Package 'spatstat.linnet'

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Title Linear Networks Functionality of the 'spatstat' Family

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Imports Matrix, spatstat.utils (>= 3.2-4), spatstat.sparse (>= 3.2-0)

Suggests goftest, locfit, spatstat (>= 3.6)

Description Defines types of spatial data on a linear network and provides functionality for geometrical operations, data analysis and modelling of data on a linear network, in the 'spatstat' family of packages.

Contains definitions and support for linear networks, including creation of networks, geometrical measurements, topological connectivity, geometrical operations such as inserting and deleting vertices, intersecting a network with another object, and interactive editing of networks.

Data types defined on a network include point patterns, pixel images, functions, and tessellations.

Exploratory methods include kernel estimation of intensity on a network, K-functions and pair correlation functions on a network, simulation envelopes, nearest neighbour distance and empty space distance, relative risk estimation with cross-validated bandwidth selection. Formal hypothesis tests of random pattern (chi-squared, Kolmogorov-Smirnov, Monte Carlo, Diggle-Cressie-Loosmore-Ford, Dao-Genton, two-stage Monte Carlo) and tests for covariate effects (Cox-Berman-Waller-Lawson, Kolmogorov-Smirnov, ANOVA) are also supported.

Parametric models can be fitted to point pattern data using the function lppm() similar to glm(). Only Poisson models are implemented so far. Models may involve dependence on covariates and dependence on marks. Models are fitted by maximum likelihood. Fitted point process models can be simulated, automatically. Formal hypothesis tests of a fitted model are supported (likelihood ratio test, analysis of deviance, Monte Carlo tests) along with basic tools for model selection (stepwise(), AIC()) and variable selection (sdr). Tools for validating the fitted model include simulation envelopes, residuals, residual plots and Q-Q plots, leverage and influence diagnostics, partial residuals, and added variable plots.

Random point patterns on a network can be generated using a variety of models.

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URL http://spatstat.org/

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`spatstat.linnet-package` *The spatstat.linnet Package*

Description

The **spatstat.linnet** package belongs to the **spatstat** family of packages. It contains the functionality for analysing spatial data on a linear network.

Details

spatstat is a family of R packages for the statistical analysis of spatial data. Its main focus is the analysis of spatial patterns of points in two-dimensional space.

The original **spatstat** package has now been split into several sub-packages.

This sub-package **spatstat.linnet** contains the user-level functions from **spatstat** that are concerned with spatial data on a linear network.

Structure of the spatstat family

The orginal **spatstat** package grew to be very large. It has now been divided into several **sub-packages**:

- **spatstat.utils** containing basic utilities
- **spatstat.sparse** containing linear algebra utilities
- **spatstat.data** containing datasets
- **spatstat.univar** containing functions for estimating probability distributions of random variables
- **spatstat.geom** containing geometrical objects and geometrical operations
- **spatstat.explore** containing the main functionality for exploratory and non-parametric analysis of spatial data
- **spatstat.model** containing the main functionality for statistical modelling and inference for spatial data
- **spatstat.linnet** containing functions for spatial data on a linear network
- **spatstat**, which simply loads the other sub-packages listed above, and provides documentation.

When you install **spatstat**, these sub-packages are also installed. Then if you load the **spatstat** package by typing `library(spatstat)`, the other sub-packages listed above will automatically be loaded or imported. For an overview of all the functions available in these sub-packages, see the help file for **spatstat** in the **spatstat** package,

Additionally there are several **extension packages:**

- **spatstat.gui** for interactive graphics
- **spatstat.local** for local likelihood (including geographically weighted regression)

- **spatstat.Knet** for additional, computationally efficient code for linear networks
- **spatstat.sphere** (under development) for spatial data on a sphere, including spatial data on the earth's surface

The extension packages must be installed separately and loaded explicitly if needed. They also have separate documentation.

Overview of spatstat.linnet

A linear network is a subset of the two-dimensional plane composed of straight line segments. It could represent a road network, for example. Our code requires that, if two segments intersect each other, then the intersection is a single point, and the intersection point is treated as a vertex of the network.

The **spatstat.linnet** package supports spatial data analysis on a linear network. The primary aim is to analyse spatial patterns of points on a network. The points could represent road accidents on a road network, for example.

The **spatstat.linnet** package provides code for handling

- `linear networks`
- `point patterns on a linear network`
- `pixel images on a linear network` (where the network is divided into small segments and a numerical value is assigned to each segment)
- `functions on a linear network` (i.e. functions that are defined at every location along the network)
- `tessellations of a linear network` (where the network is subdivided into disjoint subsets with different labels)
- `point process models on a linear network`

Here is a list of the main functionality provided in **spatstat.linnet**.

Linear networks

An object of class `"linnet"` represents a linear network. Examples of such objects include the dataset `simplenet` provided in the package.

Linear network objects can be created by the following functions:

`linnet`	create a linear network
`as.linnet`	convert other data to a network
`delaunayNetwork`	network of Delaunay triangulation
`dirichletNetwork`	network of Dirichlet edges

Utilities for manipulating networks include:

`[.linnet`	extract subset of linear network
`clickjoin`	interactively join vertices in network
`joinVertices`	join existing vertices in a network
`insertVertices`	insert new vertices at positions along network

addVertices	add new vertices, extending a network
thinNetwork	remove vertices or lines from a network
repairNetwork	repair internal format
vertices.linnet	extract the vertices of network
terminalvertices	find terminal vertices of network
affine.linnet	apply affine transformation
shift.linnet	apply vector translation
rotate.linnet	apply rotation
rescale.linnet	rescale the unit of length
scalardilate.linnet	physically rescale the network
diameter.linnet	diameter of linear network
is.connected.linnet	determine whether network is connected
lineardisc	compute disc of given radius in network
marks.linnet	extract marks of a network
marks<-.linnet	assign marks to a network
plot.linnet	plot a network
as.owin.linnet	extract window containing network
as.psp.linnet	extract line segments comprising network
nsegments.linnet	number of segments in network
nvertices.linnet	number of vertices in network
pixellate.linnet	convert network to 2D pixel image
print.linnet	print basic information
summary.linnet	print summary information
unitname.linnet	extract name of unit of length
unitname<-.linnet	assign name of unit of length
vertexdegree	number of segments meeting each vertex
volume.linnet	total length of network
Window.linnet	extract window containing network
density.linnet	smoothed 2D spatial density of lines

A network is called a tree if it has no closed loops. The following functions support the creation and manipulation of trees:

begins	check start of character string
branchlabelfun	tree branch membership labelling function
deletebranch	delete a branch of a tree
extractbranch	extract a branch of a tree
treebranchlabels	label vertices of a tree by branch membership
treeprune	prune tree to given level

Point patterns on a linear network

An object of class "lpp" represents a point pattern on a linear network (for example, road accidents on a road network).

Examples of such objects include the following datasets provided in the **spatstat.data** package:

chicago	Chicago crime data
dendrite	Dendritic spines data
spiders	Spider webs on mortar lines of brick wall

There is also a dataset provided in the extension package **spatstat.Knet**:

wacrashes	Road accidents in Western Australia

Point patterns on a network can be created by the following functions:

lpp	create a point pattern on a linear network
as.lpp	convert other data to point pattern on network
clicklpp	interactively add points on a linear Network
crossing.linnet	crossing points between network and other lines

Point patterns on a network can be generated randomly using the following functions:

rpoislpp	Poisson points on linear network
runiflpp	uniform random points on a linear network
rlpp	random points on a linear network
rSwitzerlpp	simulate Switzer-type point process on linear network
rThomaslpp	simulate Thomas process on linear network
rcelllpp	simulate cell process on linear network
rjitter.lpp	randomly perturb a point pattern on a network

Functions for manipulating a point pattern on a network include the following. An object of class "lpp" also belongs to the class "ppx", for which additional support is available.

as.ppp.lpp	convert to 2D point pattern
as.psp.lpp	extract line segments
marks.ppx	extract marks associated with points
marks<-.ppx	assign marks to points on network
nsegments.lpp	count number of segments
print.lpp	print basic information
summary.lpp	print summary information
unitname.lpp	extract name of unit of length
unitname<-.lpp	assign name of unit of length
unmark.lpp	remove marks
subset.lpp	subset of points satisfying a condition
[.lpp	extract subset of point pattern
Window.lpp	extract window containing network
as.owin.lpp	extract window containing network
affine.lpp	apply affine transformation
shift.lpp	apply vector translation
rotate.lpp	apply rotation
rescale.lpp	rescale the unit of length

scalardilate.lpp	physically rescale the network and points
connected.lpp	find connected components of point pattern on network
cut.lpp	classify points in a Point Pattern on a Network
distfun.lpp	distance map (function)
distmap.lpp	distance map (image)
domain.lpp	extract the linear network
identify.lpp	interactively identify points
is.multitype.lpp	recognize whether point pattern is multitype
nncross.lpp	nearest neighbours
nndist.lpp	nearest neighbour distances
nnfromvertex	nearest data point from each vertex
nnfun.lpp	nearest neighbour map
nnwhich.lpp	identify nearest neighbours
pairdist.lpp	pairwise shortest-path distances
plot.lpp	plot point pattern on linear Network
points.lpp	draw points on existing plot
superimpose.lpp	superimpose several point patterns
text.lpp	add text labels
unstack.lpp	separate multiple columns of marks

Pixel images on a network

An object of class "linim" represents a pixel image on a linear network. Effectively, the network is divided into small segments (lixels) and each small segment is assigned a value, which could be numeric, factor, logical or complex values.

Pixel images on a network can be created using the following functions:

linim	create pixel image on linear network
as.linim	convert other data to pixel image on network

Functions for manipulating a pixel image on a network include:

[.linim	extract subset of pixel image on linear network
[<-.linim	reset values in subset of image on linear network
Math.linim	S3 group generic methods for images on a linear network
eval.linim	evaluate expression involving pixel images on linear network
as.linnet.linim	extract linear network
integral.linim	integral of pixel image on a linear network
mean.linim	mean of pixel values
median.linim	median of pixel values
quantile.linim	quantiles of pixel values
as.data.frame.linim	convert to data frame
print.linim	print basic information
summary.linim	print summary information
affine.linim	apply affine transformation
scalardilate.linim	apply scalar dilation

shift.linim	apply vector translation
pairs.linim	scatterplot matrix for images
persp.linim	perspective view of pixel image on network
plot.linim	plot pixel image on linear network

Functions on a linear network

An object of class "linfun" represents a function defined at any location along the network. Objects of this class are created by the following functions:

linfun	create function on a linear network
as.linfun	convert other data to function on network

The following supporting code is available:

print.linfun	print basic information
summary.linfun	print summary information
plot.linfun	plot function on network
persp.linfun	perspective view of function on network
as.data.frame.linfun	convert to data frame
as.owin.linfun	extract window containing network
as.function.linfun	convert to ordinary R function

Tessellations of a linear network

An object of class "lintess" represents a tessellation of the network, that is, a subdivision of the network into disjoint subsets called 'tiles'. Objects of this class are created by the following functions:

lintess	create tessellation of network
chop.linnet	divide a linear network into tiles using infinite lines
divide.linnet	divide linear network at cut points
lineardirichlet	Dirichlet tessellation on a linear network

The following functions are provided for manipulating a tessellation on a network:

as.data.frame.lintess	convert to data frame
intersect.lintess	intersection of two tessellations on network
lineartileindex	determine which tile contains each given point on network
marks.lintess	extract marks of each tile
marks<-.lintess	assign marks to each tile
plot.lintess	plot tessellation on network
tile.lengths	compute lengths of tiles
tilenames.lintess	names of tiles

as.linfun.lintess	convert tessellation to a function

Smoothing a point pattern on a linear network:

Given a point pattern dataset on a linear network, it is often desired to estimate the spatially-varying density or intensity of points along the network. For example if the points represent road accidents, then we may wish to estimate the spatially-varying density of accidents per unit length (over a given period of time).

Related tasks include estimation of relative risk, and smoothing of of values observed at the data points.

density.lpp	kernel estimate of intensity
densityEqualSplit	kernel estimate of intensity using equal-split algorithm
densityHeat.lpp	kernel estimate of intensity using heat equation
densityQuick.lpp	kernel estimate of intensity using a 2D kernel
densityVoronoi.lpp	intensity estimate using Voronoi-Dirichlet Tessellation
densityfun.lpp	kernel estimate of intensity as a function
bw.lppl	Bandwidth selection for kernel estimate of intensity
bw.voronoi	bandwidth selection for Voronoi estimator
relrisk.lpp	kernel estimate of relative risk
bw.relrisk.lpp	Bandwidth selection for relative risk
Smooth.lpp	spatial smoothing of observations at points

Exploration of dependence on a covariate:

Another task is to investigate how the spatially-varying intensity of points depends on an explanatory variable (covariate). The covariate may be given as a pixel image on the network (class "linim") or as a function on the network (class "linfun").

rhohat.lpp	nonparametric estimate of intensity as function of a covariate
roc.lpp	Receiver Operating Characteristic for data on a network
auc.lpp	Area Under ROC Curve for data on a network
cdf.test.lpp	spatial distribution test for points on a linear network
berman.test.lpp	Berman's tests for point pattern on a network
sdr.lpp	Sufficient Dimension Reduction for a point pattern on a linear network

Summary statistics for a point pattern on a linear network:

These are for point patterns on a linear network (class lpp). For unmarked patterns:

linearK	K function on linear network
linearKinhom	inhomogeneous K function on linear network
linearpcf	pair correlation function on linear network
linearpcfinhom	inhomogeneous pair correlation on linear network
linearJinhom	inhomogeneous J function on linear network
linearKEuclid	K function on linear network using Euclidean distance

linearKEuclidInhom	inhomogeneous K function on linear network using Euclidean distance
linearpcfEuclid	pair correlation function on linear network using Euclidean distance
linearpcfEuclidInhom	inhomogeneous pair correlation on linear network using Euclidean distance

For multitype patterns:

linearKcross	K function between two types of points
linearKdot	K function from one type to any type
linearKcross.inhom	Inhomogeneous version of linearKcross
linearKdot.inhom	Inhomogeneous version of linearKdot
linearmarkconnect	Mark connection function on linear network
linearmarkequal	Mark equality function on linear network
linearpcfcross	Pair correlation between two types of points
linearpcfdot	Pair correlation from one type to any type
linearpcfcross.inhom	Inhomogeneous version of linearpcfcross
linearpcfdot.inhom	Inhomogeneous version of linearpcfdot

Related facilities:

pairdist.lpp	distances between pairs
crossdist.lpp	distances between pairs
nndist.lpp	nearest neighbour distances
nncross.lpp	nearest neighbour distances
nnwhich.lpp	find nearest neighbours
nnfun.lpp	find nearest data point
density.lpp	kernel smoothing estimator of intensity
distfun.lpp	distance transform
envelope.lpp	simulation envelopes
rpoislpp	simulate Poisson points on linear network
runiflpp	simulate random points on a linear network

It is also possible to fit point process models to lpp objects.

Point process models on a linear network:

An object of class "lpp" represents a pattern of points on a linear network. Point process models can also be fitted to these objects. Currently only Poisson models can be fitted.

lppm	point process model on linear network
anova.lppm	analysis of deviance for point process model on linear network
envelope.lppm	simulation envelopes for point process model on linear network
fitted.lppm	fitted intensity values
predict.lppm	model prediction on linear network
data.lppm	extract original data
berman.test.lppm	Berman's tests of goodness-of-fit
is.marked.lppm	Recognise whether model is marked

is.multitype.lppm	Recognise whether model is multitype
is.stationary.lppm	Recognise whether model is stationary
model.frame.lppm	Extract the variables in model
model.images.lppm	Compute images of constructed covariates
model.matrix.lppm	Extract design matrix
plot.lppm	Plot fitted point process model
pseudoR2.lppm	Calculate Pseudo-R-Squared for model
simulate.lppm	simulate fitted point process model

Licence

This library and its documentation are usable under the terms of the "GNU General Public License", a copy of which is distributed with the package.

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---

addVertices *Add New Vertices to a Linear Network*

Description

Adds new vertices to a linear network at specified locations outside the network.

Usage

```
addVertices(L, X, join=NULL, joinmarks=NULL)
```

Arguments

L	Existing linear network (object of class "linnet") or point pattern on a linear network (object of class "lpp").
X	Point pattern (object of class "ppp") specifying the new vertices.
join	Optional information specifying how to join the new vertices X to the existing network. See Details. If join=NULL (the default), the new vertices are simply added to the list of network vertices without being joined to the rest of the network.
joinmarks	Optional vector or data frame of marks associated with the new edges specified by join.

Details

This function adds new vertices to an existing linear network L, at specified locations X outside the network.

The argument L can be either a linear network (class "linnet") or some other object that includes a linear network.

The new vertex locations are points outside the network, specified as a point pattern X (object of class "ppp").

The argument join specifies how to join the new vertices to the existing network.

- If join=NULL (the default), the new vertices are simply added to the list of network vertices without being joined to the rest of the network.
- If join is a vector of integers, then these are taken to be indices of existing vertices of L in the order given in V = vertices(L). Then each new vertex X[i] will be joined to an existing vertex V[j] where j = join[i]. Each new vertex is joined to exactly one existing vertex.
- If join="vertices" then each new vertex X[i] is joined to the nearest existing vertex V[j]. Each new vertex is joined to exactly one existing vertex.
- If join="nearest" then each new vertex is projected to the nearest location along on the network; these locations are inserted as new vertices of L; and then each vertex X[i] is joined to the corresponding projected point. Each new vertex is joined to exactly one newly-inserted vertex.
- If join is a point pattern on a network (class "lpp"), it must be defined on the same network as L and it must consist of the same number of points as X. The points of join will be inserted as new vertices of L, and then each vertex X[i] is joined to the corresponding point join[i]. Each new vertex is joined to exactly one newly-inserted vertex.

The result is the modified object, with an attribute "id" such that the ith added vertex has become the id[i]th vertex of the new network.

Value

An object of the same class as L representing the result of adding the new vertices. The result also has an attribute "id" as described in Details.

Author(s)

Adrian Baddeley

See Also

insertVertices to insert vertices along an existing network.

as.lpp, linnet, methods.linnet, joinVertices, thinNetwork.

Examples

```
opa <- par(mfrow=c(1,3))
L <- simplenet
X <- runifpoint(20, Window(simplenet))
```

```
plot(L)
plot(X, add=TRUE, cols="green", pch=16, cex=2)
plot(addVertices(L, X, "nearest"), col="red")
plot(L, add=TRUE, col="grey", lwd=3)
plot(X, add=TRUE, cols="green", pch=16, cex=2)
plot(addVertices(L, X, "vertices"), col="red")
plot(L, add=TRUE, col="grey", lwd=3)
plot(X, add=TRUE, cols="green", pch=16, cex=2)
par(opa)
```

`affine.linnet` *Apply Geometrical Transformations to a Linear Network*

Description

Apply geometrical transformations to a linear network.

Usage

```
  ## S3 method for class 'linnet'
affine(X, mat=diag(c(1,1)), vec=c(0,0), ...)

  ## S3 method for class 'linnet'
flipxy(X)

  ## S3 method for class 'linnet'
shift(X, vec=c(0,0), ..., origin=NULL)

  ## S3 method for class 'linnet'
rotate(X, angle=pi/2, ..., centre=NULL)

  ## S3 method for class 'linnet'
scalardilate(X, f, ...)

  ## S3 method for class 'linnet'
rescale(X, s, unitname)
```

Arguments

`X`	Linear network (object of class `"linnet"`).
`mat`	Matrix representing a linear transformation.
`vec`	Vector of length 2 representing a translation.
`angle`	Rotation angle in radians.
`f`	Scalar dilation factor.
`s`	Unit conversion factor: the new units are `s` times the old units.
`...`	Arguments passed to other methods.

origin	Character string determining a location that will be shifted to the origin. Options are "centroid", "midpoint" and "bottomleft". Partially matched.
centre	Centre of rotation. Either a vector of length 2, or a character string (partially matched to "centroid", "midpoint" or "bottomleft"). The default is the coordinate origin c(0,0).
unitname	Optional. New name for the unit of length. A value acceptable to the function unitname<-

Details

These functions are methods for the generic functions affine, flipxy, shift, rotate, rescale and scalardilate applicable to objects of class "linnet".

All of these functions perform geometrical transformations on the object X, except for rescale, which simply rescales the units of length.

Value

Another linear network (of class "linnet") representing the result of applying the geometrical transformation.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

and Rolf Turner <rolfturner@posteo.net>

See Also

linnet and as.linnet.

Generic functions affine, flipxy, shift, rotate, scalardilate, rescale.

Examples

```
U <- rotate(simplenet, pi)
stretch <- diag(c(2,3))
Y <- affine(simplenet, mat=stretch)
shear <- matrix(c(1,0,0.6,1),ncol=2, nrow=2)
Z <- affine(simplenet, mat=shear, vec=c(0, 1))
```

---

affine.lpp *Apply Geometrical Transformations to Point Pattern on a Linear Network*

Description

Apply geometrical transformations to a point pattern on a linear network.

Usage

```
  ## S3 method for class 'lpp'
affine(X, mat=diag(c(1,1)), vec=c(0,0), ...)

  ## S3 method for class 'lpp'
flipxy(X)

  ## S3 method for class 'lpp'
shift(X, vec=c(0,0), ..., origin=NULL)

  ## S3 method for class 'lpp'
rotate(X, angle=pi/2, ..., centre=NULL)

  ## S3 method for class 'lpp'
scalardilate(X, f, ...)

  ## S3 method for class 'lpp'
rescale(X, s, unitname)
```

Arguments

X	Point pattern on a linear network (object of class "lpp").
mat	Matrix representing a linear transformation.
vec	Vector of length 2 representing a translation.
angle	Rotation angle in radians.
f	Scalar dilation factor.
s	Unit conversion factor: the new units are s times the old units.
...	Arguments passed to other methods.
origin	Character string determining a location that will be shifted to the origin. Options are "centroid", "midpoint" and "bottomleft". Partially matched.
centre	Centre of rotation. Either a vector of length 2, or a character string (partially matched to "centroid", "midpoint" or "bottomleft"). The default is the coordinate origin c(0,0).
unitname	Optional. New name for the unit of length. A value acceptable to the function unitname<-

Details

These functions are methods for the generic functions affine, flipxy, shift, rotate, rescale and scalardilate applicable to objects of class "lpp".

All of these functions perform geometrical transformations on the object X, except for rescale, which simply rescales the units of length.

Value

Another point pattern on a linear network (object of class "lpp") representing the result of applying the geometrical transformation.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Rolf Turner <rolfturner@posteo.net>

See Also

lpp.

Generic functions affine, flipxy, shift, rotate, scalardilate, rescale.

Examples

```
X <- rpoislpp(2, simplenet)
U <- rotate(X, pi)
V <- shift(X, c(0.1, 0.2))
stretch <- diag(c(2,3))
Y <- affine(X, mat=stretch)
shear <- matrix(c(1,0,0.6,1),ncol=2, nrow=2)
Z <- affine(X, mat=shear, vec=c(0, 1))
```

---

anova.lppm *ANOVA for Fitted Point Process Models on Linear Network*

Description

Performs analysis of deviance for two or more fitted point process models on a linear network.

Usage

```
  ## S3 method for class 'lppm'
anova(object, ..., test=NULL)
```

Arguments

object	A fitted point process model on a linear network (object of class "lppm").
...	One or more fitted point process models on the same linear network.
test	Character string, partially matching one of "Chisq", "F" or "Cp".

Details

This is a method for anova for fitted point process models on a linear network (objects of class "lppm", usually generated by the model-fitting function lppm).

If the fitted models are all Poisson point processes, then this function performs an Analysis of Deviance of the fitted models. The output shows the deviance differences (i.e. 2 times log likelihood ratio), the difference in degrees of freedom, and (if test="Chi") the two-sided p-values for the chi-squared tests. Their interpretation is very similar to that in anova.glm.

If some of the fitted models are *not* Poisson point processes, then the deviance difference is replaced by the adjusted composite likelihood ratio (Pace et al, 2011; Baddeley et al, 2014).

Value

An object of class "anova", or NULL.

Errors and warnings

models not nested: There may be an error message that the models are not "nested". For an Analysis of Deviance the models must be nested, i.e. one model must be a special case of the other. For example the point process model with formula ~x is a special case of the model with formula ~x+y, so these models are nested. However the two point process models with formulae ~x and ~y are not nested.

If you get this error message and you believe that the models should be nested, the problem may be the inability of R to recognise that the two formulae are nested. Try modifying the formulae to make their relationship more obvious.

different sizes of dataset: There may be an error message from anova.glmlist that "models were not all fitted to the same size of dataset". This generally occurs when the point process models are fitted on different linear networks.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

References

Ang, Q.W. (2010) *Statistical methodology for events on a network*. Master's thesis, School of Mathematics and Statistics, University of Western Australia.

Ang, Q.W., Baddeley, A. and Nair, G. (2012) Geometrically corrected second-order analysis of events on a linear network, with applications to ecology and criminology. *Scandinavian Journal of Statistics* **39**, 591–617.

Baddeley, A., Turner, R. and Rubak, E. (2015) Adjusted composite likelihood ratio test for Gibbs point processes. *Journal of Statistical Computation and Simulation* **86** (5) 922–941. DOI: 10.1080/00949655.2015.1044530.

McSwiggan, G., Nair, M.G. and Baddeley, A. (2012) Fitting Poisson point process models to events on a linear network. Manuscript in preparation.

Pace, L., Salvan, A. and Sartori, N. (2011) Adjusting composite likelihood ratio statistics. *Statistica Sinica* **21**, 129–148.

See Also

lppm

Examples

```
X <- runiflpp(10, simplenet)
mod0 <- lppm(X ~1)
modx <- lppm(X ~x)
anova(mod0, modx, test="Chi")
```

`as.data.frame.lintess` *Convert Network Tessellation to Data Frame*

Description

Converts a tessellation on a linear network into a data frame.

Usage

```
## S3 method for class 'lintess'
as.data.frame(x, ...)
```

Arguments

`x`	Tessellation on a linear network (object of class `"lintess"`).
`...`	Further arguments passed to `as.data.frame.default` to determine the row names and other features.

Details

A tessellation on a linear network is a partition of the network into non-overlapping pieces (tiles). Each tile consists of one or more line segments which are subsets of the line segments making up the network. A tile can consist of several disjoint pieces.

This function converts the tessellation `x` to a data frame. Each row of the data frame specifies one sub-segment of the network, and allocates it to a particular tile. The data frame has the following columns:

- The `seg` column specifies which line segment of the network contains the sub-segment. Values of `seg` are integer indices for the network segments in `as.psp(as.linnet(x))`.
- The `t0` and `t1` columns specify the start and end points of the sub-segment. They are numeric values between 0 and 1 inclusive, where the values 0 and 1 representing the network vertices that are joined by this network segment.
- The `tile` column specifies which tile of the tessellation includes this sub-segment. It is a factor whose levels are the names of the tiles.

The tessellation may have marks, which are attached to the *tiles* of the tessellation. If marks are present, the resulting data frame includes columns containing, for each sub-segment, the mark value of the corresponding tile.

Value

A data frame with columns named `seg`, `t0`, `t1`, `tile`, and possibly other columns.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

lintess

Examples

```
X <- lineardirichlet(runiflpp(3, simplenet))
marks(X) <- letters[1:3]
as.data.frame(X)
```

---

as.linfun *Convert Data to a Function on a Linear Network*

Description

Convert some kind of data to an object of class "linfun" representing a function on a linear network.

Usage

```
as.linfun(X, ...)

## S3 method for class 'linim'
as.linfun(X, ...)

## S3 method for class 'linnet'
as.linfun(X, ..., values=marks(X))

## S3 method for class 'lintess'
as.linfun(X, ..., values=marks(X), navalue=NA)

## S3 method for class 'linim'
as.function(x, ...)

## S3 method for class 'linnet'
as.function(x, ...)

## S3 method for class 'lintess'
as.function(x, ...)
```

Arguments

X, x	Some kind of data to be converted.
...	Other arguments passed to methods.
values	Optional. Vector of function values, one entry associated with each tile of the tessellation.
navalue	Optional. Function value associated with locations that do not belong to a tile of the tessellation.

Details

An object of class "linfun" represents a function defined on a linear network. This page documents methods for converting other kinds of objects to a "linfun" object.

The function as.linfun is generic. There are methods for converting linear networks (class "linnet"), pixel images on a linear network (class "linnet") and tessellations on a linear network (class "lintess") to functions on a network. Equivalent methods are also provided for the generic as.function.

The methods as.linfun.linim and as.function.linim convert objects of class "linim" (pixel images on a linear network) to functions on the network.

The methods as.linfun.linnet and as.function.linnet converts a linear network (object of class "linnet") to a function on the network. The function values are specified by the argument values. It should be a vector with one entry for each segment of the network; any point lying on segment number i will return the value values[i]. If values is missing or NULL, the function values are taken to be the marks attached to the segments (values=marks(X)); if there are no marks attached to the segments, the function value is the integer index of the segment (values=seq_len(nsegments(X))).

The methods as.linfun.lintess and as.function.lintess convert a tessellation on a linear network into a function with a different value on each tile of the tessellation. The function values are specified by the argument values. It should be a vector with one entry for each tile of the tessellation; any point lying in tile number i will return the value values[i]. If values is missing, the marks of the tessellation are taken as the function values. If values is missing and the tessellation has no marks, or if values is given as NULL, then the function returns factor values identifying which tile contains each given point.

Value

Object of class "linfun".

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

linfun

Examples

```
X <- runiflpp(2, simplenet)
Y <- runiflpp(5, simplenet)

# image on network
D <- density(Y, 0.1)

f <- as.linfun(D)
f
f(X)
```

```
h <- as.linfun(simplenet)

# tessellation on network
Z <- lineardirichlet(Y)
g <- as.linfun(Z)
g(X)
h <- as.linfun(Z, values = runif(5))
h(X)
```

---

as.linim *Convert to Pixel Image on Linear Network*

Description

Converts various kinds of data to a pixel image on a linear network.

Usage

```
  as.linim(X, ...)

  ## S3 method for class 'linim'
as.linim(X, ...)

  ## S3 method for class 'linfun'
as.linim(X, L=domain(X), ...,
                           eps = NULL, dimyx = NULL, xy = NULL,
                           rule.eps=c("adjust.eps",
                                      "grow.frame", "shrink.frame"),
                           delta=NULL, nd=NULL)

  ## S3 method for class 'function'
as.linim(X, L, ...,
                            eps = NULL, dimyx = NULL, xy = NULL,
                            rule.eps=c("adjust.eps",
                                       "grow.frame", "shrink.frame"),
                            delta=NULL, nd=NULL)

  ## Default S3 method:
as.linim(X, L, ...,
                           eps = NULL, dimyx = NULL, xy = NULL,
                           rule.eps=c("adjust.eps",
                                      "grow.frame", "shrink.frame"),
                           delta=NULL, nd=NULL)
```

Arguments

X	Data to be converted to a pixel image on a linear network.
L	Linear network (object of class "linnet"). Alternatively a pixel image on a network (class "linim") to be used as a template.
...	Additional arguments passed to X when X is a function.
eps, dimyx, xy, rule.eps	Optional arguments passed to as.mask to control the pixel resolution.
delta	Optional. Numeric value giving the approximate distance (in coordinate units) between successive sample points along each segment of the network, when L is a network.
nd	Optional. Integer giving the (approximate) number of sample points on the network, when L is a network. Ignored if delta is given.

Details

This function converts the data X into a pixel image on a linear network, an object of class "linim" (see linim).

The argument X may be any of the following:

- a function on a linear network, an object of class "linfun".
- a pixel image on a linear network, an object of class "linim".
- a pixel image, an object of class "im".
- a function(x,y) in the R language.
- any type of data acceptable to as.im, such as a function, numeric value, or window.

First X is converted to a pixel image object Y (object of class "im"). The conversion is performed by as.im. The arguments eps, dimyx, xy and rule.eps determine the pixel resolution.

Next Y is converted to a pixel image on a linear network using linim. The argument L determines the linear network. If L is missing or NULL, then X should be an object of class "linim", and L defaults to the linear network on which X is defined.

In addition to converting the function to a pixel image, the algorithm also generates a fine grid of sample points evenly spaced along each segment of the network. The function values at these sample points are stored in the resulting object as a data frame (the argument df of linim). This mechanism allows greater accuracy for some calculations (such as integral.linim). If L is a "linim" object, then it is used as a template; the sample points are determined by the sample points in L. Otherwise, L is treated as a network (class "linnet"), and new sample points are constructed by placing them evenly-spaced along each segment of the network with separation delta.

Value

An image object on a linear network; an object of class "linim".

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>

See Also

as.im

Examples

```
f <- function(x,y){ x + y }
plot(as.linim(f, simplenet))
```

---

as.linnet.linim *Extract Linear Network from Data on a Linear Network*

Description

Given some kind of data on a linear network, the command as.linnet extracts the linear network itself.

Usage

```
 ## S3 method for class 'linim'
as.linnet(X, ...)

 ## S3 method for class 'linfun'
as.linnet(X, ...)

 ## S3 method for class 'lintess'
as.linnet(X, ...)

 ## S3 method for class 'lpp'
as.linnet(X, ..., fatal=TRUE, sparse)
```

Arguments

X	Data on a linear network. A point pattern (class "lpp"), pixel image (class "linim"), function (class "linfun") or tessellation (class "lintess") on a linear network.
...	Ignored.
fatal	Logical value indicating whether data in the wrong format should lead to an error (fatal=TRUE) or a warning (fatal=FALSE).
sparse	Logical value indicating whether to use a sparse matrix representation, as explained in linnet. Default is to keep the same representation as in X.

Details

These are methods for the generic as.linnet for various classes.

The network on which the data are defined is extracted.

Value

A linear network (object of class "linnet").

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

linnet, methods.linnet.

Examples

```
# make some data
xcoord <- linfun(function(x,y,seg,tp) { x }, simplenet)
as.linnet(xcoord)
X <- as.linim(xcoord)
as.linnet(X)
```

---

as.linnet.psp *Convert Line Segment Pattern to Linear Network*

Description

Converts a line segment pattern to a linear network.

Usage

```
 ## S3 method for class 'psp'
as.linnet(X, ..., eps, sparse=FALSE, chop=TRUE, fuse=TRUE)
```

Arguments

X	Line segment pattern (object of class "psp").
...	Ignored.
eps	Optional. Distance threshold. If two segment endpoints are closer than eps units apart, they will be treated as the same point, and will become a single vertex in the linear network. Ignored if fuse=FALSE.
sparse	Logical value indicating whether to use a sparse matrix representation, as explained in linnet.
chop	Logical value specifying whether segments which cross each other should be subdivided into separate segments of the network which meet at the intersection point.
fuse	Logical value specifying whether two vertices lyin closer than eps should be treated as a single vertex.

Details

This command converts any collection of line segments into a linear network by guessing the connectivity of the network.

If chop=TRUE (the default), then if any segments in X cross over each other, they are first cut into pieces using selfcut.psp.

If fuse=TRUE (the default), then any pair of segment endpoints lying closer than eps units apart, is treated as a single vertex.

After these modifications, the linear network is constructed using linnet.

If chop=FALSE and fuse=FALSE, each segment in the segment pattern X becomes an edge in the resulting network, and no other edges or vertices are created.

It would be wise to check the result by plotting the degree of each vertex, as shown in the Examples.

If X has marks, then these are stored in the resulting linear network Y <- as.linnet(X), and can be extracted as marks(as.psp(Y)) or marks(Y$lines).

Value

A linear network (object of class "linnet").

The result also has an attribute "camefrom" indicating the provenance of each line in the resulting network. For example camefrom[3]=2 means that the third line segment in the result is a piece of the second segment of X.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

linnet, selfcut.psp, methods.linnet.

Examples

```
# make some data
A <- psp(0.09, 0.55, 0.79, 0.80, window=owin())
B <- superimpose(A, as.psp(simplenet))

# convert to a linear network
L <- as.linnet(B)

# check validity
L
plot(L)
text(vertices(L), labels=vertexdegree(L))

# show the pieces that came from original segment number 1
S <- as.psp(L)
(camefrom <- attr(L, "camefrom"))
parts <- which(camefrom == 1)
```

```
plot(S[parts], add=TRUE, col="green", lwd=2)

# convert to a network without changing the geometry
H <- as.linnet(B, chop=FALSE, fuse=FALSE)
```

`as.lpp` *Convert Data to a Point Pattern on a Linear Network*

Description

Convert various kinds of data to a point pattern on a linear network.

Usage

```
as.lpp(x=NULL, y=NULL, seg=NULL, tp=NULL, ...,
       marks=NULL, L=NULL, check=FALSE, sparse)
```

Arguments

`x, y`	Vectors of cartesian coordinates, or any data acceptable to `xy.coords`. Alternatively `x` can be a point pattern on a linear network (object of class `"lpp"`) or a planar point pattern (object of class `"ppp"`).
`seg, tp`	Optional local coordinates. Vectors of the same length as `x,y`. See Details.
`...`	Ignored.
`marks`	Optional marks for the point pattern. A vector or factor with one entry for each point, or a data frame or hyperframe with one row for each point.
`L`	Linear network (object of class `"linnet"`) on which the points lie.
`check`	Logical. Whether to check the validity of the spatial coordinates.
`sparse`	Optional logical value indicating whether to store the linear network data in a sparse matrix representation or not. See `linnet`.

Details

This function converts data in various formats into a point pattern on a linear network (object of class `"lpp"`).

The possible formats are:

- `x` is already a point pattern on a linear network (object of class `"lpp"`). Then `x` is returned unchanged.
- `x` is a planar point pattern (object of class `"ppp"`). Then `x` is converted to a point pattern on the linear network `L` using `lpp`.
- `x,y,seg,tp` are vectors of equal length. These specify that the `i`th point has Cartesian coordinates `(x[i],y[i])`, and lies on segment number `seg[i]` of the network `L`, at a fractional position `tp[i]` along that segment (with `tp=0` representing one endpoint and `tp=1` the other endpoint of the segment).

- x,y are missing and seg,tp are vectors of equal length as described above.
- seg,tp are NULL, and x,y are data in a format acceptable to xy.coords specifying the Cartesian coordinates.
- Only the arguments x and L are given, and x is a data frame with one of the following types:
  - two columns labelled seg,tp interpreted as local coordinates on the network.
  - two columns labelled x,y interpreted as Cartesian coordinates.
  - four columns labelled x,y,seg,tp interpreted as Cartesian coordinates and local coordinates.

Value

A point pattern on a linear network (object of class "lpp").

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

and Rolf Turner <rolfturner@posteo.net>

See Also

lpp.

Examples

```
A <- as.psp(simplenet)
X <- runifpointOnLines(10, A)
is.ppp(X)
Y <- as.lpp(X, L=simplenet)
```

---

as.owin.lpp *Convert Data on a Network to class owin*

Description

Converts data on a linear network into an object of class "owin".

Usage

```
 ## S3 method for class 'lpp'
as.owin(W, ..., fatal=TRUE)

 ## S3 method for class 'lppm'
as.owin(W, ..., fatal=TRUE)
```

Arguments

W	Data specifying an observation window, in any of several formats described under *Details* below.
fatal	Logical value determining what to do if the data cannot be converted to an observation window. See Details.
...	Ignored.

Details

The class "owin" is a way of specifying the observation window for a point pattern. See owin.object for an overview.

The function as.owin converts data in any of several formats into an object of class "owin" for use by the **spatstat** package. The function as.owin is generic, with methods for different classes of objects, and a default method.

A long list of methods for as.owin is documented in the help file for as.owin in the **spatstat.geom** package.

This help file documents additional methods applicable when W is

- an object of class "lpp" representing a point pattern on a linear network. In this case, as.owin extracts the linear network and returns a window containing this network.
- an object of class "lppm" representing a fitted point process model on a linear network. In this case, as.owin extracts the linear network and returns a window containing this network.

If the argument W cannot be converted to a window, then an error will be generated (if fatal=TRUE) or a value of NULL will be returned (if fatal=FALSE).

Value

An object of class "owin" (see owin.object) specifying an observation window.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

as.owin, owin.object, owin.

Additional methods for as.owin may be provided by other packages outside the **spatstat** family.

Examples

```
as.owin(simplenet)
```

auc.lpp *Area Under ROC Curve for Network Data*

Description

Compute the AUC (area under the Receiver Operating Characteristic curve) for a point pattern on a network, or a fitted point process model on a network.

Usage

```
## S3 method for class 'lpp'
auc(X, covariate, ..., high = TRUE,
                    subset=NULL)

## S3 method for class 'lppm'
auc(X, ..., subset=NULL)
```

Arguments

X	Point pattern on a network (object of class "lpp") or fitted point process model on a network (object of class "lppm").
covariate	Spatial covariate. Either a function(x,y), a pixel image (object of class "im" or "linim"), or one of the strings "x" or "y" indicating the Cartesian coordinates.
...	Arguments passed to roc, and arguments passed to as.mask controlling the pixel resolution for calculations.
high	Logical value indicating whether the threshold operation should favour high or low values of the covariate.
subset	Optional. A spatial window (object of class "owin") specifying a subset of the data, for which the AUC should be calculated.

Details

The generic auc computes the AUC, the area under the curve of the Receiver Operating Characteristic. The ROC curve itself is computed by the generic roc.

The functions auc.lpp and auc.lppm are methods for auc for point patterns on a linear network (class "lpp") and fitted point process models on a linear network (class "lppm").

For a point pattern X and a covariate Z, the AUC is a numerical index that measures the ability of the covariate to separate the spatial domain into areas of high and low density of points. Let x_i be a randomly-chosen data point from X and U a randomly-selected location in the study region. The AUC is the probability that $Z(x_i) > Z(U)$ assuming high=TRUE. That is, AUC is the probability that a randomly-selected data point has a higher value of the covariate Z than does a randomly-selected spatial location. The AUC is a number between 0 and 1. A value of 0.5 indicates a complete lack of discriminatory power.

For a fitted point process model X, the AUC measures the ability of the fitted model intensity to separate the spatial domain into areas of high and low density of points. Suppose $\lambda(u)$ is the intensity function of the model. The AUC is the probability that $\lambda(x_i) > \lambda(U)$. That is, AUC is the probability that a randomly-selected data point has higher predicted intensity than does a randomly-selected spatial location. The AUC is **not** a measure of the goodness-of-fit of the model (Lobo et al, 2007).

Value

Numeric. For auc.lpp, the result is a single number giving the AUC value.

For auc.lppm, the result is a numeric vector of length 2 giving the AUC value and the theoretically expected AUC value for this model.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Ege Rubak <rubak@math.aau.dk> and Suman Rakshit <Suman.Rakshit@curtin.edu.au>.

References

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See Also

roc.

auc, auc.ppm.

youden.

Examples

```
Crimes <- unmark(chicago)
fit <- lppm(Crimes ~ x)
auc(fit)
auc(Crimes, "x")
```

begins *Check Start of Character String*

Description

Checks whether a character string begins with a particular prefix.

Usage

```
begins(x, firstbit)
```

Arguments

x	Character string, or vector of character strings, to be tested.
firstbit	A single character string.

Details

This simple wrapper function checks whether (each entry in) x begins with the string firstbit, and returns a logical value or logical vector with one entry for each entry of x. This function is useful mainly for reducing complexity in model formulae.

Value

Logical vector of the same length as x.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

Rolf Turner <rolfturner@posteo.net>

and Ege Rubak <rubak@math.aau.dk>

Examples

```
begins(c("Hello", "Goodbye"), "Hell")
begins("anything", "")
```

berman.test.lpp *Berman's Tests for Point Process Model on a Network*

Description

Tests the goodness-of-fit of a Poisson point process model on a linear network, using the approach of Berman (1986).

Usage

```
## S3 method for class 'lpp'
berman.test(X, covariate,
                          which = c("Z1", "Z2"),
        alternative = c("two.sided", "less", "greater"), ...)

## S3 method for class 'lppm'
berman.test(model, covariate,
                          which = c("Z1", "Z2"),
               alternative = c("two.sided", "less", "greater"), ...)
```

Arguments

X	A point pattern (object of class "lpp").
model	A fitted point process model (object of class "lppm").
covariate	The spatial covariate on which the test will be based. An image (object of class "im" or "linim") or a function.
which	Character string specifying the choice of test.
alternative	Character string specifying the alternative hypothesis.
...	Additional arguments controlling the pixel resolution (arguments dimyx and eps passed to as.mask) or other undocumented features.

Details

These functions perform a goodness-of-fit test of a Poisson point process model fitted to point pattern data. The observed distribution of the values of a spatial covariate at the data points, and the predicted distribution of the same values under the model, are compared using either of two test statistics Z_1 and Z_2 proposed by Berman (1986). The Z_1 test is also known as the Lawson-Waller test.

The function berman.test is generic, with methods for point patterns ("ppp" or "lpp") and point process models ("ppm" or "lppm").

See the help file for berman.test for information on the generic function and the methods for data in two-dimensional space, classes "ppp" and "ppm".

This help file describes the methods for data on a linear network, classes "lpp" and "lppm".

- If X is a point pattern dataset (object of class "ppp" or "lpp"), then berman.test(X, ...) performs a goodness-of-fit test of the uniform Poisson point process (Complete Spatial Randomness, CSR) for this dataset.
- If model is a fitted point process model (object of class "ppm" or "lppm") then berman.test(model, ...) performs a test of goodness-of-fit for this fitted model. In this case, model should be a Poisson point process.

The test is performed by comparing the observed distribution of the values of a spatial covariate at the data points, and the predicted distribution of the same covariate under the model. Thus, you must nominate a spatial covariate for this test.

The argument covariate should be either a function(x,y) or a pixel image (object of class "im" containing the values of a spatial function. If covariate is an image, it should have numeric values, and its domain should cover the observation window of the model. If covariate is a function, it should expect two arguments x and y which are vectors of coordinates, and it should return a numeric vector of the same length as x and y.

First the original data point pattern is extracted from model. The values of the covariate at these data points are collected.

Next the values of the covariate at all locations in the observation window are evaluated. The point process intensity of the fitted model is also evaluated at all locations in the window.

- If which="Z1", the test statistic Z_1 is computed as follows. The sum S of the covariate values at all data points is evaluated. The predicted mean μ and variance σ^2 of S are computed from the values of the covariate at all locations in the window. Then we compute $Z_1 = (S - \mu)/\sigma$. Closely-related tests were proposed independently by Waller et al (1993) and Lawson (1993) so this test is often termed the Lawson-Waller test in epidemiological literature.
- If which="Z2", the test statistic Z_2 is computed as follows. The values of the covariate at all locations in the observation window, weighted by the point process intensity, are compiled into a cumulative distribution function F. The probability integral transformation is then applied: the values of the covariate at the original data points are transformed by the predicted cumulative distribution function F into numbers between 0 and 1. If the model is correct, these numbers are i.i.d. uniform random numbers. The standardised sample mean of these numbers is the statistic Z_2.

In both cases the null distribution of the test statistic is the standard normal distribution, approximately.

The return value is an object of class "htest" containing the results of the hypothesis test. The print method for this class gives an informative summary of the test outcome.

Value

An object of class "htest" (hypothesis test) and also of class "bermantest", containing the results of the test. The return value can be plotted (by plot.bermantest) or printed to give an informative summary of the test.

Warning

The meaning of a one-sided test must be carefully scrutinised: see the printed output.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

References

Berman, M. (1986) Testing for spatial association between a point process and another stochastic process. *Applied Statistics* **35**, 54–62.

Lawson, A.B. (1993) On the analysis of mortality events around a prespecified fixed point. *Journal of the Royal Statistical Society, Series A* **156** (3) 363–377.

Waller, L., Turnbull, B., Clark, L.C. and Nasca, P. (1992) Chronic Disease Surveillance and testing of clustering of disease and exposure: Application to leukaemia incidence and TCE-contaminated dumpsites in upstate New York. *Environmetrics* **3**, 281–300.

See Also

cdf.test, quadrat.test, ppm lppm

Examples

```
#' test of complete randomness
berman.test(spiders, "x")
#' test of fitted model
fit <- lppm(spiders ~ x)
berman.test(fit, "y", "Z2")
```

---

branchlabelfun *Tree Branch Membership Labelling Function*

Description

Creates a function which returns the tree branch membership label for any location on a linear network.

Usage

```
branchlabelfun(L, root = 1)
```

Arguments

L	Linear network (object of class "linnet"). The network must have no loops.
root	Root of the tree. An integer index identifying which point in vertices(L) is the root of the tree.

Details

The linear network L must be an acyclic graph (i.e. must not contain any loops) so that it can be interpreted as a tree.

The result of f <- branchlabelfun(L, root) is a function f which gives, for each location on the linear network L, the tree branch label at that location.

Tree branch labels are explained in treebranchlabels.

The result f also belongs to the class "linfun". It can be called using several different kinds of data, as explained in the help for linfun. The values of the function are character strings.

Value

A function (of class "linfun").

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

Rolf Turner <rolfturner@posteo.net>

and Ege Rubak <rubak@math.aau.dk>

See Also

treebranchlabels, linfun

Examples

```
# make a simple tree
m <- simplenet$m
m[8,10] <- m[10,8] <- FALSE
L <- linnet(vertices(simplenet), m)
# make function
f <- branchlabelfun(L, 1)
plot(f)
X <- runiflpp(5, L)
f(X)
```

---

bw.lppl *Likelihood Cross Validation Bandwidth Selection for Kernel Density on a Linear Network*

Description

Uses likelihood cross-validation to select a smoothing bandwidth for the kernel estimation of point process intensity on a linear network.

Usage

```
bw.lppl(X, ..., srange=NULL, ns=16, sigma=NULL, weights=NULL,
        distance=c("euclidean", "path"), shortcut=TRUE, warn=TRUE)
```

Arguments

X	A point pattern on a linear network (object of class "lpp").
srange	Optional numeric vector of length 2 giving the range of values of bandwidth to be searched.
ns	Optional integer giving the number of values of bandwidth to search.
sigma	Optional. Vector of values of the bandwidth to be searched. Overrides the values of ns and srange.
weights	Optional. Numeric vector of weights for the points of X. Argument passed to density.lpp.
distance	Argument passed to density.lpp controlling the type of kernel estimator.
...	Additional arguments passed to density.lpp.
shortcut	Logical value indicating whether to speed up the calculation by omitting the integral term in the cross-validation criterion.
warn	Logical. If TRUE, issue a warning if the maximum of the cross-validation criterion occurs at one of the ends of the search interval.

Details

This function selects an appropriate bandwidth sigma for the kernel estimator of point process intensity computed by density.lpp.

The argument X should be a point pattern on a linear network (class "lpp").

The bandwidth σ is chosen to maximise the point process likelihood cross-validation criterion

$$\mathrm{LCV}(\sigma) = \sum_i \log \hat{\lambda}_{-i}(x_i) - \int_L \hat{\lambda}(u)\,\mathrm{d}u$$

where the sum is taken over all the data points x_i, where $\hat{\lambda}_{-i}(x_i)$ is the leave-one-out kernel-smoothing estimate of the intensity at x_i with smoothing bandwidth σ, and $\hat{\lambda}(u)$ is the kernel-smoothing estimate of the intensity at a spatial location u with smoothing bandwidth σ. See Loader(1999, Section 5.3).

The value of $\mathrm{LCV}(\sigma)$ is computed directly, using density.lpp, for ns different values of σ between srange[1] and srange[2].

The result is a numerical value giving the selected bandwidth. The result also belongs to the class "bw.optim" which can be plotted to show the (rescaled) mean-square error as a function of sigma.

If shortcut=TRUE, the computation is accelerated by omitting the integral term in the equation above. This is valid because the integral is approximately constant.

Value

A single numerical value giving the selected bandwidth. The result also belongs to the class "bw.optim" (see bw.optim.object) which can be plotted to show the bandwidth selection criterion as a function of sigma.

Author(s)

Greg McSwiggan, Suman Rakshit and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

References

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

McSwiggan, G., Baddeley, A. and Nair, G. (2019) Estimation of relative risk for events on a linear network. *Statistics and Computing* **30** (2) 469–484.

See Also

density.lpp, bw.scott.

bw.optim.object.

For point patterns in two-dimensional space, use bw.ppl.

Examples

```
if(interactive()) {
  b <- bw.lppl(spiders)
  plot(b, main="Likelihood cross validation for spiders")
  plot(density(spiders, b, distance="e"))
} else {
  b1 <- bw.lppl(spiders, ns=2)
  b2 <- bw.lppl(spiders, ns=2, shortcut=FALSE)
}
```

---

bw.relrisk.lpp *Cross Validated Bandwidth Selection for Relative Risk Estimation on a Network*

Description

Uses cross-validation to select a smoothing bandwidth for the estimation of relative risk on a linear network.

Usage

```
  ## S3 method for class 'lpp'
bw.relrisk(X, ...,
    method = c("likelihood", "leastsquares", "KelsallDiggle", "McSwiggan"),
    distance=c("path", "euclidean"),
    hmin = NULL, hmax = NULL, nh = NULL,
    fast = TRUE, fastmethod = "onestep",
    floored = TRUE, reference = c("thumb", "uniform", "sigma"),
    allow.infinite = TRUE, epsilon = 1e-20, fudge = 0,
    verbose = FALSE, warn = TRUE)
```

Arguments

X	A multitype point pattern on a linear network (object of class "lpp" which has factor-valued marks).
...	Arguments passed to density.lpp to control the resolution of the algorithm.
method	Character string (partially matched) determining the cross-validation method. See Details.
distance	Character string (partially matched) specifying the type of smoothing kernel. See density.lpp.
hmin, hmax	Optional. Numeric values. Range of trial values of smoothing bandwith sigma to consider. There is a sensible default.
nh	Number of trial values of smoothing bandwidth sigma to consider.
fast	Logical value specifying whether the leave-one-out density estimates should be computed using a fast approximation (fast=TRUE, the default) or exactly (fast=FALSE).
fastmethod, floored	Developer use only.
reference	Character string (partially matched) specifying the bandwidth for calculating the reference intensities used in the McSwiggan method (modified Kelsall-Diggle method). reference="sigma" means the maximum bandwidth considered, which is given by the argument sigma. reference="thumb" means the bandwidths selected by Scott's rule of thumb bw.scott.iso. reference="uniform" means infinite bandwidth corresponding to uniform intensity.
allow.infinite	Logical value indicating whether an infinite bandwidth (corresponding to a constant relative risk) should be permitted as a possible choice of bandwidth.
epsilon	A small constant value added to the reference density in some of the cross-validation calculations, to improve performance.
fudge	Fudge factor to prevent very small density estimates in the leave-one-out calculation. If fudge > 0, then the lowest permitted value for a leave-one-out estimate of intensity is fudge/L, where L is the total length of the network.
verbose	Logical value indicating whether to print progress reports,
warn	Logical. If TRUE, issue a warning if the minimum of the cross-validation criterion occurs at one of the ends of the search interval.

Details

This function is a method for the generic bw.relrisk. It computes an optimal value of smoothing bandwidth for the nonparametric estimation of relative risk on a linear network using relrisk.lpp. The optimal value is found by minimising a cross-validation criterion.

The cross-validation criterion is selected by the argument method:

method="likelihood"	(negative) likelihood cross-validation
method="leastsquares"	least squares cross-validation
method="KelsallDiggle"	Kelsall and Diggle (1995) density ratio cross-validation
method="McSwiggan"	McSwiggan et al (2019) modified density ratio cross-validation

See McSwiggan et al (2019) for details.

The result is a numerical value giving the selected bandwidth `sigma`. The result also belongs to the class `"bw.optim"` allowing it to be printed and plotted. The plot shows the cross-validation criterion as a function of bandwidth. The 'optimal' bandwidth is the value of bandwidth which minimises the cross-validation criterion.

The range of values for the smoothing bandwidth `sigma` is set by the arguments `hmin, hmax`. There is a sensible default, based on the linear network version of Scott's rule `bw.scott.iso`.

If the optimal bandwidth is achieved at an endpoint of the interval `[hmin, hmax]`, the algorithm will issue a warning (unless `warn=FALSE`). If this occurs, then it is probably advisable to expand the interval by changing the arguments `hmin, hmax`.

The cross-validation procedure is based on kernel estimates of intensity, which are computed by `density.lpp`. Any arguments `...` are passed to `density.lpp` to control the kernel estimation procedure. This includes the argument `distance` which specifies the type of kernel. The default is `distance="path"`; the fastest option is `distance="euclidean"`.

Value

A single numerical value giving the selected bandwidth. The result also belongs to the class `"bw.optim"` (see `bw.optim.object`) which can be plotted to show the bandwidth selection criterion as a function of `sigma`.

Author(s)

Greg McSwiggan and Adrian Baddeley `<Adrian.Baddeley@curtin.edu.au>`.

References

Kelsall, J.E. and Diggle, P.J. (1995) Kernel estimation of relative risk. *Bernoulli* **1**, 3–16.

McSwiggan, G., Baddeley, A. and Nair, G. (2019) Estimation of relative risk for events on a linear network. *Statistics and Computing* **30** (2) 469–484.

See Also

`relrisk.lpp`, `bw.relrisk`, `bw.optim.object`

Examples

```
set.seed(2020)
X <- superimpose(A=runiflpp(20, simplenet),
                 B=runifpointOnLines(20, as.psp(simplenet)[1]))
plot(bw.relrisk(X, hmin=0.13, hmax=0.22, method="McSwiggan"))
plot(bw.relrisk(X, hmin=0.1, hmax=0.2, nh=8, distance="euclidean"))
```

bw.voronoi *Cross Validated Bandwidth Selection for Voronoi Estimator of Intensity on a Network*

Description

Uses cross-validation to select a smoothing bandwidth for the Voronoi estimate of point process intensity on a linear network.

Usage

```
bw.voronoi(X, ..., probrange = c(0.2, 0.8), nprob = 10,
           prob = NULL, nrep = 100,
           metric=c("shortestpath", "Euclidean"),
           verbose = TRUE, warn=TRUE)
```

Arguments

X	Point pattern on a linear network (object of class "lpp").
...	Ignored.
probrange	Numeric vector of length 2 giving the range of bandwidths (retention probabilities) to be assessed.
nprob	Integer. Number of bandwidths to be assessed.
prob	Optional. A numeric vector of bandwidths (retention probabilities) to be assessed. Entries must be probabilities between 0 and 1. Overrides nprob and probrange.
nrep	Number of simulated realisations to be used for the computation.
metric	Character string (partially matched) specifying the distance metric used to define the Dirichlet tessellation. Argument passed to lineardirichlet.
verbose	Logical value indicating whether to print progress reports.
warn	Logical. If TRUE, issue a warning if the maximum of the cross-validation criterion occurs at one of the ends of the search interval.

Details

This function uses likelihood cross-validation to choose the optimal value of the thinning fraction f (the retention probability) to be used in the smoothed Voronoi estimator of point process intensity densityVoronoi.lpp.

Value

A single numerical value giving the selected bandwidth. The result also belongs to the class "bw.optim" (see bw.optim.object) which can be plotted to show the bandwidth selection criterion as a function of sigma.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk> and Mehdi Moradi <m2.moradi@yahoo.com>.

References

Moradi, M., Cronie, 0., Rubak, E., Lachieze-Rey, R., Mateu, J. and Baddeley, A. (2019) Resample-smoothing of Voronoi intensity estimators. *Statistics and Computing* **29** (5) 995–1010.

See Also

densityVoronoi.lpp, bw.optim.object

Examples

```
if(interactive()) {
  X <- spiders
  np <- 10
  nr <- 100
} else {
  X <- runiflpp(4, simplenet)
  np <- 3
  nr <- 2
}
b <- bw.voronoi(X, nprob=np, nrep=nr)
b
plot(b)
bE <- bw.voronoi(X, nprob=np, nrep=nr, metric="E")
bE
```

---

cdf.test.lpp *Spatial Distribution Test for Points on a Linear Network*

Description

Performs a test of goodness-of-fit of a point process model on a linear network. The observed and predicted distributions of the values of a spatial covariate are compared using either the Kolmogorov-Smirnov test, Cramér-von Mises test or Anderson-Darling test. For non-Poisson models, a Monte Carlo test is used.

Usage

```
## S3 method for class 'lpp'
cdf.test(X, covariate,  test=c("ks", "cvm", "ad"), ...,
        interpolate=TRUE, jitter=TRUE)

## S3 method for class 'lppm'
cdf.test(model, covariate,  test=c("ks", "cvm", "ad"), ...,
          interpolate=TRUE, jitter=TRUE, nsim=99, verbose=TRUE)
```

Arguments

X	A point pattern on a linear network (object of class "lpp").
model	A fitted point process model on a linear network (object of class "lppm")
covariate	The spatial covariate on which the test will be based. A function, a pixel image (object of class "im" or "linim"), a list of pixel images, or one of the characters "x" or "y" indicating the Cartesian coordinates.
test	Character string identifying the test to be performed: "ks" for Kolmogorov-Smirnov test, "cvm" for Cramér-von Mises test or "ad" for Anderson-Darling test.
...	Arguments passed to ks.test (from the **stats** package) or cvm.test or ad.test (from the **goftest** package) to control the test.
interpolate	Logical flag indicating whether to interpolate pixel images. If interpolate=TRUE, the value of the covariate at each point of X will be approximated by interpolating the nearby pixel values. If interpolate=FALSE, the nearest pixel value will be used.
jitter	Logical flag. If jitter=TRUE, values of the covariate will be slightly perturbed at random, to avoid tied values in the test.
nsim	Number of simulated realisations from the model to be used for the Monte Carlo test, when model is not a Poisson process.
verbose	Logical value indicating whether to print progress reports when performing a Monte Carlo test.

Details

These functions perform a goodness-of-fit test of a Poisson point process model fitted to point pattern data on a linear network. The observed distribution of the values of a spatial covariate at the data points, and the predicted distribution of the same values under the model, are compared using the Kolmogorov-Smirnov test, the Cramér-von Mises test or the Anderson-Darling test. For Gibbs models, a Monte Carlo test is performed using these test statistics.

The function cdf.test is generic, with methods for point patterns ("ppp" or "lpp"), point process models ("ppm" or "lppm") and spatial logistic regression models ("slrm").

See the help file for cdf.test for information on the generic function and the methods for data in two-dimensional space, classes "ppp", "ppm" and "slrm".

This help file describes the methods for data on a linear network, classes "lpp" and "lppm".

- If X is a point pattern on a linear network (object of class "lpp"), then cdf.test(X, ...) performs a goodness-of-fit test of the uniform Poisson point process (Complete Spatial Randomness, CSR) for this dataset. For a multitype point pattern, the uniform intensity is assumed to depend on the type of point (sometimes called Complete Spatial Randomness and Independence, CSRI).
- If model is a fitted point process model on a network (object of class "lppm") then cdf.test(model, ...) performs a test of goodness-of-fit for this fitted model.

The test is performed by comparing the observed distribution of the values of a spatial covariate at the data points, and the predicted distribution of the same covariate under the model, using a classical goodness-of-fit test. Thus, you must nominate a spatial covariate for this test.

If `X` is a point pattern that does not have marks, the argument `covariate` should be either a `function(x,y)` or a pixel image (object of class `"im"` or `"linim"`) containing the values of a spatial function, or one of the characters `"x"` or `"y"` indicating the Cartesian coordinates. If `covariate` is an image, it should have numeric values, and its domain should cover the observation window of the `model`. If `covariate` is a function, it should expect two arguments `x` and `y` which are vectors of coordinates, and it should return a numeric vector of the same length as `x` and `y`.

If `X` is a multitype point pattern, the argument `covariate` can be either a `function(x,y,marks)`, or a pixel image, or a list of pixel images corresponding to each possible mark value, or one of the characters `"x"` or `"y"` indicating the Cartesian coordinates.

First the original data point pattern is extracted from `model`. The values of the `covariate` at these data points are collected.

The predicted distribution of the values of the `covariate` under the fitted `model` is computed as follows. The values of the `covariate` at all locations in the observation window are evaluated, weighted according to the point process intensity of the fitted model, and compiled into a cumulative distribution function F using `ewcdf`.

The probability integral transformation is then applied: the values of the `covariate` at the original data points are transformed by the predicted cumulative distribution function F into numbers between 0 and 1. If the model is correct, these numbers are i.i.d. uniform random numbers. The A goodness-of-fit test of the uniform distribution is applied to these numbers using `stats::ks.test`, `goftest::cvm.test` or `goftest::ad.test`.

This test was apparently first described (in the context of two-dimensional spatial data, and using Kolmogorov-Smirnov) by Berman (1986). See also Baddeley et al (2005).

If `model` is not a Poisson process, then a Monte Carlo test is performed, by generating `nsim` point patterns which are simulated realisations of the `model`, re-fitting the model to each simulated point pattern, and calculating the test statistic for each fitted model. The Monte Carlo p value is determined by comparing the simulated values of the test statistic with the value for the original data.

The return value is an object of class `"htest"` containing the results of the hypothesis test. The print method for this class gives an informative summary of the test outcome.

The return value also belongs to the class `"cdftest"` for which there is a plot method `plot.cdftest`. The plot method displays the empirical cumulative distribution function of the covariate at the data points, and the predicted cumulative distribution function of the covariate under the model, plotted against the value of the covariate.

The argument `jitter` controls whether covariate values are randomly perturbed, in order to avoid ties. If the original data contains any ties in the covariate (i.e. points with equal values of the covariate), and if `jitter=FALSE`, then the Kolmogorov-Smirnov test implemented in `ks.test` will issue a warning that it cannot calculate the exact p-value. To avoid this, if `jitter=TRUE` each value of the covariate will be perturbed by adding a small random value. The perturbations are normally distributed with standard deviation equal to one hundredth of the range of values of the covariate. This prevents ties, and the p-value is still correct. There is a very slight loss of power.

Value

An object of class "htest" containing the results of the test. See ks.test for details. The return value can be printed to give an informative summary of the test.

The value also belongs to the class "cdftest" for which there is a plot method.

Warning

The outcome of the test involves a small amount of random variability, because (by default) the coordinates are randomly perturbed to avoid tied values. Hence, if cdf.test is executed twice, the p-values will not be exactly the same. To avoid this behaviour, set jitter=FALSE.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Rolf Turner <rolfturner@posteo.net>

References

Baddeley, A., Turner, R., Møller, J. and Hazelton, M. (2005) Residual analysis for spatial point processes. *Journal of the Royal Statistical Society, Series B* **67**, 617–666.

Berman, M. (1986) Testing for spatial association between a point process and another stochastic process. *Applied Statistics* **35**, 54–62.

See Also

plot.cdftest, quadrat.test, berman.test, ks.test, goftest::cvm.test, goftest::ad.test, lppm

Examples

```
op <- options(useFancyQuotes=FALSE)

# test of CSR using x coordinate
cdf.test(spiders, "x")

# fit inhomogeneous Poisson model and test
model <- lppm(spiders ~x)
cdf.test(model, "y")

# test of CSR using a function of x and y
fun <- function(x,y){2* x + y}
cdf.test(spiders, fun)

# test of CSR using an image covariate
fim <- as.linim(fun, domain(spiders))
cdf.test(spiders, fim)

options(op)
```

chop.linnet *Divide a Linear Network into Tiles Using Infinite Lines*

Description

Given a linear network and a set of infinite lines, divide the network into tiles demarcated by the lines. The result is a tessellation of the network.

Usage

```
chop.linnet(X, L)
```

Arguments

X	Linear network (object of class "linnet") or data acceptable to as.linnet.
L	Infinite line or lines (object of class "infline").

Details

The first line of L divides X into two tiles. Subsequent lines divide each of these tiles. The result is a tessellation of X. Tiles are not necessarily connected sets.

Value

Tessellation on a linear network (object of class "lintess").

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

See Also

crossing.linnet to determine the crossing points between the lines and the network.

divide.linnet to divide a network into a tessellation using arbitrary cut points.

Examples

```
L <- infline(p=runif(3), theta=runif(3, max=pi/2))
Y <- chop.linnet(simplenet, L)
plot(Y, main="")
plot(L, col="red")
```

clickjoin *Interactively join vertices on a plot*

Description

Given a point pattern representing a set of vertices, this command gives a point-and-click interface allowing the user to join pairs of selected vertices by edges.

Usage

```
clickjoin(X, ..., add = TRUE, m = NULL, join = TRUE)
```

Arguments

X	Point pattern of vertices. An object of class "ppp".
...	Arguments passed to segments to control the plotting of the new edges.
add	Logical. Whether the point pattern X should be added to the existing plot (add=TRUE) or a new plot should be created (add=FALSE).
m	Optional. Logical matrix specifying an initial set of edges. There is an edge between vertices i and j if m[i,j] = TRUE.
join	Optional. If TRUE, then each user click will join a pair of vertices. If FALSE, then each user click will delete an existing edge. This is only relevant if m is supplied.

Details

This function makes it easier for the user to create a linear network or a planar graph, given a set of vertices.

The function first displays the point pattern X, then repeatedly prompts the user to click on a pair of points in X. Each selected pair of points will be joined by an edge. The function returns a logical matrix which has entries equal to TRUE for each pair of vertices joined by an edge.

The selection of points is performed using identify.ppp which typically expects the user to click the left mouse button. This point-and-click interaction continues until the user terminates it, by pressing the middle mouse button, or pressing the right mouse button and selecting stop.

The return value can be used in linnet to create a linear network.

Value

Logical matrix m with value m[i,j] = TRUE for every pair of vertices X[i] and X[j] that should be joined by an edge.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

See Also

linnet, clickppp

clicklpp *Interactively Add Points on a Linear Network*

Description

Allows the user to create a point pattern on a linear network by point-and-click in the display.

Usage

```
clicklpp(L, n=NULL, types=NULL, ...,
         add=FALSE, main=NULL, hook=NULL)
```

Arguments

L	Linear network on which the points will be placed. An object of class "linnet".
n	Number of points to be added (if this is predetermined).
types	Vector of types, when creating a multitype point pattern.
...	Optional extra arguments to be passed to locator to control the display.
add	Logical value indicating whether to create a new plot (add=FALSE) or draw over the existing plot (add=TRUE).
main	Main heading for plot.
hook	For internal use only. Do not use this argument.

Details

This function allows the user to create a point pattern on a linear network by interactively clicking on the screen display.

First the linear network L is plotted on the current screen device. Then the user is prompted to point the mouse at any desired locations and click the left mouse button to add each point. Interactive input stops after n clicks (if n was given) or when the middle mouse button is pressed.

The return value is a point pattern on the network L, containing the locations of all the clicked points, after they have been projected onto the network L. Any points that were clicked outside the bounding window of the network will be ignored.

If the argument types is given, then a multitype point pattern will be created. The user is prompted to input the locations of points of type type[i], for each successive index i. (If the argument n was given, there will be n points of *each* type.) The return value is a multitype point pattern on a linear network.

This function uses the R command locator to input the mouse clicks. It only works on screen devices such as 'X11', 'windows' and 'quartz'. Arguments that can be passed to locator through ... include pch (plotting character), cex (character expansion factor) and col (colour). See locator and par.

Value

A point pattern (object of class "lpp").

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>, based on an idea by Dominic Schuhmacher.

See Also

clickppp, identify.lpp, locator, clickpoly, clickbox, clickdist

---

connected.linnet *Connected Components of a Linear Network*

Description

Find the topologically-connected components of a linear network.

Usage

```
## S3 method for class 'linnet'
connected(X, ..., what = c("labels", "components"))
```

Arguments

X	A linear network (object of class "linnet").
...	Ignored.
what	Character string specifying the kind of result.

Details

The function connected is generic. This is the method for linear networks (objects of class "linnet").

Two vertices of the network are connected if they are joined by a path in the network. This function divides the network into subsets, such that all points in a subset are connected to each other.

If what="labels" the return value is a factor with one entry for each vertex of X, identifying which connected component the vertex belongs to.

If what="components" the return value is a list of linear networks, which are the connected components of X.

Value

If what="labels", a factor. If what="components", a list of linear networks.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Suman Rakshit.

See Also

thinNetwork

Examples

```
# remove some edges from a network to make it disconnected
plot(simplenet, col="grey", main="", lty=2)
A <- thinNetwork(simplenet, retainedges=-c(3,5))
plot(A, add=TRUE, lwd=2)
# find the connected components
connected(A)
cA <- connected(A, what="components")
plot(cA[[1]], add=TRUE, col="green", lwd=2)
plot(cA[[2]], add=TRUE, col="blue", lwd=2)
```

---

connected.lpp *Connected Components of a Point Pattern on a Linear Network*

Description

Finds the topologically-connected components of a point pattern on a linear network, when all pairs of points closer than a threshold distance are joined.

Usage

```
## S3 method for class 'lpp'
connected(X, R=Inf, ..., dismantle=TRUE)
```

Arguments

X	A linear network (object of class "lpp").
R	Threshold distance. Pairs of points will be joined together if they are closer than R units apart, measured by the shortest path in the network. The default R=Inf implies that points will be joined together if they are mutually connected by any path in the network.
dismantle	Logical. If TRUE (the default), the network itself will be divided into its path-connected components using connected.linnet.
...	Ignored.

Details

The function connected is generic. This is the method for point patterns on a linear network (objects of class "lpp"). It divides the point pattern X into one or more groups of points.

If R=Inf (the default), then X is divided into groups such that any pair of points in the same group can be joined by a path in the network.

If R is a finite number, then two points of X are declared to be *R-close* if they lie closer than R units apart, measured by the length of the shortest path in the network. Two points are *R-connected* if they can be reached by a series of steps between R-close pairs of points of X. Then X is divided into groups such that any pair of points in the same group is R-connected.

If dismantle=TRUE (the default) the algorithm first checks whether the network is connected (i.e. whether any pair of vertices can be joined by a path in the network), and if not, the network is decomposed into its connected components.

Value

A point pattern (of class "lpp") with marks indicating the grouping, or a list of such point patterns.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

See Also

thinNetwork

Examples

```
## behaviour like connected.ppp
U <- runiflpp(20, simplenet)
plot(connected(U, 0.15, dismantle=FALSE))

## behaviour like connected.owin
## remove some edges from a network to make it disconnected
plot(simplenet, col="grey", main="", lty=2)
A <- thinNetwork(simplenet, retainedges=-c(3,5))
plot(A, add=TRUE, lwd=2)
X <- runiflpp(10, A)
## find the connected components
cX <- connected(X)
plot(cX[[1]], add=TRUE, col="blue", lwd=2)
```

---

crossdist.lpp *Pairwise distances between two point patterns on a linear network*

Description

Computes the distances between pairs of points taken from two different point patterns on the same linear network.

Usage

```
  ## S3 method for class 'lpp'
crossdist(X, Y, ..., method="C", check=TRUE)
```

Arguments

X, Y	Point patterns on a linear network (objects of class "lpp"). They must lie on the *same* network.
...	Ignored.
method	String specifying which method of calculation to use when the network data use the non-sparse representation. Values are "C" and "interpreted".
check	Logical value specifying whether to check that X and Y are defined on the same network. Default is check=TRUE. Setting check=FALSE will save time, but should only be used if it is certain that the two networks are identical.

Details

Given two point patterns on a linear network, this function computes the distance from each point in the first pattern to each point in the second pattern, measuring distance by the shortest path along the network.

This is a method for the generic function crossdist for the class of point patterns on a linear network (objects of class "lpp").

This function expects two point pattern objects X and Y on the *same* linear network, and returns the matrix whose [i,j] entry is the shortest-path distance from X[i] to Y[j].

If two points cannot be joined by a path, the distance between them is infinite (Inf).

The argument method is not normally used. It is retained only for developers to check the validity of the software.

Value

A matrix whose [i,j] entry is the distance from the i-th point in X to the j-th point in Y. Matrix entries are nonnegative numbers or infinity (Inf).

Algorithms and accuracy

Distances are accurate within the numerical tolerance of the network, summary(X)$toler.

For network data stored in the non-sparse representation described in linnet, then pairwise distances are computed using the matrix of path distances between vertices of the network, using R code if method = "interpreted", or using C code if method="C" (the default).

For networks stored in the sparse representation, the argument method has no effect, and the distances are computed using an efficient C algorithm.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

See Also

crossdist, crossdist.ppp, pairdist, nndist

Examples

```
v <- split(chicago)
X <- v$cartheft
Y <- v$burglary
d <- crossdist(X, Y)
d[1:3,1:4]
```

`crossing.linnet` *Crossing Points between Linear Network and Other Lines*

Description

Find all the crossing-points between a linear network and another pattern of lines or line segments.

Usage

```
crossing.linnet(X, Y)
```

Arguments

`X`	Linear network (object of class `"linnet"`).
`Y`	A linear network, or a spatial pattern of line segments (class `"psp"`) or infinite lines (class `"infline"`).

Details

All crossing-points between `X` and `Y` are determined. The result is a point pattern on the network `X`.

Value

Point pattern on a linear network (object of class `"lpp"`).

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

See Also

`crossing.psp`

Examples

```
plot(simplenet, main="")
L <- infline(p=runif(3), theta=runif(3, max=pi/2))
plot(L, col="red")
Y <- crossing.linnet(simplenet, L)
plot(Y, add=TRUE, cols="blue")
```

cut.lpp *Classify Points in a Point Pattern on a Network*

Description

For a point pattern on a linear network, classify the points into distinct types according to the numerical marks in the pattern, or according to another variable.

Usage

```
  ## S3 method for class 'lpp'
cut(x, z=marks(x), ...)
```

Arguments

x	A point pattern on a linear network (object of class "lpp").
z	Data determining the classification. A numeric vector, a factor, a pixel image on a linear network (class "linim"), a function on a linear network (class "linfun"), a tessellation on a linear network (class "lintess"), a string giving the name of a column of marks, or one of the coordinate names "x", "y", "seg" or "tp".
...	Arguments passed to cut.default. They determine the breakpoints for the mapping from numerical values in z to factor values in the output. See cut.default.

Details

This function has the effect of classifying each point in the point pattern x into one of several possible types. The classification is based on the dataset z, which may be either

- a factor (of length equal to the number of points in z) determining the classification of each point in x. Levels of the factor determine the classification.
- a numeric vector (of length equal to the number of points in z). The range of values of z will be divided into bands (the number of bands is determined by ...) and z will be converted to a factor using cut.default.
- a pixel image on a network (object of class "linim"). The value of z at each point of x will be used as the classifying variable.
- a function on a network (object of class "linfun", see linfun). The value of z at each point of x will be used as the classifying variable.
- a tessellation on a network (object of class "lintess", see lintess). Each point of x will be classified according to the tile of the tessellation into which it falls.
- a character string, giving the name of one of the columns of marks(x), if this is a data frame.
- a character string identifying one of the coordinates: the spatial coordinates "x", "y" or the segment identifier "seg" or the fractional coordinate along the segment, "tp".

The default is to take z to be the vector of marks in x (or the first column in the data frame of marks of x, if it is a data frame). If the marks are numeric, then the range of values of the numerical marks is divided into several intervals, and each interval is associated with a level of a factor. The result is a marked point pattern, on the same linear network, with the same point locations as x, but with the numeric mark of each point discretised by replacing it by the factor level. This is a convenient way to transform a marked point pattern which has numeric marks into a multitype point pattern, for example to plot it or analyse it. See the examples.

To select some points from x, use the subset operators [.lpp or subset.lpp instead.

Value

A multitype point pattern on the same linear network, that is, a point pattern object (of class "lpp") with a marks vector that is a factor.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

cut, lpp, lintess, linfun, linim

Examples

```
X <- runiflpp(20, simplenet)
f <- linfun(function(x,y,seg,tp) { x }, simplenet)
plot(cut(X, f, breaks=4))
plot(cut(X, "x", breaks=4))
plot(cut(X, "seg"))
```

---

data.lppm *Extract Original Data from a Fitted Point Process Model on a Network*

Description

Given a fitted point process model on a linear network, this function extracts the original point pattern dataset to which the model was fitted.

Usage

```
data.lppm(object)
```

Arguments

object	fitted point process model on a linear network (an object of class "lppm").

Details

An object of class "lppm" represents a point process model that has been fitted to a point pattern dataset on a linear network. It is typically produced by the model-fitting algorithm lppm. The object contains complete information about the original data point pattern to which the model was fitted. This function extracts the original data pattern.

Value

A point pattern on a linear network (object of class "lpp").

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

lppm, data.ppm

Examples

```
fit <- lppm(spiders ~ x)
X <- data.lppm(fit)
# 'X' is identical to 'spiders'
```

---

delaunayNetwork *Linear Network of Delaunay Triangulation or Dirichlet Tessellation*

Description

Computes the edges of the Delaunay triangulation or Dirichlet tessellation of a point pattern, and returns the result as a linear network object.

Usage

```
delaunayNetwork(X)

dirichletNetwork(X, ...)
```

Arguments

X	A point pattern (object of class "ppp").
...	Arguments passed to as.linnet.psp

Details

For delaunayNetwork, points of X which are neighbours in the Delaunay triangulation (see delaunay) will be joined by a straight line. The result will be returned as a linear network (object of class "linnet").

For dirichletNetwork, the Dirichlet tessellation is computed (see dirichlet) and the edges of the tiles of the tessellation are extracted. This is converted to a linear network using as.linnet.psp.

Value

Linear network (object of class "linnet") or NULL.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

Rolf Turner <rolfturner@posteo.net>

and Ege Rubak <rubak@math.aau.dk>

See Also

delaunay, dirichlet, delaunayDistance

Examples

```
LE <- delaunayNetwork(cells)
LI <- dirichletNetwork(cells)
```

---

deletebranch *Delete or Extract a Branch of a Tree*

Description

Deletes or extracts a given branch of a tree.

Usage

```
deletebranch(X, ...)

## S3 method for class 'linnet'
deletebranch(X, code, labels, ...)

## S3 method for class 'lpp'
deletebranch(X, code, labels, ...)

extractbranch(X, ...)

## S3 method for class 'linnet'
```

```
extractbranch(X, code, labels, ..., which=NULL)

## S3 method for class 'lpp'
extractbranch(X, code, labels, ..., which=NULL)
```

Arguments

X	Linear network (object of class "linnet") or point pattern on a linear network (object of class "lpp").
code	Character string. Label of the branch to be deleted or extracted.
labels	Vector of character strings. Branch labels for the vertices of the network, usually obtained from treebranchlabels.
...	Arguments passed to methods.
which	Logical vector indicating which vertices of the network should be extracted. Overrides code and labels.

Details

The linear network L <- X or L <- as.linnet(X) must be a tree, that is, it has no loops.

The argument labels should be a character vector giving tree branch labels for each vertex of the network. It is usually obtained by calling treebranchlabels.

The branch designated by the string code will be deleted or extracted.

The return value is the result of deleting or extracting this branch from X along with any data associated with this branch (such as points or marks).

Value

Another object of the same type as X obtained by deleting or extracting the specified branch.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>

See Also

treebranchlabels, branchlabelfun, linnet

Examples

```
# make a simple tree
m <- simplenet$m
m[8,10] <- m[10,8] <- FALSE
L <- linnet(vertices(simplenet), m)
plot(L, main="")
# compute branch labels
tb <- treebranchlabels(L, 1)
tbc <- paste0("[", tb, "]")
```

```
text(vertices(L), labels=tbc, cex=2)

# delete branch B
LminusB <- deletebranch(L, "b", tb)
plot(LminusB, add=TRUE, col="green")

# extract branch B
LB <- extractbranch(L, "b", tb)
plot(LB, add=TRUE, col="red")
```

`density.linnet` *Kernel Smoothing of Linear Network*

Description

Compute a kernel smoothed intensity function for the line segments of a linear network.

Usage

```
  ## S3 method for class 'linnet'
density(x, ...)
```

Arguments

`x`	Linear network (object of class `"linnet"`)
`...`	Arguments passed to `density.psp` to control the amount of smoothing and the spatial resolution of the result.

Details

This is the method for the generic function `density` for the class `"linnet"` (linear networks).

The network `x` is first converted to a line segment pattern (object of class `"psp"`). Then the method `density.psp` is applied to the segment pattern.

A kernel estimate of the intensity of the line segment pattern is computed. The result is the convolution of the isotropic Gaussian kernel, of standard deviation `sigma`, with the line segments.

The intensity of a line segment pattern is the (spatially-varying) amount of segment length per unit area, expressed in the same units as the coordinates of `x`. If the units of `x` are in metres, then an intensity value of 3 means that there are 3 metres of segment length per square metre of spatial domain.

See `density.psp` for more details.

Value

A pixel image in two dimensions (object of class `"im"`) or a numeric vector.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

density.psp, im.object, density.

Examples

```
D <- density(simplenet, 0.1)
plot(D)
plot(simplenet, add=TRUE, col="white")
## compare with average intensity
volume(simplenet)/area(Window(simplenet))
```

---

density.lpp *Kernel Estimate of Intensity on a Linear Network*

Description

Estimates the intensity of a point process on a linear network by applying kernel smoothing to the point pattern data.

Usage

```
## S3 method for class 'lpp'
density(x, sigma=NULL, ...,
        weights=NULL,
        distance=c("path", "euclidean"),
        continuous=TRUE,
        kernel="gaussian")

## S3 method for class 'splitppx'
density(x, sigma=NULL, ...)
```

Arguments

x	Point pattern on a linear network (object of class "lpp") to be smoothed.
sigma	Smoothing bandwidth (standard deviation of the kernel). A single numerical value in the same units as the spatial coordinates of x. Alternatively sigma may be a function which selects a bandwidth when applied to X, for example, bw.scott.iso or bw.lppl. There is a sensible default.
...	Additional arguments controlling the algorithm and the spatial resolution of the result. These arguments are passed either to densityQuick.lpp, densityHeat.lpp or densityEqualSplit depending on the algorithm chosen.

weights	Optional weights associated with the points of x. A numeric or logical valued vector, pixel image, function or expression, or one of the strings "x" or "y" representing the cartesian coordinates. The expression may involve the variables x,y,marks representing the coordinates and marks of the point pattern. Numerical weights may be positive, negative or zero.
distance	Character string (partially matched) specifying whether to use a kernel based on paths in the network (distance="path", the default) or a two-dimensional kernel (distance="euclidean").
kernel	Character string specifying the smoothing kernel. See dkernel for possible options.
continuous	Logical value indicating whether to compute the "equal-split continuous" smoother (continuous=TRUE, the default) or the "equal-split discontinuous" smoother (continuous=FALSE). Applies only when distance="path".

Details

Kernel smoothing is applied to the points of x using either a kernel based on path distances in the network, or a two-dimensional kernel. The result is a pixel image on the linear network (class "linim") which can be plotted.

- If distance="path" (the default) then the smoothing is performed using a kernel based on path distances in the network, as described in described in Okabe and Sugihara (2012) and McSwiggan et al (2016).
  - If continuous=TRUE (the default), smoothing is performed using the "equal-split continuous" rule described in Section 9.2.3 of Okabe and Sugihara (2012). The resulting function is continuous on the linear network.
  - If continuous=FALSE, smoothing is performed using the "equal-split discontinuous" rule described in Section 9.2.2 of Okabe and Sugihara (2012). The resulting function is continuous except at the network vertices.
  - In the default case (where distance="path" and continuous=TRUE and kernel="gaussian"), computation is performed rapidly by solving the classical heat equation on the network, as described in McSwiggan et al (2016). The arguments are passed to densityHeat.lpp which performs the computation. Computational time is short, but increases quadratically with sigma.
  - In all other cases, computation is performed by path-tracing as described in Okabe and Sugihara (2012); the arguments are passed to densityEqualSplit which performs the computation. Computation time can be extremely long, and increases exponentially with sigma.
- If distance="euclidean", the smoothing is performed using a two-dimensional kernel. The arguments are passed to densityQuick.lpp to perform the computation. Computation time is very short. See the help for densityQuick.lpp for further details.

There is also a method for split point patterns on a linear network (class "splitppx") which will return a list of pixel images.

The argument sigma specifies the smoothing bandwidth. If sigma is missing or NULL, the default is one-eighth of the length of the shortest side of the bounding box of x. If sigma is a function in the R language, it is assumed to be a bandwidth selection rule, and it will be applied to x to compute the bandwidth value.

Value

A pixel image on the linear network (object of class "linim"), or in some cases, a numeric vector of length equal to npoints(x).

Infinite bandwidth

If sigma=Inf, the resulting density estimate is constant over all locations, and is equal to the average density of points per unit length. (If the network is not connected, then this rule is applied separately to each connected component of the network).

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Greg McSwiggan.

References

McSwiggan, G., Baddeley, A. and Nair, G. (2016) Kernel density estimation on a linear network. *Scandinavian Journal of Statistics* **44**, 324–345.

Okabe, A. and Sugihara, K. (2012) *Spatial analysis along networks*. Wiley.

See Also

lpp, linim, densityQuick.lpp, densityHeat.lpp, densityVoronoi.lpp

Examples

```
X <- runiflpp(3, simplenet)
D <- density(X, 0.2, verbose=FALSE)
plot(D, style="w", main="", adjust=2)
Dq <- density(X, 0.2, distance="euclidean")
plot(Dq, style="w", main="", adjust=2)
Dw <- density(X, 0.2, weights=c(1,2,-1), verbose=FALSE)
De <- density(X, 0.2, kernel="epanechnikov", verbose=FALSE)
Ded <- density(X, 0.2, kernel="epanechnikov", continuous=FALSE, verbose=FALSE)
```

---

densityEqualSplit *Equal-Split Algorithm for Kernel Density on a Network*

Description

Computes a kernel density estimate on a linear network using the Okabe-Sugihara equal-split algorithms.

Usage

```
densityEqualSplit(x, sigma = NULL, ...,
                  at = c("pixels", "points"),
                  leaveoneout=TRUE,
                  weights = NULL,
                  kernel = "epanechnikov", continuous = TRUE,
                epsilon = 1e-06, verbose = TRUE, debug = FALSE, savehistory = TRUE)
```

Arguments

x	Point pattern on a linear network (object of class "lpp") to be smoothed.
sigma	Smoothing bandwidth (standard deviation of the kernel). A numeric value in the same units as the spatial coordinates of x. Alternatively sigma may be a function which selects a bandwidth when applied to X, for example, bw.scott.iso or bw.lppl. There is a sensible default.
...	Arguments passed to as.mask determining the resolution of the result.
at	String (partially matched) specifying whether to compute the intensity values at a fine grid of locations on the network (at="pixels", the default) or only at the points of x (at="points").
leaveoneout	Logical value indicating whether to compute a leave-one-out estimator. Applicable only when at="points".
weights	Optional. Numeric vector of weights associated with the points of x. Weights may be positive, negative or zero.
kernel	Character string specifying the smoothing kernel. See dkernel for possible options.
continuous	Logical value indicating whether to compute the "equal-split continuous" smoother (continuous=TRUE, the default) or the "equal-split discontinuous" smoother (continuous=FALSE).
epsilon	Tolerance value. A tail of the kernel with total mass less than epsilon may be deleted.
verbose	Logical value indicating whether to print progress reports.
debug	Logical value indicating whether to print debugging information.
savehistory	Logical value indicating whether to save the entire history of the algorithm, for the purposes of evaluating performance.

Details

Kernel smoothing is applied to the points of x using a kernel based on path distances in the network. The result is a pixel image on the linear network (class "linim") which can be plotted.

Smoothing is performed using one of the "equal-split" rules described in Okabe and Sugihara (2012).

- If continuous=TRUE (the default), smoothing is performed using the "equal-split continuous" rule described in Section 9.2.3 of Okabe and Sugihara (2012). The resulting function is continuous on the linear network.

- If continuous=FALSE, smoothing is performed using the "equal-split discontinuous" rule described in Section 9.2.2 of Okabe and Sugihara (2012). The resulting function is not continuous.

Computation is performed by path-tracing as described in Okabe and Sugihara (2012).

It is advisable to choose a kernel with bounded support such as kernel="epanechnikov". With a Gaussian kernel, computation time can be long, and increases exponentially with sigma.

Faster algorithms are available through density.lpp.

The argument sigma specifies the smoothing bandwidth. If sigma is missing or NULL, the default is one-eighth of the length of the shortest side of the bounding box of x. If sigma is a function in the R language, it is assumed to be a bandwidth selection rule, and it will be applied to x to compute the bandwidth value.

Value

If at="pixels" (the default), a pixel image on the linear network (object of class "linim").

If at="points", a numeric vector with one entry for each point of x.

Infinite bandwidth

If sigma=Inf, the resulting density estimate is constant over all locations, and is equal to the average density of points per unit length. (If the network is not connected, then this rule is applied separately to each connected component of the network).

Discretisation

The kernel estimate is computed exactly (apart from numerical error) but only at a discrete set of sample points along the network. The spacing of sample points is determined by the default pixel resolution. To increase accuracy, a finer pixellation should be specified using one of the arguments dimyx, eps or xy passed to as.mask. To increase accuracy for the rest of the R session, specify a larger value of spatstat.options('npixel'). For example dimyx=512 or spatstat.options(npixel=512)would specify a 512 x 512 pixel grid, reducing the sample spacing by a factor of 4 from the default 128 x 128 grid. Refining the sample spacing will increase computation time.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Greg McSwiggan.

References

Okabe, A. and Sugihara, K. (2012) *Spatial analysis along networks*. Wiley.

See Also

density.lpp

Examples

```
X <- runiflpp(3, simplenet)
De <- density(X, 0.2, kernel="epanechnikov", verbose=FALSE)
Ded <- density(X, 0.2, kernel="epanechnikov", continuous=FALSE, verbose=FALSE)
```

---

densityfun.lpp *Kernel Estimate of Intensity on a Linear Network as a Spatial Function*

Description

Computes a kernel estimate of the intensity of a point process on a linear network, and returns the intensity estimate as a function of spatial location.

Usage

```
## S3 method for class 'lpp'
densityfun(X, sigma, ..., weights=NULL, nsigma=1, verbose=FALSE)
```

Arguments

X	Point pattern on a linear network (object of class "lpp").
sigma	Bandwidth of kernel (standard deviation of Gaussian kernel), in the same units of length as X.
...	Arguments passed to density.lpp to control the discretisation.
weights	Optional numeric vector of weights associated with the points of X.
nsigma	Integer. The number of different bandwidths for which a result should be returned. If nsigma=1 (the default), the result is a function giving kernel estimate with bandwidth sigma. If nsigma > 1, the result is a function with an additional argument k containing the kernel estimates for the nsigma+1 equally-spaced time steps from 0 to sigma^2.
verbose	Logical value indicating whether to print progress reports.

Details

Kernel smoothing is applied to the points of X using the diffusion algorithm of McSwiggan et al (2016). The result is a function on the linear network (object of class "linfun") that can be printed, plotted and evaluated at any location.

This is a method for the generic function densityfun for the class "lpp" of point patterns on a linear network.

Value

Function on a linear network (object of class "linfun").

If nsigma=1 (the default), the result is a function giving kernel estimate with bandwidth sigma.

If nsigma > 1, the result is a function with an additional argument k. If k is specified, the function returns the kernel estimate for bandwidth tau = sigma * sqrt(k/nsigma). If k is not specified, results are returned for all k = 1, 2, ..., nsigma.

The result also has attributes

- attr(result, "dt") giving the time step Δt;
- attr(result, "dx") giving the spacing Δx between sample points in the numerical algorithm;
- attr(result, "sigma") giving the smoothing bandwidth σ used (or the successive bandwidths used at each sampled time step, if nsigma > 1).

Author(s)

Greg McSwiggan, with tweaks by Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

References

McSwiggan, G., Baddeley, A. and Nair, G. (2016) Kernel Density Estimation on a Linear Network. *Scandinavian Journal of Statistics* **44**, 324–345.

See Also

density.lpp which returns a pixel image on the linear network.

methods.linfun for methods applicable to "linfun" objects.

Examples

```
X <- unmark(chicago)
# single bandwidth
g <- densityfun(X, 30)
plot(g)
Y <- X[1:5]
g(Y)
# weighted
gw <- densityfun(X, 30, weights=runif(npoints(X)))
# sequence of bandwidths
g10 <- densityfun(X, 30, nsigma=10)
g10(Y, k=10)
g10(Y)
plot(as.linim(g10, k=5))
```

densityHeat.lpp *Kernel Density on a Network using Heat Equation*

Description

Given a point pattern on a linear network, compute a kernel estimate of intensity, by solving the heat equation.

Usage

```
  ## S3 method for class 'lpp'
densityHeat(x, sigma=NULL, ...,
              at=c("pixels", "points"), leaveoneout=TRUE,
              weights = NULL,
              dx = NULL, dt = NULL, iterMax = 1e+06,
              finespacing = TRUE, verbose=FALSE)
```

Arguments

x	Point pattern on a linear network (object of class "lpp") to be smoothed.
sigma	Smoothing bandwidth (standard deviation of the kernel). A numeric value in the same units as the spatial coordinates of x. Alternatively sigma may be a function which selects a bandwidth when applied to X, for example, bw.scott.iso or bw.lppl. There is a sensible default.
...	Arguments passed to as.mask determining the resolution of the result. (Any other arguments are ignored.)
at	String specifying whether to compute the intensity values at a fine grid of pixel locations on the network (at="pixels", the default) or only at the data points of x (at="points").
leaveoneout	Logical value indicating whether to compute a leave-one-out estimator. Applicable only when at="points".
weights	Optional. Numeric vector of weights associated with the points of x. Weights may be positive, negative or zero.
dx	Optional. Spacing of the sampling points along the network. A single number giving a distance value in the same units as x.
dt	Optional. Time step in the heat equation solver. A single number.
iterMax	Maximum number of iterations.
finespacing	Logical value specifying whether the discrete approximation is required to be accurate along every segment of the network, no matter how short the segment is. See the section on Discretisation.
verbose	Logical value specifying whether to print progress reports.

Details

The function densityHeat is generic. This is the method for the class "lpp" of points on a linear network.

Kernel smoothing is applied to the points of x using a kernel based on path distances in the network. If at="pixels" (the default), the result is a pixel image on the linear network (class "linim") which can be plotted. If at="points" the result is a numeric vector giving the density estimates at the data points of x.

The smoothing operation is equivalent to the "equal-split continuous" rule described in Section 9.2.3 of Okabe and Sugihara (2012). However, the actual computation is performed rapidly, by solving the classical time-dependent heat equation on the network, as described in McSwiggan et al (2016). Computational time is short, but increases quadratically with sigma.

If at="points" and leaveoneout=TRUE, a leave-one-out estimate is computed at each data point (that is, the estimate at each data point x[i] is based on all of the points except x[i]) using the truncated series approximation of McSwiggan et al (2019).

The argument sigma specifies the smoothing bandwidth. If sigma is missing or NULL, the default is one-eighth of the length of the shortest side of the bounding box of x. If sigma is a function in the R language, it is assumed to be a bandwidth selection rule, and it will be applied to x to compute the bandwidth value.

Value

If at="pixels" (the default), a pixel image on the linear network (object of class "linim").

If at="points", a numeric vector with one entry for each point of x.

Infinite bandwidth

If sigma=Inf, the resulting density estimate is constant over all locations, and is equal to the average density of points per unit length. (If the network is not connected, then this rule is applied separately to each connected component of the network).

Discretisation and Error Messages

The computation is performed by discretising the network. Accuracy of the result can be increased by using a finer discretisation, at the cost of slower computation.

The simplest way to increase accuracy is to specify the argument dx which controls the spacing between sample points on the network. However, specifying a very small value of dx may result in an error, because it implies a very large number of sample points or a very large number of iterations.

If dx is not specified, then it will be determined by other arguments according to a set of rules. The argument finespacing determines which rule will be applied.

- If finespacing=TRUE (the default), then the sample points will be chosen to ensure sufficient accuracy along every segment of the network. The sample point spacing dx must not exceed one-third of the length of the shortest segment of the network. The default value of dx is smaller than this. This ensures that the discrete approximation is accurate along every segment, no matter how short the segment is. However, this may not be feasible if it implies a very large number of sample points, or a large number of iterations: in such cases, the code

may terminate with an error about illegal values of dx, dt or iterMax. The user may increase the value of iterMax to relax this constraint.

- If finespacing=FALSE, then the sample points will be chosen to ensure adequate accuracy at every pixel in the default pixellation of the window of x. The default spacing of sample points dx will be about one-half the width of a pixel. This is usually a much coarser resolution than the one selected by finespacing=TRUE. If it is too coarse, the pixel resolution can be refined by specifying one of the arguments dimyx, eps or xy which are passed to as.mask. For example, dimyx=512 would specify a 512 x 512 pixel grid and would increase accuracy relative to the default 128 x 128 grid. The default pixel resolution can be changed for the remainder of the R session by spatstat.options('npixel').

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Greg McSwiggan.

References

McSwiggan, G., Baddeley, A. and Nair, G. (2016) Kernel density estimation on a linear network. *Scandinavian Journal of Statistics* **44**, 324–345.

McSwiggan, G., Baddeley, A. and Nair, G. (2019) Estimation of relative risk for events on a linear network. *Statistics and Computing* **30**, 469–484.

Okabe, A. and Sugihara, K. (2012) *Spatial analysis along networks*. Wiley.

See Also

density.lpp

Examples

```
X <- runiflpp(3, simplenet)
D <- densityHeat(X, 0.2)
plot(D, style="w", main="", adjust=2)
densityHeat.lpp(X, 0.2, at="points")
Dw <- densityHeat(X, 0.2, weights=c(1,2,-1))
```

---

densityQuick.lpp *Kernel Estimation of Intensity on a Network using a 2D Kernel*

Description

Estimates the intensity of a point process on a linear network using a two-dimensional smoothing kernel.

Usage

```
densityQuick.lpp(x, sigma=NULL, ...,
         kernel="gaussian",
         at = c("pixels", "points"),
         what = c("estimate", "se", "var"),
         leaveoneout = TRUE,
         diggle = FALSE,
         edge2D = FALSE,
         weights = NULL,
         positive = FALSE)
```

Arguments

x	Point pattern on a linear network (object of class "lpp").
sigma	Smoothing bandwidth. A single numeric value, in the same units as the coordinates of x. Alternatively sigma may be a function which selects a bandwidth when applied to x, for example, bw.scott.iso or bw.lppl. There is a sensible default.
...	Additional arguments passed to as.mask to determine the pixel resolution, or arguments passed to sigma if it is a function.
kernel	String (partially matched) specifying the smoothing kernel. Current options are "gaussian", "epanechnikov", "quartic" or "disc".
at	String (partially matched) specifying whether to compute the intensity values at a fine grid of locations on the network (at="pixels", the default) or only at the points of x (at="points").
what	String (partially matched) specifying whether to calculate the intensity estimate, or its estimated standard error, or its estimated variance.
leaveoneout	Logical value indicating whether to compute a leave-one-out estimator. Applicable only when at="points".
diggle	Logical value specifying whether to use the 'Diggle' correction.
edge2D	Logical value specifying whether to apply the usual two-dimensional edge correction procedure to the numerator and denominator of the estimate.
weights	Optional weights to be attached to the points. A numeric vector, an expression, or a pixel image.
positive	Logical value indicating whether to force the resulting values to be positive. Default is FALSE for the sake of speed.

Details

Kernel smoothing is applied to the points of x using a two-dimensional Gaussian kernel, as described in Rakshit et al (2019). The result is a pixel image on the linear network (class "linim") which can be plotted.

Other techniques for kernel smoothing on a network are implemented in density.lpp. The main advantages of using a two-dimensional kernel are very fast computation and insensitivity to changes

in the network geometry. The main disadvantage is that it ignores the connectivity of the network. See Rakshit et al (2019) for further explanation.

The argument `sigma` specifies the smoothing bandwidth. If `sigma` is missing or `NULL`, the default is one-eighth of the length of the shortest side of the bounding box of `x`. If `sigma` is a function in the R language, it is assumed to be a bandwidth selection rule, and it will be applied to `x` to compute the bandwidth value.

Value

If `at="pixels"` (the default), a pixel image on the linear network (object of class `"linim"`).

If `at="points"`, a numeric vector with one entry for each point of `x`.

Infinite bandwidth

If `sigma=Inf`, the resulting density estimate is constant over all locations, and is equal to the average density of points per unit length. (If the network is not connected, then this rule is applied separately to each connected component of the network).

Author(s)

Adrian Baddeley, Suman Rakshit and Tilman Davies

References

Rakshit, S., Davies, T., Moradi, M., McSwiggan, G., Nair, G., Mateu, J. and Baddeley, A. (2019) Fast kernel smoothing of point patterns on a large network using 2D convolution. *International Statistical Review* **87** (3) 531–556. DOI: 10.1111/insr.12327.

See Also

`density.lpp`, the main function for density estimation on a network.

`bw.scott`, `bw.scott.iso`, `bw.lppl`for bandwidth selection.

Examples

```
X <- unmark(chicago)
plot(densityQuick.lpp(X, 500))
plot(densityQuick.lpp(X, 500, diggle=TRUE))
plot(densityQuick.lpp(X, bw.scott.iso))
plot(densityQuick.lpp(X, 500, what="se"))
```

densityVoronoi.lpp *Intensity Estimate of Point Pattern on Linear Network Using Voronoi-Dirichlet Tessellation*

Description

Computes an adaptive estimate of the intensity function of a point pattern on a linear network, using the Dirichlet-Voronoi tessellation on the network.

Usage

```
## S3 method for class 'lpp'
densityVoronoi(X, f = 1, ...,
               metric=c("shortestpath", "Euclidean"),
               nrep = 1, verbose = TRUE)
```

Arguments

X	Point pattern on a linear network (object of class "lpp").
f	Fraction (between 0 and 1 inclusive) of the data points that will be used to build a tessellation for the intensity estimate.
...	Arguments passed to linim determining the pixel resolution of the result.
metric	Character string (partially matched) specifying the distance metric used to define the Dirichlet tessellation. Argument passed to lineardirichlet.
nrep	Number of independent repetitions of the randomised procedure.
verbose	Logical value indicating whether to print progress reports.

Details

This function is an alternative to density.lpp. It computes an estimate of the intensity function of a point pattern dataset on a linear network. The result is a pixel image on the network, giving the estimated intensity.

This function is a method for the generic densityVoronoi for the class "lpp" of point patterns on a linear network.

If f=1 (the default), the Voronoi estimate (Barr and Schoenberg, 2010) is computed: the point pattern X is used to construct a Voronoi/Dirichlet tessellation on the network (see lineardirichlet); the lengths of the Dirichlet tiles are computed; the estimated intensity in each tile is the reciprocal of the tile length. The result is a pixel image of intensity estimates which are constant on each tile of the tessellation.

If f=0, the intensity estimate at every location is equal to the average intensity (number of points divided by network length). The result is a pixel image of intensity estimates which are constant.

If f is strictly between 0 and 1, the smoothed Voronoi estimate (Moradi et al, 2019) is computed. The dataset X is randomly thinned by deleting or retaining each point independently, with probability f of retaining a point. The thinned pattern is used to construct a Dirichlet tessellation and form the

Voronoi estimate, which is then adjusted by a factor `1/f`. This procedure is repeated `nrep` times and the results are averaged to obtain the smoothed Voronoi estimate.

The value `f` can be chosen automatically by bandwidth selection using `bw.voronoi`.

Value

Pixel image on a linear network (object of class `"linim"`).

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk> and Mehdi Moradi <m2.moradi@yahoo.com>.

References

Moradi, M., Cronie, 0., Rubak, E., Lachieze-Rey, R., Mateu, J. and Baddeley, A. (2019) Resample-smoothing of Voronoi intensity estimators. *Statistics and Computing* **29** (5) 995–1010.

See Also

`densityVoronoi` is the generic, with a method for class `"ppp"`.

`lineardirichlet` computes the Dirichlet-Voronoi tessellation on a network.

`bw.voronoi` performs bandwidth selection of the fraction `f`.

See also `density.lpp`.

Examples

```
if(interactive()) {
  X <- spiders
  nr <- 100
} else {
  X <- runiflpp(10, simplenet)
  nr <- 3
}
plot(densityVoronoi(X))
plot(densityVoronoi(X, 0.1, nrep=nr))
plot(densityVoronoi(X, metric="E"))
plot(dirichlet(as.ppp(X)), add=TRUE, lty=2)
```

---

diagnose.lppm *Diagnostic Plots for Fitted Point Process Model on a Linear Network*

Description

Given a point process model fitted to a point pattern on a linear network, produce diagnostic plots based on residuals.

Usage

```
  ## S3 method for class 'lppm'
diagnose(object, ..., type="raw", which="all", sigma=NULL,
               cumulative=TRUE,
               plot.it=TRUE, rv = NULL,
               compute.sd=is.poisson(object), compute.cts=TRUE,
               envelope=FALSE, nsim=39, nrank=1,
               typename,  oldstyle=FALSE, splineargs=list(spar=0.5))

  ## S3 method for class 'diaglppm'
plot(x, ..., which,
               plot.neg=c("image", "discrete"),
               plot.smooth=c("image", "persp"),
               plot.sd, spacing=0.1, outer=3,
               srange=NULL, monochrome=FALSE, main=NULL)
```

Arguments

object	The fitted point process model (an object of class "lppm") for which diagnostics should be produced. This object is usually obtained from lppm.
type	String indicating the type of residuals or weights to be used. Current options are "eem" for the Stoyan-Grabarnik exponential energy weights, "raw" for the raw residuals, "inverse" for the inverse-lambda residuals, and "pearson" for the Pearson residuals. A partial match is adequate.
which	Character string or vector indicating the choice(s) of plots to be generated. Options are "all", "marks", "smooth", "x", "y" and "sum". Multiple choices may be given but must be matched exactly. See Details.
sigma	Bandwidth for kernel smoother in "smooth" option.
cumulative	Logical flag indicating whether the lurking variable plots for the x and y coordinates will be the plots of cumulative sums of marks (cumulative=TRUE) or the plots of marginal integrals of the smoothed residual field (cumulative=FALSE).
plot.it	Logical value indicating whether plots should be shown. If plot.it=FALSE, the computed diagnostic quantities are returned without plotting them.
plot.neg	String indicating how the density part of the residual measure should be plotted.
plot.smooth	String indicating how the smoothed residual field should be plotted.
compute.sd, plot.sd	Logical values indicating whether error bounds should be computed and added to the "x" and "y" plots. The default is TRUE for Poisson models and FALSE for non-Poisson models. See Details.
envelope, nsim, nrank	Arguments passed to envelope.lppm in order to plot simulation envelopes for the lurking variable plots.
rv	Usually absent. Advanced use only. If this argument is present, the values of the residuals will not be calculated from the fitted model object but will instead be taken directly from rv.

spacing	The spacing between plot panels (when a four-panel plot is generated) expressed as a fraction of the width of the window of the point pattern.
outer	The distance from the outermost line of text to the nearest plot panel, expressed as a multiple of the spacing between plot panels.
srange	Vector of length 2 that will be taken as giving the range of values of the smoothed residual field, when generating an image plot of this field. This is useful if you want to generate diagnostic plots for two different fitted models using the same colour map.
monochrome	Flag indicating whether images should be displayed in greyscale (suitable for publication) or in colour (suitable for the screen). The default is to display in colour.
oldstyle	Logical flag indicating whether error bounds should be plotted using the approximation given in the original paper (`oldstyle=TRUE`), or using the correct asymptotic formula (`oldstyle=FALSE`).
splineargs	Argument passed to `smooth.spline` to control the smoothing in the lurking variable plot.
x	The value returned from a previous call to `diagnose.lppm`. An object of class `"diaglppm"`.
typename	String to be used as the name of the residuals.
main	Main title for the plot.
...	Extra arguments, controlling either the resolution of the smoothed image (passed from `diagnose.lppm` to `density.lpp`) or the appearance of the plots (passed from `diagnose.lppm` to `plot.diaglppm` and from `plot.diaglppm` to `plot.default`).
compute.cts	Advanced use only.

Details

The function `diagnose.lppm` generates several diagnostic plots for a fitted point process model. The plots display the residuals from the fitted model (Baddeley et al, 2005) or alternatively the 'exponential energy marks' (Stoyan and Grabarnik, 1991). These plots can be used to assess goodness-of-fit, to identify outliers in the data, and to reveal departures from the fitted model.

The function `diagnose` is generic, with a method for class `"lppm"` which is documented in this page.

The argument `object` must be a fitted point process model (object of class `"lppm"`) typically produced by the maximum pseudolikelihood fitting algorithm `lppm`).

The argument `type` selects the type of residual or weight that will be computed. Current options are:

`"eem"`: exponential energy marks (Stoyan and Grabarnik, 1991) computed by `eem.lppm`. These are positive weights attached to the data points (i.e. the points of the point pattern dataset to which the model was fitted). If the fitted model is correct, then the sum of these weights for all data points in a spatial region B has expected value equal to the area of B. See `eem.lppm` for further explanation.

`"raw"`, `"inverse"` **or** `"pearson"`**:** point process residuals (Baddeley et al, 2005) computed by the function `residuals.lppm`. These are residuals attached both to the data points and to some other points in the window of observation (namely, to the dummy points of the quadrature scheme used to fit the model). If the fitted model is correct, then the sum of the residuals in a spatial region B has mean zero. The options are

- `"raw"`: the raw residuals;
- `"inverse"`: the 'inverse-lambda' residuals, a counterpart of the exponential energy weights;
- `"pearson"`: the Pearson residuals.

See `residuals.lppm` for further explanation.

The argument `which` selects the type of plot that is produced. Options are:

`"marks"`**:** plot the residual measure. For the exponential energy weights (`type="eem"`) this displays circles centred at the points of the data pattern, with radii proportional to the exponential energy weights. For the residuals (`type="raw"`, `type="inverse"` or `type="pearson"`) this again displays circles centred at the points of the data pattern with radii proportional to the (positive) residuals, while the plotting of the negative residuals depends on the argument `plot.neg`. If `plot.neg="image"` then the negative part of the residual measure, which is a density, is plotted as a colour image. If `plot.neg="discrete"` then the discretised negative residuals (obtained by approximately integrating the negative density using the quadrature scheme of the fitted model) are plotted as squares centred at the dummy points with side lengths proportional to the (negative) residuals. [To control the size of the circles and squares, use the argument `maxsize`.]

`"smooth"`**:** plot a kernel-smoothed version of the residual measure. Each data or dummy point is taken to have a 'mass' equal to its residual or exponential energy weight. (Note that residuals can be negative). This point mass is then replaced by a bivariate isotropic Gaussian density with standard deviation `sigma`. The value of the smoothed residual field at any point in the window is the sum of these weighted densities. If the fitted model is correct, this smoothed field should be flat, and its height should be close to 0 (for the residuals) or 1 (for the exponential energy weights). The field is plotted either as an image, contour plot or perspective view of a surface, according to the argument `plot.smooth`. The range of values of the smoothed field is printed if the option `which="sum"` is also selected.

`"x"`**:** produce a 'lurking variable' plot for the x coordinate. This is a plot of $h(x)$ against x (solid lines) and of $E(h(x))$ against x (dashed lines), where $h(x)$ is defined below, and $E(h(x))$ denotes the expectation of $h(x)$ assuming the fitted model is true.

- if `cumulative=TRUE` then $h(x)$ is the cumulative sum of the weights or residuals for all points which have X coordinate less than or equal to x. For the residuals $E(h(x)) = 0$, and for the exponential energy weights $E(h(x))$ = area of the subset of the window to the left of the line $X = x$.
- if `cumulative=FALSE` then $h(x)$ is the marginal integral of the smoothed residual field (see the case `which="smooth"` described above) on the x axis. This is approximately the derivative of the plot for `cumulative=TRUE`. The value of $h(x)$ is computed by summing the values of the smoothed residual field over all pixels with the given x coordinate. For the residuals $E(h(x)) = 0$, and for the exponential energy weights $E(h(x))$ = length of the intersection between the observation window and the line $X = x$.

If `plot.sd = TRUE`, then superimposed on the lurking variable plot are the pointwise two-standard-deviation error limits for $h(x)$ calculated for the inhomogeneous Poisson process.

The default is plot.sd = TRUE for Poisson models and plot.sd = FALSE for non-Poisson models.

"y": produce a similar lurking variable plot for the y coordinate.

"sum": print the sum of the weights or residuals for all points in the window (clipped by a margin rbord if required) and the area of the same window. If the fitted model is correct the sum of the exponential energy weights should equal the area of the window, while the sum of the residuals should equal zero. Also print the range of values of the smoothed field displayed in the "smooth" case.

"all": All four of the diagnostic plots listed above are plotted together in a two-by-two display. Top left panel is "marks" plot. Bottom right panel is "smooth" plot. Bottom left panel is "x" plot. Top right panel is "y" plot, rotated 90 degrees.

The argument rbord ensures there are no edge effects in the computation of the residuals. The diagnostic calculations will be confined to those points of the data pattern which are at least rbord units away from the edge of the window. The value of rbord should be greater than or equal to the range of interaction permitted in the model.

By default, the two-standard-deviation limits are calculated from the exact formula for the asymptotic variance of the residuals under the asymptotic normal approximation, equation (37) of Baddeley et al (2006). However, for compatibility with the original paper of Baddeley et al (2005), if oldstyle=TRUE, the two-standard-deviation limits are calculated using the innovation variance, an over-estimate of the true variance of the residuals. (However, see the section about Replicated Data).

The argument rv would normally be used only by experts. It enables the user to substitute arbitrary values for the residuals or marks, overriding the usual calculations. If rv is present, then instead of calculating the residuals from the fitted model, the algorithm takes the residuals from the object rv, and plots them in the manner appropriate to the type of residual or mark selected by type. If type ="eem" then rv should be similar to the return value of eem.lppm, namely, a numeric vector of length equal to the number of points in the original data point pattern. Otherwise, rv should be similar to the return value of residuals.lppm, that is, it should be an object of class "msr" (see msr) representing a signed measure.

The return value of diagnose.lppm is an object of class "diaglppm". The plot method for this class is documented here. There is also a print method. See the Examples.

In plot.diaglppm, if a four-panel diagnostic plot is produced (the default), then the extra arguments xlab, ylab, rlab determine the text labels for the x and y coordinates and the residuals, respectively. The undocumented arguments col.neg and col.smooth control the colour maps used in the top left and bottom right panels respectively.

Value

An object of class "diaglppm" which contains the coordinates needed to reproduce the selected plots. This object can be plotted using plot.diaglppm and printed using print.diaglppm.

Replicated Data

Note that if object is a model that was obtained by first fitting a model to replicated point pattern data using mppm and then using subfits to extract a model for one of the individual point patterns, then the variance calculations are only implemented for the innovation variance (oldstyle=TRUE) and this is the default in such cases.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

References

Baddeley, A., Turner, R., Møller, J. and Hazelton, M. (2005) Residual analysis for spatial point processes. *Journal of the Royal Statistical Society, Series B* **67**, 617–666.

Baddeley, A., Møller, J. and Pakes, A.G. (2008) Properties of residuals for spatial point processes. *Annals of the Institute of Statistical Mathematics* **60**, 627–649.

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See Also

residuals.lppm, eem.lppm, lppm, lurking.lppm.

Examples

```
if(interactive()) {
  X <- unmark(chicago)
} else {
  g <- function(x, y, seg, tp) { exp(x + 3*y) }
  lambda <- linfun(g, simplenet)
  X <- rpoislpp(lambda)
}
fit <- lppm(X ~ x + y)
diagnose(fit)

diagnose(fit, type="pearson")


diagnose(fit, which="marks")

diagnose(fit, type="raw", plot.neg="discrete")

diagnose(fit, type="pearson", which="smooth")

# save the diagnostics and plot them later
u <- diagnose(fit, plot.it=FALSE)
if(interactive()) {
  plot(u)
  plot(u, which="marks")
}
```

diameter.linnet *Diameter and Bounding Radius of a Linear Network*

Description

Compute the diameter or bounding radius of a linear network measured using the shortest path distance.

Usage

```
## S3 method for class 'linnet'
diameter(x)

## S3 method for class 'linnet'
boundingradius(x, ...)
```

Arguments

x	Linear network (object of class "linnet").
...	Ignored.

Details

The diameter of a linear network (in the shortest path distance) is the maximum value of the shortest-path distance between any two points u and v on the network.

The bounding radius of a linear network (in the shortest path distance) is the minimum value, over all points u on the network, of the maximum shortest-path distance from u to another point v on the network.

The functions boundingradius and diameter are generic; the functions boundingradius.linnet and diameter.linnet are the methods for objects of class linnet.

Value

A single numeric value.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

See Also

boundingradius, diameter, linnet

Examples

```
diameter(simplenet)
boundingradius(simplenet)
```

distbdry.lpp *Distance To Boundary in a Linear Network*

Description

For a point pattern on a linear network, compute the distance from each point to the nearest terminal vertex of the network.

Usage

```
## S3 method for class 'lpp'
distbdry(X)
```

Arguments

X	A point pattern on a linear network (class "lpp").

Details

This function computes the distance from each data point X[i] to the nearest terminal vertex of the network. A terminal vertex is a vertex which is the endpoint of exactly one segment of the network. Distance is measured by the length of the shortest path in the network.

The function distbdry is generic, with methods for class "ppp", "pp3", "lpp" and other classes.

Value

A numeric vector with one entry for each point of X.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

distbdry

Examples

```
X <- if(interactive()) chicago else spiders
b <- distbdry(X)
plot(X %mark% b, main=expression(distbdry(X)),
     pch=16, size=1, cols=topo.colors(128))
L <- domain(X)
V <- vertices(L)
d <- vertexdegree(L)
Terminal <- V[d == 1]
points(Terminal, pch=2, col="red")
```

distfun.lpp *Distance Map on Linear Network*

Description

Compute the distance function of a point pattern on a linear network.

Usage

```
  ## S3 method for class 'lpp'
distfun(X, ..., k=1)
```

Arguments

X	A point pattern on a linear network (object of class "lpp").
k	An integer. The distance to the kth nearest point will be computed.
...	Extra arguments are ignored.

Details

On a linear network L, the "geodesic distance function" of a set of points A in L is the mathematical function f such that, for any location s on L, the function value f(s) is the shortest-path distance from s to A.

The command distfun.lpp is a method for the generic command distfun for the class "lpp" of point patterns on a linear network.

If X is a point pattern on a linear network, f <- distfun(X) returns a *function* in the R language that represents the distance function of X. Evaluating the function f in the form v <- f(x,y), where x and y are any numeric vectors of equal length containing coordinates of spatial locations, yields the values of the distance function at these locations. More efficiently f can be called in the form v <- f(x, y, seg, tp) where seg and tp are the local coordinates on the network. It can also be called as v <- f(x) where x is a point pattern on the same linear network.

The function f obtained from f <- distfun(X) also belongs to the class "linfun". It can be printed and plotted immediately as shown in the Examples. It can be converted to a pixel image using as.linim.

Value

A function with arguments x,y and optional arguments seg,tp. It also belongs to the class "linfun" which has methods for plot, print etc.

Distance values

The values returned by the distance function f <- distfun(X) are distances, expressed as multiples of the unit of length of the spatial coordinates in X. The unit of length is given by unitname(X).

Note that, if the unit of length in X is a composite expression such as '2 microns', then the values of f are expressed as multiples of 2 microns, rather than being expressed in microns.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

linfun, methods.linfun.

To identify *which* point is the nearest neighbour, see nnfun.lpp.

Examples

```
X <- runiflpp(3, simplenet)
f <- distfun(X)
f
plot(f)

# using a distfun as a covariate in a point process model:
Y <- runiflpp(4, simplenet)
fit <- lppm(Y ~D, covariates=list(D=f))

f(Y)
```

---

distmap.lpp *Distance Map of Point Pattern on Linear Network*

Description

Computes the distance from each pixel to the nearest point in the given point pattern on a linear network.

Usage

```
  ## S3 method for class 'lpp'
distmap(X, ..., k=1)
```

Arguments

X	A point pattern on a linear network (object of class "lpp").
k	Integer. The distance to the k-th nearest data point will be computed.
...	Arguments passed to as.linim.linfun to control pixel resolution.

Details

This is a method for the generic function distmap. It computes the distance map of the point pattern X as a pixel image on the network.

At a pixel u, the greyscale value equals the distance from u to the nearest point of the pattern X (or the k-th nearest point of X).

Value

A pixel image on the network (object of class "linim") whose greyscale values are the values of the distance map.

Distance values

The pixel values in the image distmap(X) are distances, expressed as multiples of the unit of length of the spatial coordinates in X. The unit of length is given by unitname(X).

Note that, if the unit of length in X is a composite expression such as '2 microns', then the values in distmap(X) are expressed as multiples of 2 microns, rather than being expressed in microns.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

Generic function distmap and methods.

Examples

```
plot(distmap(spiders))
```

---

divide.linnet *Divide Linear Network at Cut Points*

Description

Make a tessellation of a linear network by dividing it into pieces demarcated by the points of a point pattern.

Usage

```
divide.linnet(X)
```

Arguments

X	Point pattern on a linear network (object of class "lpp").

Details

The points X are interpreted as dividing the linear network L=as.linnet(X) into separate pieces.

Two locations on L belong to the same piece if and only if they can be joined by a path in L that does not cross any of the points of X.

The result is a tessellation of the network (object of class "lintess") representing the division of L into pieces.

Value

A tessellation on a linear network (object of class "lintess").

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk> and Greg McSwiggan.

See Also

linnet, lintess.

Examples

```
X <- runiflpp(5, simplenet)
plot(divide.linnet(X))
plot(X, add=TRUE, pch=16, show.network=FALSE)
```

---

domain.lpp *Extract the Linear Network on which Spatial Data are Defined*

Description

Given a spatial object representing data on a linear network, extract the network.

Usage

```
 ## S3 method for class 'lpp'
domain(X, ...)

 ## S3 method for class 'lppm'
domain(X, ...)

 ## S3 method for class 'linfun'
domain(X, ...)

 ## S3 method for class 'lintess'
domain(X, ...)
```

Arguments

X	A spatial object representing data on a linear network. An object of class "lpp", "lppm", "linfun" or "lintess".
...	Extra arguments. They are ignored by all the methods listed here.

Details

The function domain is generic, with methods for many classes.

For a spatial object X domain(X) extracts the spatial domain in which X is defined.

For a two-dimensional object X, typically domain(X) is the same as Window(X).

The exception is that, if X is a point pattern on a linear network (class "lpp") or a point process model on a linear network (class "lppm"), then domain(X) is the linear network on which the points lie, while Window(X) is the two-dimensional window containing the linear network.

Value

A linear network (object of class "linnet").

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

domain, domain.rmhmodel, domain.ppm.

Window, Frame

Examples

```
domain(chicago)
```

---

eem.lppm *Exponential Energy Marks on a Linear Network*

Description

Given a point process model fitted to a point pattern on a linear network, compute the Stoyan-Grabarnik diagnostic "exponential energy marks" for the data points.

Usage

```
## S3 method for class 'lppm'
eem(fit, ...)
```

Arguments

fit	The fitted point process model. An object of class "lppm".
...	Ignored.

Details

Stoyan and Grabarnik (1991) proposed a diagnostic tool for point process models fitted to spatial point pattern data. Each point x_i of the data pattern X is given a 'mark' or 'weight'

$$m_i = \frac{1}{\hat{\lambda}(x_i, X)}$$

where $\hat{\lambda}(x_i, X)$ is the conditional intensity of the fitted model. If the fitted model is correct, then the sum of these marks for all points in a region B has expected value equal to the area of B.

The function `eem` is generic, with methods for various classes of models. This page documents the method `eem.lppm` for the class `"lppm"`.

The argument `fit` must be a fitted point process model on a linear network (object of class `"lppm"`). Such objects are produced by the fitting algorithm `lppm`). This fitted model object contains complete information about the original data pattern and the model that was fitted to it.

The value returned by `eem` is the vector of weights $m[i]$ associated with the points $x[i]$ of the original data pattern. The original data pattern (in corresponding order) can be extracted from `fit` using `response.lppm`.

The function `diagnose.lppm` produces a set of sensible diagnostic plots based on these weights.

Value

A vector containing the values of the exponential energy mark for each point in the pattern.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

References

Stoyan, D. and Grabarnik, P. (1991) Second-order characteristics for stochastic structures connected with Gibbs point processes. *Mathematische Nachrichten*, 151:95–100.

See Also

`diagnose.ppm`, `residuals.lppm`, `lppm`

Examples

```
fit <- lppm(spiders ~ x + y)
ee <- eem(fit)
sum(ee)/volume(domain(spiders)) # should be about 1 if model is correct
```

envelope.lpp *Envelope for Point Patterns on Linear Network*

Description

Enables envelopes to be computed for point patterns on a linear network.

Usage

```
  ## S3 method for class 'lpp'
envelope(Y, fun=linearK, nsim=99, nrank=1, ...,
  funargs=list(), funYargs=funargs,
  simulate=NULL, fix.n=FALSE, fix.marks=FALSE, verbose=TRUE,
  transform=NULL,global=FALSE,ginterval=NULL,
  use.theory=NULL, theoryfun=NULL,
  alternative=c("two.sided", "less", "greater"),
  scale=NULL, clamp=FALSE,
  savefuns=FALSE, savepatterns=FALSE,
  nsim2=nsim, VARIANCE=FALSE, nSD=2, Yname=NULL,
  maxnerr=nsim, rejectNA=FALSE, silent=FALSE,
  do.pwrong=FALSE, envir.simul=NULL)


  ## S3 method for class 'lppm'
envelope(Y, fun=linearK, nsim=99, nrank=1, ...,
  funargs=list(), funYargs=funargs,
  simulate=NULL, fix.n=FALSE, fix.marks=FALSE, verbose=TRUE,
  transform=NULL,global=FALSE,ginterval=NULL,
  use.theory=NULL, theoryfun=NULL,
  alternative=c("two.sided", "less", "greater"),
  scale=NULL, clamp=FALSE,
  savefuns=FALSE, savepatterns=FALSE,
  nsim2=nsim, VARIANCE=FALSE, nSD=2, Yname=NULL,
  maxnerr=nsim, rejectNA=FALSE, silent=FALSE,
  do.pwrong=FALSE, envir.simul=NULL)
```

Arguments

Y	A point pattern on a linear network (object of class "lpp") or a fitted point process model on a linear network (object of class "lppm").
fun	Function that is to be computed for each simulated pattern.
nsim	Number of simulations to perform.
nrank	Integer. Rank of the envelope value amongst the nsim simulated values. A rank of 1 means that the minimum and maximum simulated values will be used.
...	Extra arguments passed to fun.

funargs	A list, containing extra arguments to be passed to fun.
funYargs	Optional. A list, containing extra arguments to be passed to fun when applied to the original data Y only.
simulate	Optional. Specifies how to generate the simulated point patterns. If simulate is an expression in the R language, then this expression will be evaluated nsim times, to obtain nsim point patterns which are taken as the simulated patterns from which the envelopes are computed. If simulate is a function, then this function will be repeatedly applied to the data pattern Y to obtain nsim simulated patterns. If simulate is a list of point patterns, then the entries in this list will be treated as the simulated patterns from which the envelopes are computed. Alternatively simulate may be an object produced by the envelope command: see Details.
fix.n	Logical. If TRUE, simulated patterns will have the same number of points as the original data pattern.
fix.marks	Logical. If TRUE, simulated patterns will have the same number of points *and* the same marks as the original data pattern. In a multitype point pattern this means that the simulated patterns will have the same number of points *of each type* as the original data.
verbose	Logical flag indicating whether to print progress reports during the simulations.
transform	Optional. A transformation to be applied to the function values, before the envelopes are computed. An expression object (see Details).
global	Logical flag indicating whether envelopes should be pointwise (global=FALSE) or simultaneous (global=TRUE).
ginterval	Optional. A vector of length 2 specifying the interval of r values for the simultaneous critical envelopes. Only relevant if global=TRUE.
use.theory	Logical value indicating whether to use the theoretical value, computed by fun, as the reference value for simultaneous envelopes. Applicable only when global=TRUE.
theoryfun	Optional. A function(r) in the R language which calculates the theoretical or reference value of the summary function fun.
alternative	Character string determining whether the envelope corresponds to a two-sided test (side="two.sided", the default) or a one-sided test with a lower critical boundary (side="less") or a one-sided test with an upper critical boundary (side="greater").
scale	Optional. Scaling function for global envelopes. A function in the R language which determines the relative scale of deviations, as a function of distance r, when computing the global envelopes. Applicable only when global=TRUE. Summary function values for distance r will be *divided* by scale(r) before the maximum deviation is computed. The resulting global envelopes will have width proportional to scale(r).
clamp	Logical value indicating how to compute envelopes when alternative="less" or alternative="greater". Deviations of the observed summary function from the theoretical summary function are initially evaluated as signed real numbers, with large positive values indicating consistency with the alternative hypothesis. If clamp=FALSE (the default), these values are not changed. If clamp=TRUE, any negative values are replaced by zero.

savefuns	Logical flag indicating whether to save all the simulated function values.
savepatterns	Logical flag indicating whether to save all the simulated point patterns.
nsim2	Number of extra simulated point patterns to be generated if it is necessary to use simulation to estimate the theoretical mean of the summary function. Only relevant when global=TRUE and the simulations are not based on CSR.
VARIANCE	Logical. If TRUE, critical envelopes will be calculated as sample mean plus or minus nSD times sample standard deviation.
nSD	Number of estimated standard deviations used to determine the critical envelopes, if VARIANCE=TRUE.
Yname	Character string that should be used as the name of the data point pattern Y when printing or plotting the results.
maxnerr	Maximum number of rejected patterns. If fun yields a fatal error when applied to a simulated point pattern (for example, because the pattern is empty and fun requires at least one point), the pattern will be rejected and a new random point pattern will be generated. If this happens more than maxnerr times, the algorithm will give up.
rejectNA	Logical value specifying whether to reject a simulated pattern if the resulting values of fun are all equal to NA, NaN or infinite. If FALSE (the default), then simulated patterns are rejected only when fun gives a fatal error.
silent	Logical value specifying whether to print a report each time a simulated pattern is rejected.
do.pwrong	Logical. If TRUE, the algorithm will also estimate the true significance level of the "wrong" test (the test that declares the summary function for the data to be significant if it lies outside the *pointwise* critical boundary at any point). This estimate is printed when the result is printed.
envir.simul	Environment in which to evaluate the expression simulate, if not the current environment.

Details

This is a method for the generic function envelope applicable to point patterns on a linear network.

The argument Y can be either a point pattern on a linear network, or a fitted point process model on a linear network. The function fun will be evaluated for the data and also for nsim simulated point patterns on the same linear network. The upper and lower envelopes of these evaluated functions will be computed as described in envelope.

The type of simulation is determined as follows.

- if Y is a point pattern (object of class "lpp") and simulate is missing or NULL, then random point patterns will be generated according to a Poisson point process on the linear network on which Y is defined, with intensity estimated from Y.
- if Y is a fitted point process model (object of class "lppm") and simulate is missing or NULL, then random point patterns will be generated by simulating from the fitted model.
- If simulate is present, it specifies the type of simulation as explained below.

- If simulate is an expression (typically including a call to a random generator), then the expression will be repeatedly evaluated, and should yield random point patterns on the same linear network as Y.
- If simulate is a function (typically including a call to a random generator), then the function will be repeatedly applied to the original point pattern Y, and should yield random point patterns on the same linear network as Y.
- If simulate is a list of point patterns, then these will be taken as the simulated point patterns. They should be on the same linear network as Y.

The function fun should accept as its first argument a point pattern on a linear network (object of class "lpp") and should have another argument called r or a ... argument.

For further information, see the help for envelope.

Value

Function value table (object of class "fv") with additional information, as described in envelope.

Author(s)

Ang Qi Wei <aqw07398@hotmail.com> and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

References

Ang, Q.W. (2010) *Statistical methodology for events on a network*. Master's thesis, School of Mathematics and Statistics, University of Western Australia.

Ang, Q.W., Baddeley, A. and Nair, G. (2012) Geometrically corrected second-order analysis of events on a linear network, with applications to ecology and criminology. *Scandinavian Journal of Statistics* **39**, 591–617.

Okabe, A. and Yamada, I. (2001) The K-function method on a network and its computational implementation. *Geographical Analysis* **33**, 271-290.

See Also

envelope, linearK

Examples

```
if(interactive()) {
  ns <- 39
  np <- 40
} else { ns <- np <- 3 }
X <- runiflpp(np, simplenet)

# uniform Poisson: random numbers of points
envelope(X, nsim=ns)

# uniform Poisson: conditional on observed number of points
envelope(X, fix.n=TRUE, nsim=ns)
```

```
# nonuniform Poisson
fit <- lppm(X ~x)
envelope(fit, nsim=ns)

#multitype
marks(X) <- sample(letters[1:2], np, replace=TRUE)
envelope(X, nsim=ns)
```

`eval.linim` *Evaluate Expression Involving Pixel Images on Linear Network*

Description

Evaluates any expression involving one or more pixel images on a linear network, and returns a pixel image on the same linear network.

Usage

```
eval.linim(expr, envir, harmonize=TRUE, warn=TRUE)
```

Arguments

`expr`	An expression in the R language, involving the names of objects of class `"linim"`.
`envir`	Optional. The environment in which to evaluate the expression.
`harmonize`	Logical. Whether to resolve inconsistencies between the pixel grids.
`warn`	Logical. Whether to issue a warning if the pixel grids were inconsistent.

Details

This function a wrapper to make it easier to perform pixel-by-pixel calculations. It is one of several functions whose names begin with `eval` which work on objects of different types. This particular function is designed to work with objects of class `"linim"` which represent pixel images on a linear network.

Suppose `X` is a pixel image on a linear network (object of class `"linim"`. Then `eval.linim(X+3)` will add 3 to the value of every pixel in `X`, and return the resulting pixel image on the same linear network.

Suppose `X` and `Y` are two pixel images on the same linear network, with compatible pixel dimensions. Then `eval.linim(X + Y)` will add the corresponding pixel values in `X` and `Y`, and return the resulting pixel image on the same linear network.

In general, `expr` can be any expression in the R language involving (a) the *names* of pixel images, (b) scalar constants, and (c) functions which are vectorised. See the Examples.

First `eval.linim` determines which of the *variable names* in the expression `expr` refer to pixel images. Each such name is replaced by a matrix containing the pixel values. The expression is then evaluated. The result should be a matrix; it is taken as the matrix of pixel values.

The expression `expr` must be vectorised. There must be at least one linear pixel image in the expression.

All images must have compatible dimensions. If harmonize=FALSE, images that are incompatible will cause an error. If harmonize=TRUE, images that have incompatible dimensions will be resampled so that they are compatible; if warn=TRUE, a warning will be issued.

Value

An image object of class "linim".

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Rolf Turner <rolfturner@posteo.net>

See Also

eval.im, linim

Examples

```
M <- psp2mask(as.psp(simplenet))
Z <- as.im(function(x,y) {x-y}, W=M)
X <- linim(simplenet, Z)
X

Y <- linfun(function(x,y,seg,tp){y^2+x}, simplenet)
Y <- as.linim(Y)

eval.linim(X + 3)
eval.linim(X - Y)
eval.linim(abs(X - Y))
Z <- eval.linim(sin(X * pi) + Y)
```

Extract.linim *Extract Subset of Pixel Image on Linear Network*

Description

Extract a subset of a pixel image on a linear network.

Usage

```
  ## S3 method for class 'linim'
x[i, ..., drop=TRUE]
```

Arguments

x	A pixel image on a linear network (object of class "linim").
i	Spatial window defining the subregion. Either a spatial window (an object of class "owin"), or a logical-valued pixel image, or any type of index that applies to a matrix, or a point pattern (an object of class "lpp" or "ppp"), or something that can be converted to a point pattern by as.lpp (using the network on which x is defined).
...	Additional arguments passed to [.im.
drop	Logical value indicating whether NA values should be omitted from the result.

Details

This function is a method for the subset operator "[" for pixel images on linear networks (objects of class "linim").

The pixel image x will be restricted to the domain specified by i.

Pixels outside the domain of x are assigned the value NA; if drop=TRUE (the default) such NA values are deleted from the result; if drop=FALSE, then NA values are retained.

If i is a window (or a logical-valued pixel image) then x[i] is another pixel image of class "linim", representing the restriction of x to the spatial domain specified by i.

If i is a point pattern, then x[i] is the vector of pixel values of x at the locations specified by i.

Value

Another pixel image on a linear network (object of class "linim") or a vector of pixel values.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

See Also

thinNetwork to extract the data lying on selected edges of the network.

linim to make a pixel image on a network.

Examples

```
M <- psp2mask(as.psp(simplenet))
Z <- as.im(function(x,y){x}, W=M)
Y <- linim(simplenet, Z)
X <- runiflpp(4, simplenet)
Y[X]
Y[square(c(0.3, 0.6))]
```

`Extract.linnet` *Extract Subset of Linear Network*

Description

Extract a subset of a linear network.

Usage

```
  ## S3 method for class 'linnet'
x[i, ..., snip=TRUE]
```

Arguments

`x`	A linear network (object of class `"linnet"`).
`i`	Spatial window defining the subregion. An object of class `"owin"`.
`snip`	Logical. If `TRUE` (the default), segments of `x` which cross the boundary of `i` will be cut by the boundary. If `FALSE`, these segments will be deleted.
`...`	Ignored.

Details

This function computes the intersection between the linear network `x` and the domain specified by `i`.

This function is a method for the subset operator `"["` for linear networks (objects of class `"linnet"`). It is provided mainly for completeness.

The index `i` should be a window.

The argument `snip` specifies what to do with segments of `x` which cross the boundary of `i`. If `snip=FALSE`, such segments are simply deleted. If `snip=TRUE` (the default), such segments are cut into pieces by the boundary of `i`, and those pieces which lie inside the window `i` are included in the resulting network.

Value

Another linear network (object of class `"linnet"`).

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net>, Ege Rubak <rubak@math.aau.dk> and Suman Rakshit.

Examples

```
p <- par(mfrow=c(1,2), mar=0.2+c(0,0,1,0))
B <- owin(c(0.1,0.7),c(0.19,0.6))

plot(simplenet, main="x[w, snip=TRUE]")
plot(simplenet[B], add=TRUE, col="green", lwd=3)
plot(B, add=TRUE, border="red", lty=3)

plot(simplenet, main="x[w, snip=FALSE]")
plot(simplenet[B, snip=FALSE], add=TRUE, col="green", lwd=3)
plot(B, add=TRUE, border="red", lty=3)

par(p)
```

`Extract.lpp` *Extract Subset of Point Pattern on Linear Network*

Description

Extract a subset of a point pattern on a linear network.

Usage

```
  ## S3 method for class 'lpp'
x[i, j, drop=FALSE, ..., snip=TRUE]
```

Arguments

`x`	A point pattern on a linear network (object of class `"lpp"`).
`i`	Subset index. A valid subset index in the usual R sense, indicating which points should be retained.
`j`	Spatial window (object of class `"owin"`) delineating the region that should be retained.
`drop`	Logical value indicating whether to remove unused levels of the marks, if the marks are a factor.
`snip`	Logical. If `TRUE` (the default), segments of the network which cross the boundary of the window `j` will be cut by the boundary. If `FALSE`, these segments will be deleted.
`...`	Ignored.

Details

This function extracts a designated subset of a point pattern on a linear network.

The function `[.lpp` is a method for `[` for the class `"lpp"`. It extracts a designated subset of a point pattern. The argument `i` should be a subset index in the usual R sense: either a numeric vector of positive indices (identifying the points to be retained), a numeric vector of negative indices

(identifying the points to be deleted) or a logical vector of length equal to the number of points in the point pattern `x`. In the latter case, the points `(x$x[i], x$y[i])` for which `subset[i]=TRUE` will be retained, and the others will be deleted.

The argument `j`, if present, should be a spatial window. The pattern inside the region will be retained. *Line segments that cross the boundary of the window are deleted* in the current implementation.

The argument `drop` determines whether to remove unused levels of a factor, if the point pattern is multitype (i.e. the marks are a factor) or if the marks are a data frame or hyperframe in which some of the columns are factors.

The argument `snip` specifies what to do with segments of the network which cross the boundary of the window `j`. If `snip=FALSE`, such segments are simply deleted. If `snip=TRUE` (the default), such segments are cut into pieces by the boundary of `j`, and those pieces which lie inside the window `ji` are included in the resulting network.

Use `unmark` to remove all the marks in a marked point pattern, and `subset.lpp` to remove only some columns of marks.

Value

A point pattern on a linear network (of class `"lpp"`).

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Rolf Turner <rolfturner@posteo.net>

See Also

`lpp`, `subset.lpp`

Examples

```
# Chicago crimes data - remove cases of assault
chicago[marks(chicago) != "assault"]
# equivalent to subset(chicago, select=-assault)

# spatial window subset
B <- owin(c(350, 700), c(600, 1000))
plot(chicago)
plot(B, add=TRUE, lty=2, border="red", lwd=3)
op <- par(mfrow=c(1,2), mar=0.6+c(0,0,1,0))
plot(B, main="chicago[B, snip=FALSE]", lty=3, border="red")
plot(chicago[, B, snip=FALSE], add=TRUE)
plot(B, main="chicago[B, snip=TRUE]", lty=3, border="red")
plot(chicago[, B, snip=TRUE], add=TRUE)
par(op)
```

fitted.lppm *Fitted Intensity for Point Process on Linear Network*

Description

Given a point process model fitted to a point pattern on a linear network, compute the fitted intensity of the model at the points of the pattern, or at the points of the quadrature scheme used to fit the model.

Usage

```
## S3 method for class 'lppm'
fitted(object, ...,
                       dataonly = FALSE, new.coef = NULL,
      leaveoneout = FALSE)
```

Arguments

object	Fitted point process model on a linear network (object of class "lppm").
...	Ignored.
dataonly	Logical value indicating whether to computed fitted intensities at the points of the original point pattern dataset (dataonly=TRUE) or at all the quadrature points of the quadrature scheme used to fit the model (dataonly=FALSE, the default).
new.coef	Numeric vector of parameter values to replace the fitted model parameters coef(object).
leaveoneout	Logical. If TRUE the fitted value at each data point will be computed using a leave-one-out method. See Details.

Details

This is a method for the generic function fitted for the class "lppm" of fitted point process models on a linear network.

The locations u at which the fitted conditional intensity/trend is evaluated, are the points of the quadrature scheme used to fit the model in ppm. They include the data points (the points of the original point pattern dataset x) and other "dummy" points in the window of observation.

If leaveoneout=TRUE, fitted values will be computed for the data points only, using a 'leave-one-out' rule: the fitted value at X[i] is effectively computed by deleting this point from the data and re-fitting the model to the reduced pattern X[-i], then predicting the value at X[i]. (Instead of literally performing this calculation, we apply a Taylor approximation using the influence function computed in dfbetas.ppm.

Value

A vector containing the values of the fitted spatial trend.

Entries in this vector correspond to the quadrature points (data or dummy points) used to fit the model. The quadrature points can be extracted from object by union.quad(quad.ppm(object)).

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

lppm, predict.lppm

Examples

```
fit <- lppm(spiders~x+y)
a <- fitted(fit)
b <- fitted(fit, dataonly=TRUE)
```

---

harmonise.linim *Make Pixel Images on a Network Compatible*

Description

Convert several pixel images to a common pixel raster.

Usage

```
## S3 method for class 'linim'
harmonise(...)

## S3 method for class 'linim'
harmonize(...)
```

Arguments

...	Any number of pixel images on a network (objects of class "linim") or data which can be converted to pixel images on a network by as.linim.

Details

This function makes any number of pixel images on a network compatible, by converting them all to a common pixel grid.

The command harmonise is generic. This is the method for objects of class "linim".

At least one of the arguments ... must be a pixel image on a network (object of class "linim") or a network (class "linnet") so that the network is defined.

If several arguments contain network information then they must specify the same network.

Other arguments may be two-dimensional images (class "im"), windows (class "owin"), functions (function(x,y)) or numerical constants. These will be converted to images using as.linim.

The return value is a list, with entries corresponding to the input arguments, in which each entry is a pixel image on the same network. If the arguments were named (name=value) then the return value also carries these names.

Value

A list, of length equal to the number of arguments . . . , whose entries are pixel images on a network.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

harmonise, harmonise.im, as.linim

Examples

```
g <- linfun(function(x,y, seg, tp) { seg }, simplenet)
Image1 <- as.linim(g)
Distfun <- distfun(runiflpp(3, simplenet))
Image2 <- as.im(function(x,y) { x }, Window(simplenet))
harmonise(Image1, Distfun, Image2)
```

---

heatkernelapprox *Approximation to Heat Kernel on Linear Network at Source Point*

Description

Computes an approximation to the value of the heat kernel on a network evaluated at its source location.

Usage

```
heatkernelapprox(X, sigma, nmax = 20, floored=TRUE)
```

Arguments

X	Point pattern on a linear network (object of class "lpp").
sigma	Numeric. Bandwidth for kernel.
nmax	Number of terms to be used in the sum.
floored	Logical. If TRUE, all values are constrained to be greater than or equal to $1/L$ where L is the total length of the network. This the exact value of the heat kernel when the bandwidth is infinite.

Details

For each point `X[i]` in the pattern `X`, this algorithm computes an approximation to the value of the heat kernel with source point `X[i]` evaluated at the same location.

The heat kernel $\kappa(u, v)$ for a source location u evaluated at location v can be expressed as an infinite sum of contributions from all possible paths from u to v. This algorithm applies to the special case $u = v$ where the source point and the query point are the same.

The algorithm computes an approximation to $\kappa(u, u)$ by taking only the contributions from paths which (a) remain in the line segment containing the point u and (b) visit a vertex at most `nmax` times.

Value

Numeric vector with one entry for each point in `X`.

Author(s)

Greg McSwiggan and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

See Also

`hotrod`

Examples

```
X <- runiflpp(3,simplenet)
heatkernelapprox(X, 0.5)
```

`identify.linnet` *Interactively Identify Segments of a Linear Network*

Description

If a linear network is plotted in the graphics window, then each time the left mouse button is pressed, this function will find the network segment which is closest the mouse position, and print its serial number.

Usage

```
  ## S3 method for class 'linnet'
identify(x, ...)
```

Arguments

`x`	A linear network (object of class `"linnet"`).
`...`	Arguments passed to `identify.psp` and ultimately to `identify.default`.

Details

This is a method for the generic function identify for linear networks.

The network x should first be plotted using plot.linnet, plot.lpp or plot.linim. Then identify(x) reads the position of the graphics pointer each time the left mouse button is pressed. It then determines which network segment lies closest to the mouse position. The index of this segment (and its mark if any) will be returned as part of the value of the call.

Each time a segment is identified, text will be displayed at the midpoint of the segment, showing its serial number.

Value

A vector containing the serial numbers of the network segments of x that were identified.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

identify, identify.psp, plot.linnet.

---

identify.lintess *Interactively Identify Tiles of a Tessellation on a Network*

Description

If a tessellation on a linear network is plotted in the graphics window, then each time the left mouse button is pressed, this function will find the tile which contains the mouse position, print the serial number of the tile containing this position, and draw the tile in a different colour.

Usage

```
  ## S3 method for class 'lintess'
identify(x, ..., labels=tilenames(x),
                            n=nobjects(x), plot=TRUE, paint=plot,
                            paint.args=list())
```

Arguments

x	A tessellation on a linear network (object of class "lintess").
...	Arguments passed to identify.default.
labels	Labels associated with the tiles of the tessellation, to be plotted when the tiles are identified. A character vector or numeric vector of length equal to the number of tiles of x.
n	Maximum number of tiles to be identified.

plot	Logical. Whether to plot the labels when a tile is identified.
paint	Logical. Whether to redraw each identified tile, using a different colour.
paint.args	Optional list of arguments passed to plot.psp determining the colour and style in which each identified tile will be redrawn, if paint=TRUE.

Details

This is a method for the generic function identify for tessellations on a linear network.

The tessellation x, or the underlying network, should first be plotted using plot.lintess or plot.linnet.

Then identify(x) reads the position of the graphics pointer each time the left mouse button is pressed. It then determines which tile of x contains the mouse position. The index of this tile will be returned as part of the value of the call.

Each time a tile is identified, text will be displayed alongside the tile showing the name of the tile, and the tile will be re-drawn in a different colour.

The procedure terminates when the right mouse button is pressed.

Value

A data.frame with columns id and name containing the serial numbers and names of the tiles of x that were identified, in the order that they were identified; If x is marked, subsequent columns contain the marks for these tiles.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

identify, plot.lintess, plot.psp

---

identify.lpp *Identify Points in a Point Pattern on a Linear Network*

Description

If a point pattern on a network is plotted in the graphics window, this function will find the point of the pattern which is nearest to the mouse position, and print its mark value (or its serial number if there is no mark).

Usage

```
 ## S3 method for class 'lpp'
identify(x, ...)
```

Arguments

x	A point pattern on a linear network (object of class "lpp").
...	Arguments passed to identify.default.

Details

This is a method for the generic function identify for point patterns on a linear network (objects of class "lpp").

The point pattern x should first be plotted using plot.lpp. Then identify(x) reads the position of the graphics pointer each time the left mouse button is pressed. It then finds the point of the pattern x closest to the mouse position. If this closest point is sufficiently close to the mouse pointer, its index (and its mark if any) will be returned as part of the value of the call.

Each time a point of the pattern is identified, text will be displayed next to the point, showing its serial number (if x is unmarked) or its mark value (if x is marked).

Value

If x is unmarked, the result is a vector containing the serial numbers of the points in the pattern x that were identified. If x is marked, the result is a 2-column matrix, the first column containing the serial numbers and the second containing the marks for these points.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

identify.ppp, identify, clicklpp

---

insertVertices *Insert New Vertices in a Linear Network*

Description

Adds new vertices to a linear network at specified locations along the network.

Usage

```
insertVertices(L, ...)
```

Arguments

L	Linear network (object of class "linnet") or point pattern on a linear network (object of class "lpp").
...	Additional arguments passed to as.lpp specifying the positions of the new vertices along the network.

Details

This function adds new vertices at locations along an existing linear network.

The argument L can be either a linear network (class "linnet") or some other object that includes a linear network.

The new vertex locations can be specified either as a point pattern (class "lpp" or "ppp") or using coordinate vectors x,y or seg,tp or x,y,seg,tp as explained in the help for as.lpp.

This function breaks the existing line segments of L into pieces at the locations specified by the coordinates seg,tp and creates new vertices at these locations.

The result is the modified object, with an attribute "id" such that the ith added vertex has become the id[i]th vertex of the new network.

Value

An object of the same class as L representing the result of adding the new vertices. The result also has an attribute "id" as described in Details.

Author(s)

Adrian Baddeley

See Also

addVertices to create new vertices at locations which are not yet on the network.

as.lpp, linnet, methods.linnet, joinVertices, thinNetwork.

Examples

```
opa <- par(mfrow=c(1,3), mar=rep(0,4))
simplenet

plot(simplenet, main="")
plot(vertices(simplenet), add=TRUE)

# add two new vertices at specified local coordinates
L <- insertVertices(simplenet, seg=c(3,7), tp=c(0.2, 0.5))
L
plot(L, main="")
plot(vertices(L), add=TRUE)
id <- attr(L, "id")
id
plot(vertices(L)[id], add=TRUE, pch=16)

# add new vertices at three randomly-generated points
X <- runiflpp(3, simplenet)
LL <- insertVertices(simplenet, X)
plot(LL, main="")
plot(vertices(LL), add=TRUE)
ii <- attr(LL, "id")
plot(vertices(LL)[ii], add=TRUE, pch=16)
```

```
par(opa)
```

`integral.linim` *Integral on a Linear Network*

Description

Computes the integral (total value) of a function or pixel image over a linear network.

Usage

```
## S3 method for class 'linim'
integral(f, domain=NULL, weight=NULL, ...)

## S3 method for class 'linfun'
integral(f, domain=NULL, weight=NULL, ..., exact=FALSE, delta, nd)
```

Arguments

`f`	A pixel image on a linear network (class `"linim"`) or a function on a linear network (class `"linfun"`).
`domain`	Optional window specifying the domain of integration. Alternatively a tessellation (class `"tess"` or `"lintess"`).
`weight`	Optional numerical weight function for the integration. A pixel image (object of class `"linim"` or `"im"`), a function (object of class `"linfun"`, `"funxy"` or a a `function(x,y)`) or anything acceptable to `as.linim`.
`...`	Ignored.
`exact`	Logical value specifying whether to use a more accurate (and slower) calculation method. See Details.
`delta`	Optional. The step length (in coordinate units) for computing the approximate integral (if `exact=FALSE`). A single positive number.
`nd`	Optional. Integer giving the approximate number of sample points on the network (if `exact=FALSE`).

Details

The integral (total value of the function over the network) is calculated.

If `domain` is a window (class `"owin"`) then the integration will be restricted to this window. If `domain` is a tessellation (class `"tess"` or `"lintess"`) then the integral of `f` in each tile of `domain` will be computed.

If `weight` is given, effectively the integral of `weight * f` is computed.

For objects of class `"linfun"` there is the option of using a more accurate calculation method in which the integral along each segment of the network is computed separately using the utility `integrate` from the **stats** package. If `exact=TRUE`, additional arguments `...` are passed to `integrate` to control the computation.

Value

A single numeric or complex value (or a vector of such values if domain is a tessellation).

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

linim, integral.im, integrate

Examples

```
# make a function and image data
xcoord <- linfun(function(x,y,seg,tp) { x }, simplenet)
integral(xcoord)
integral(xcoord, exact=TRUE)
X <- as.linim(xcoord)
integral(X)

# integrals inside each tile of a tessellation
A <- quadrats(Frame(simplenet), 3)
integral(X, A)
```

---

intensity.lpp *Empirical Intensity of Point Pattern on Linear Network*

Description

Computes the average number of points per unit length in a point pattern on a linear network.

Usage

```
## S3 method for class 'lpp'
intensity(X, ...)
```

Arguments

X	A point pattern on a linear network (object of class "lpp").
...	Ignored.

Details

This is a method for the generic function intensity It computes the empirical intensity of a point pattern on a linear network (object of class "lpp"), i.e. the average density of points per unit length.

If the point pattern is multitype, the intensities of the different types are computed separately.

Value

A numeric value (giving the intensity) or numeric vector (giving the intensity for each possible type).

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Rolf Turner <rolfturner@posteo.net>

See Also

intensity, intensity.ppp

Examples

```
intensity(chicago)
```

---

intensity.lppm *Intensity of Fitted Point Process Model on a Linear Network*

Description

Computes the intensity of a fitted point process model on a linear network.

Usage

```
## S3 method for class 'lppm'
intensity(X, ...)
```

Arguments

X	A fitted point process model on a linear network (object of class "lppm").
...	Arguments passed to predict.lppm.

Details

This is a method for the generic function intensity for fitted point process models on a linear network (objects of class "lppm") created by the model-fitting function lppm).

The intensity of a point process model on a linear network is the expected number of random points per unit length (McSwiggan, 2019; Baddeley, Rubak and Turner, 2015, Chapter 17).

The result of intensity.lppm(X) is a numerical value if X is a homogeneous Poisson point process, and a pixel image if X is inhomogeneous. (In the latter case, the resolution of the pixel image is controlled by the arguments ... which are passed to predict.lppm.)

Value

A numeric value or numeric vector (if the model is homogeneous) or a pixel image (object of class "linim")

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Greg McSwiggan.

References

Baddeley, A., Rubak, E. and Turner, R. (2015) *Spatial Point Patterns: Methodology and Applications with R*. Chapman and Hall/CRC Press. .

McSwiggan, G. (2019) Spatial point process methods for linear networks with applications to road accident analysis. PhD thesis, University of Western Australia.

See Also

`intensity`, `intensity.lpp`, `intensity.ppm`.

Type `methods(intensity)` to see methods for other classes.

Examples

```
m1 <- lppm(spiders ~ 1)
intensity(m1)
mx <- lppm(spiders ~ x)
intensity(mx)
```

---

intersect.lintess *Intersection of Tessellations on a Linear Network*

Description

Yields the intersection (common refinement) of two tessellations on a linear network.

Usage

```
intersect.lintess(X, Y)
```

Arguments

`X`, `Y`	Tessellations (objects of class `"lintess"`) on the same linear network, or data that define such tessellations. See Details.

Details

`X` and `Y` should be tessellations on a linear network (objects of class `"lintess"`) and should be defined on the same network. The algorithm finds the common refinement of the two tessellations. Each tile in the resulting tessellation is the intersection of a tile of `X` with a tile of `Y`.

Alternatively, one of the arguments `X` or `Y` can be a two-dimensional tessellation (object of class `"tess"`) while the other argument is a network or a tessellation on a network. The two-dimensional tessellation will be intersected with the network to produce a tessellation on the network, then intersected with the other tessellation on the network.

Value

Another tessellation (object of class "lintess") on the same linear network as X and Y.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

See Also

lintess, divide.linnet, chop.linnet

Examples

```
X <- divide.linnet(runiflpp(4, simplenet))
Y <- divide.linnet(runiflpp(3, simplenet))
opa <- par(mfrow=c(1,3))
plot(X)
plot(Y)
plot(intersect.lintess(X,Y))
par(opa)
```

---

is.connected.linnet *Determine Whether a Linear Network is Connected*

Description

Determine whether a linear network is topologically connected.

Usage

```
## S3 method for class 'linnet'
is.connected(X, ...)
```

Arguments

X	A linear network (object of class "linnet").
...	Arguments passed to connected.linnet to determine the connected components.

Details

The command is.connected(X) returns TRUE if the network X consists of a single, topologically-connected piece, and returns FALSE if X consists of several pieces which are not joined together.

The function is.connected is generic, with methods for several classes. This help file documents the method for linear networks, is.connected.linnet.

Value

A logical value.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

is.connected, connected, connected.lpp.

Examples

```
is.connected(simplenet)
```

---

is.marked.lppm *Test Whether A Point Process Model is Marked*

Description

Tests whether a fitted point process model on a network involves "marks" attached to the points.

Usage

```
  ## S3 method for class 'lppm'
is.marked(X, ...)
```

Arguments

X	Fitted point process model on a linear networ (object of class "lppm") usually obtained from lppm.
...	Ignored.

Details

"Marks" are observations attached to each point of a point pattern. For example the chicago dataset contains the locations of crimes, each crime location being marked by the type of crime.

The argument X is a fitted point process model on a network (an object of class "lppm") typically obtained by fitting a model to point pattern data using lppm.

This function returns TRUE if the *original data* (to which the model X was fitted) were a marked point pattern.

Note that this is not the same as testing whether the model involves terms that depend on the marks (i.e. whether the fitted model ignores the marks in the data). See the Examples for a trick to do this.

If this function returns TRUE, the implications are (for example) that any simulation of this model will require simulation of random marks as well as random point locations.

Value

Logical value, equal to TRUE if X is a model that was fitted to a marked point pattern dataset.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Rolf Turner <rolfturner@posteo.net>

See Also

is.marked.

Examples

```
fit <- lppm(chicago ~ x)
is.marked(fit)
## result is TRUE, i.e. the data are marked

## To check whether the model involves marks:
"marks" %in% spatstat.utils::variablesinformula(formula(fit))
```

---

is.multitype.lpp *Test Whether A Point Pattern on a Network is Multitype*

Description

Tests whether a point pattern on a network has "marks" attached to the points which classify the points into several types.

Usage

```
  ## S3 method for class 'lpp'
is.multitype(X, na.action="warn", ...)
```

Arguments

X	Point pattern on a linear networl (object of class "lpp").
na.action	String indicating what to do if NA values are encountered amongst the marks. Options are "warn", "fatal" and "ignore".
...	Ignored.

Details

"Marks" are observations attached to each point of a point pattern. For example the chicago dataset contains the locations of crimes, each crime location being marked by the type of crime.

This function tests whether the point pattern X contains or involves marked points, **and** that the marks are a factor. It is a method for the generic function is.multitype.

The argument na.action determines what action will be taken if the point pattern has a vector of marks but some or all of the marks are NA. Options are "fatal" to cause a fatal error; "warn" to issue a warning and then return TRUE; and "ignore" to take no action except returning TRUE.

Value

Logical value, equal to TRUE if X is a multitype point pattern.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Rolf Turner <rolfturner@posteo.net>

See Also

is.multitype, is.multitype.lppm

Examples

```
is.multitype(chicago)
```

---

is.multitype.lppm *Test Whether A Point Process Model is Multitype*

Description

Tests whether a fitted point process model on a network involves "marks" attached to the points that classify the points into several types.

Usage

```
  ## S3 method for class 'lppm'
is.multitype(X, ...)
```

Arguments

X	Fitted point process model on a linear network (object of class "lppm") usually obtained from lppm.
...	Ignored.

Details

"Marks" are observations attached to each point of a point pattern. For example the chicago dataset contains the locations of crimes, each crime location being marked by the type of crime.

The argument X is a fitted point process model on a network (an object of class "lppm") typically obtained by fitting a model to point pattern data on a network using lppm.

This function returns TRUE if the *original data* (to which the model X was fitted) were a multitype point pattern.

Note that this is not the same as testing whether the model involves terms that depend on the marks (i.e. whether the fitted model ignores the marks in the data). See the Examples for a trick for doing this.

If this function returns TRUE, the implications are (for example) that any simulation of this model will require simulation of random marks as well as random point locations.

Value

Logical value, equal to TRUE if X is a model that was fitted to a multitype point pattern dataset.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Rolf Turner <rolfturner@posteo.net>

See Also

is.multitype, is.multitype.lpp

Examples

```
fit <- lppm(chicago ~ x)
is.multitype(fit)
# TRUE because chicago data are multitype

## To check whether the model involves marks:
"marks" %in% spatstat.utils::variablesinformula(formula(fit))
```

---

is.stationary.lppm *Recognise Stationary and Poisson Point Process Models on a Network*

Description

Given a point process model that has been fitted to data on a network, determine whether the model is a stationary point process, and whether it is a Poisson point process.

Usage

```
## S3 method for class 'lppm'
is.stationary(x)

## S3 method for class 'lppm'
is.poisson(x)
```

Arguments

x	A fitted spatial point process model on a linear network (object of class "lppm").

Details

The argument x represents a fitted spatial point process model on a linear network.

is.stationary(x) returns TRUE if x represents a stationary point process, and FALSE if not.

is.poisson(x) returns TRUE if x represents a Poisson point process, and FALSE if not.

The functions is.stationary and is.poisson are generic, with methods for many classes of models.

Value

A logical value.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

`is.marked` to determine whether a model is a marked point process.

`is.stationary`, `is.poisson` for generics.

`summary.lppm` for detailed information.

Model-fitting function `lppm`.

Examples

```
fit <- lppm(spiders ~ x)
is.stationary(fit)
is.poisson(fit)
```

---

joinVertices *Join Vertices in a Network*

Description

Join the specified vertices in a linear network, creating a new network.

Usage

```
joinVertices(L, from, to, marks=NULL)
```

Arguments

`L`	A linear network (object of class `"linnet"`) or point pattern on a linear network (object of class `"lpp"`).
`from`, `to`	Integers, or integer vectors of equal length, specifying the vertices which should be joined. Alternatively `from` can be a 2-column matrix of integers and `to` is missing or `NULL`.
`marks`	Optional vector or data frame of values associated with the new edges.

Details

Vertices of the network are numbered by their order of appearance in the point pattern `vertices(L)`.

If `from` and `to` are single integers, then the pair of vertices numbered `from` and `to` will be joined to make a new segment of the network. If `from` and `to` are vectors of integers, then vertex `from[i]` will be joined to vertex `to[i]` for each `i = 1,2,...`

If `L` is a network (class `"linnet"`), the result is another network, created by adding new segments. If `L` is a point pattern on a network (class `"lpp"`), the result is another point pattern object, created by adding new segments to the underlying network, and retaining the points.

In the resulting object, the new line segments are appended to the existing list of line segments.

Value

A linear network (object of class `"linnet"`) or point pattern on a linear network (object of class `"lpp"`).

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

`linnet`, `methods.linnet`, `thinNetwork`

Examples

```
snet <- joinVertices(simplenet, 4, 8)
plot(solist(simplenet, snet), main="")
X <- runiflpp(3, simplenet)
Y <- joinVertices(X, 4, 8)
```

`lineardirichlet` *Dirichlet Tessellation on a Linear Network*

Description

Given a point pattern on a linear network, compute the Dirichlet (or Voronoi or Thiessen) tessellation induced by the points.

Usage

```
lineardirichlet(X, metric=c("shortestpath", "Euclidean"))
```

Arguments

`X`	Point pattern on a linear network (object of class `"lpp"`).
`metric`	Character string (partially matched) specifying the distance metric used to define the Dirichlet tessellation.

Details

The Dirichlet tessellation induced by a point pattern X on a linear network L is a partition of L into subsets. The subset L[i] associated with the data point X[i] is the part of L lying closer to X[i] than to any other data point X[j].

If metric="shortestpath" (the default), distance between points on the network is measured by the shortest path in the network. If metric="Euclidean", distance is measured by the Euclidean distance in two dimensions.

Value

A tessellation on a linear network (object of class "lintess").

Missing tiles

If the linear network is not connected, and if one of the connected components contains no data points, then the Dirichlet tessellation using metric="shortestpath" is mathematically undefined inside this component. The resulting tessellation object includes a tile with label NA, which contains this component of the network. A plot of the tessellation will not show this tile.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

See Also

lintess.

For the Dirichlet tessellation in two-dimensional space, see dirichlet.

Examples

```
X <- runiflpp(5, simplenet)
plot(lineardirichlet(X), lwd=3)
points(X)
plot(lineardirichlet(X, metric="E"), lwd=3)
points(X)
plot(dirichlet(as.ppp(X)), add=TRUE, lty=2)
```

---

lineardisc *Compute Disc of Given Radius in Linear Network*

Description

Computes the 'disc' of given radius and centre in a linear network.

Usage

```
lineardisc(L, x = locator(1), r, plotit = TRUE,
           cols=c("blue", "red","green"), add=TRUE)

lineardisclength(L, x = locator(1), r)

countends(L, x = locator(1), r, toler=NULL, internal=list())
```

Arguments

L	Linear network (object of class "linnet").
x	Location of centre of disc. Either a point pattern (object of class "ppp") containing exactly 1 point, or a numeric vector of length 2.
r	Radius of disc.
plotit	Logical. Whether to plot the disc.
add	Logical. If add=TRUE (the default), the disc will be plotted on the current plot frame. If add=FALSE, a new plot frame will be started, the entire network will be displayed, and then the disc will be plotted over this.
cols	Colours for plotting the disc. A numeric or character vector of length 3 specifying the colours of the disc centre, disc lines and disc endpoints respectively.
toler	Optional. Distance threshold for countends. See Details. There is a sensible default.
internal	Argument for internal use by the package.

Details

The 'disc' $B(u, r)$ of centre x and radius r in a linear network L is the set of all points u in L such that the shortest path distance from x to u is less than or equal to r. This is a union of line segments contained in L.

The *relative boundary* of the disc $B(u, r)$ is the set of points v such that the shortest path distance from x to u is *equal* to r.

The function lineardisc computes the disc of radius r and its relative boundary, optionally plots them, and returns them. The faster function lineardisclength computes only the total length of the disc, and countends computes only the number of endpoints of the disc.

Note that countends requires the linear network L to be given in the non-sparse matrix format (see the argument sparse in linnet or as.linnet) while lineardisc and lineardisclength accept both sparse and non-sparse formats.

The optional threshold toler is used to suppress numerical errors in countends. If the distance from u to a network vertex v is between r-toler and r+toler, the vertex will be treated as lying on the relative boundary.

Value

The value of lineardisc is a list with two entries:

lines	Line segment pattern (object of class "psp") representing the interior disc

endpoints Point pattern (object of class "ppp") representing the relative boundary of the disc.

The value of lineardisclength is a single number giving the total length of the disc.

The value of countends is an integer giving the number of points in the relative boundary.

Author(s)

Ang Qi Wei <aqw07398@hotmail.com> and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

References

Ang, Q.W. (2010) *Statistical methodology for events on a network*. Master's thesis, School of Mathematics and Statistics, University of Western Australia.

Ang, Q.W., Baddeley, A. and Nair, G. (2012) Geometrically corrected second-order analysis of events on a linear network, with applications to ecology and criminology. *Scandinavian Journal of Statistics* **39**, 591–617.

See Also

linnet

Examples

```
 # letter 'A'
 v <- ppp(x=(-2):2, y=3*c(0,1,2,1,0), c(-3,3), c(-1,7))
 edg <- cbind(1:4, 2:5)
 edg <- rbind(edg, c(2,4))
 letterA <- linnet(v, edges=edg)
 plot(letterA)

di <- lineardisc(letterA, c(0,3), 1.6)
di

# count the endpoints more efficiently
countends(letterA, c(0,3), 1.6)
# cross-check
npoints(di$endpoints)

# measure the length more efficiently
lineardisclength(letterA, c(0,3), 1.6)
# cross-check
sum(lengths_psp(di$lines))
```

`linearJinhom` *Inhomogeneous Linear J-function for Point Processes on Linear Networks*

Description

Computes an estimate of the inhomogeneous linear J-function for a point pattern on a linear network.

Usage

```
linearJinhom(X, lambda = NULL, lmin=NULL,
             ...,
             r=NULL, rmax=NULL,
             distance=c("path","euclidean"),
             densitymethod=c("kernel", "Voronoi"),
             sigma=bw.scott.iso,
             f=0.2, nrep=200, ngrid=256)
```

Arguments

`X`	Point pattern on linear network (object of class `"lpp"`).
`lambda`	Intensity values for the point pattern. Either a numeric vector, a `function`, a pixel image (object of class `"im"` or `"linim"`) or a fitted point process model (object of class `"ppm"` or `"lppm"`).
`lmin`	Optional. The minimum possible value of the intensity over the network. A positive numerical value.
`r`	Optional. Numeric vector of values of the function argument r. There is a sensible default.
`rmax`	Optional. Numeric value specifying the largest desired value of r. There is a sensible default.
`distance`	A string (partially matched) specifying the metric that will be used to measure distances between points on the network: `distance="path"` is the shortest-path distance, and `distance="euclidean"` is the Euclidean distance.
`densitymethod`	String (partially matched) specifying the method that will be used to estimate the intensity `lambda`, if `lambda` is not given: `densitymethod="kernel"` specifies kernel smoothing and `densitymethod="Voronoi"` specifies Voronoi estimation. See Details.
`sigma`	Smoothing bandwidth used to estimate `lambda` by kernel smoothing, if `lambda` is not given and `densitymethod="kernel"`. Either a numeric value, or a function that can be applied to `X` to compute the bandwidth.
`f`, `nrep`	Arguments passed to the algorithm for estimating the intensity by Voronoi estimation, if `lambda` is not given and `densitymethod="Voronoi"`.
`...`	Additional arguments passed to the algorithms that estimate the intensity, if `lambda` is not given.

ngrid — Integer specifying the number of sample points on the network that will be used to estimate the inhomogeneous empty space function F.

Details

This function computes the geometrically corrected inhomogeneous linear J-function for point processes on linear networks defined by Cronie et al (2020).

The argument lambda is the (estimated) intensity of the underlying point process. It should be either a numeric vector (giving intensity values at the points of X), a function, a pixel image (object of class "im" or "linim") or a fitted point process model (object of class "ppm" or "lppm").

If lambda is not given, it will be estimated from the observed point pattern X as follows:

- If densitymethod="kernel", the intensity will be estimated by kernel smoothing, using the fast estimator densityQuick.lpp introduced by Rakshit et al (2019). The smoothing bandwidth sigma is required. It may be specified as a numeric value, or as a function that can be applied to X to obtain a bandwidth value. Examples of the latter include bw.scott.iso and bw.lppl. Additional arguments ... will be passed to sigma and to densityQuick.lpp.
- If densitymethod = "Voronoi", the intensity will be estimated using the resample-smoothed Voronoi estimator densityVoronoi.lpp introduced by Moradi et al (2019). The arguments f and nrep are passed to densityVoronoi.lpp and determine the retention probability and the number of replicates, respectively. Additional arguments ... will be passed to densityVoronoi.lpp.

Value

Function value table (object of class "fv").

Author(s)

Mehdi Moradi <m2.moradi@yahoo.com> and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

References

Cronie, O., Moradi, M., and Mateu, J. (2020) Inhomogeneous higher-order summary statistics for point processes on linear networks. *Statistics and Computing* **30** (6) 1221–1239.

Moradi, M., Cronie, 0., Rubak, E., Lachieze-Rey, R., Mateu, J. and Baddeley, A. (2019) Resample-smoothing of Voronoi intensity estimators. *Statistics and Computing* **29** (5) 995–1010.

Rakshit, S., Davies, T., Moradi, M., McSwiggan, G., Nair, G., Mateu, J. and Baddeley, A. (2019) Fast kernel smoothing of point patterns on a large network using 2D convolution. *International Statistical Review* **87** (3) 531–556. DOI: 10.1111/insr.12327.

See Also

bw.scott.iso, bw.lppl, densityVoronoi.lpp, densityQuick.lpp

linearKinhom

Jinhom

Examples

```
if(interactive()) {
  plot(linearJinhom(spiders))
} else {
  bottomhalf <- owin(c(0, 1125), c(0, 500))
  plot(linearJinhom(spiders[bottomhalf]))
}
```

---

linearK *Linear K Function*

Description

Computes an estimate of the linear K function for a point pattern on a linear network.

Usage

```
linearK(X, r=NULL, ..., correction="Ang", ratio=FALSE)
```

Arguments

X	Point pattern on linear network (object of class "lpp").
r	Optional. Numeric vector of values of the function argument r. There is a sensible default.
...	Ignored.
correction	Geometry correction. Either "none" or "Ang". See Details.
ratio	Logical. If TRUE, the numerator and denominator of the estimate will also be saved, for use in analysing replicated point patterns.

Details

This command computes the linear K function from point pattern data on a linear network.

If correction="none", the calculations do not include any correction for the geometry of the linear network. The result is the network K function as defined by Okabe and Yamada (2001).

If correction="Ang", the pair counts are weighted using Ang's correction (Ang, 2010; Ang et al, 2012).

Value

Function value table (object of class "fv").

Author(s)

Ang Qi Wei <aqw07398@hotmail.com> and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

References

Ang, Q.W. (2010) Statistical methodology for spatial point patterns on a linear network. MSc thesis, University of Western Australia.

Ang, Q.W., Baddeley, A. and Nair, G. (2012) Geometrically corrected second-order analysis of events on a linear network, with applications to ecology and criminology. *Scandinavian Journal of Statistics* **39**, 591–617.

Okabe, A. and Yamada, I. (2001) The K-function method on a network and its computational implementation. *Geographical Analysis* **33**, 271-290.

See Also

`compileK`, `lpp`

Examples

```
X <- rpoislpp(5, simplenet)
linearK(X)
linearK(X, correction="none")
```

`linearKcross` *Multitype K Function (Cross-type) for Linear Point Pattern*

Description

For a multitype point pattern on a linear network, estimate the multitype K function which counts the expected number of points of type j within a given distance of a point of type i.

Usage

```
linearKcross(X, i, j, r=NULL, ..., correction="Ang")
```

Arguments

`X`	The observed point pattern, from which an estimate of the cross type K function $K_{ij}(r)$ will be computed. An object of class `"lpp"` which must be a multitype point pattern (a marked point pattern whose marks are a factor).
`i`	Number or character string identifying the type (mark value) of the points in `X` from which distances are measured. Defaults to the first level of `marks(X)`.
`j`	Number or character string identifying the type (mark value) of the points in `X` to which distances are measured. Defaults to the second level of `marks(X)`.
`r`	numeric vector. The values of the argument r at which the K-function $K_{ij}(r)$ should be evaluated. There is a sensible default. First-time users are strongly advised not to specify this argument. See below for important conditions on r.
`correction`	Geometry correction. Either `"none"` or `"Ang"`. See Details.
`...`	Ignored.

Details

This is a counterpart of the function Kcross for a point pattern on a linear network (object of class "lpp").

The arguments i and j will be interpreted as levels of the factor marks(X). If i and j are missing, they default to the first and second level of the marks factor, respectively.

The argument r is the vector of values for the distance r at which $K_{ij}(r)$ should be evaluated. The values of r must be increasing nonnegative numbers and the maximum r value must not exceed the radius of the largest disc contained in the window.

Value

An object of class "fv" (see fv.object).

Warnings

The arguments i and j are interpreted as levels of the factor marks(X). Beware of the usual trap with factors: numerical values are not interpreted in the same way as character values.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

References

Baddeley, A, Jammalamadaka, A. and Nair, G. (2014) Multitype point process analysis of spines on the dendrite network of a neuron. *Applied Statistics* (Journal of the Royal Statistical Society, Series C), **63**, 673–694.

See Also

linearKdot, linearK.

Examples

```
K <- linearKcross(chicago, "assault", "robbery")
```

---

linearKcross.inhom *Inhomogeneous multitype K Function (Cross-type) for Linear Point Pattern*

Description

For a multitype point pattern on a linear network, estimate the inhomogeneous multitype K function which counts the expected number of points of type j within a given distance of a point of type i.

Usage

```
linearKcross.inhom(X, i, j, lambdaI=NULL, lambdaJ=NULL,
                   r=NULL, ..., correction="Ang", normalise=TRUE,
                   sigma=NULL)
```

Arguments

X	The observed point pattern, from which an estimate of the cross type K function $K_{ij}(r)$ will be computed. An object of class "lpp" which must be a multitype point pattern (a marked point pattern whose marks are a factor).
i	Number or character string identifying the type (mark value) of the points in X from which distances are measured. Defaults to the first level of marks(X).
j	Number or character string identifying the type (mark value) of the points in X to which distances are measured. Defaults to the second level of marks(X).
lambdaI	Intensity values for the points of type i. Either a numeric vector, a function, a pixel image (object of class "im" or "linim") or a fitted point process model (object of class "ppm" or "lppm") or NULL.
lambdaJ	Intensity values for the points of type j. Either a numeric vector, a function, a pixel image (object of class "im" or "linim") or a fitted point process model (object of class "ppm" or "lppm") or NULL.
r	numeric vector. The values of the argument r at which the K-function $K_{ij}(r)$ should be evaluated. There is a sensible default. First-time users are strongly advised not to specify this argument. See below for important conditions on r.
correction	Geometry correction. Either "none" or "Ang". See Details.
...	Arguments passed to lambdaI and lambdaJ if they are functions.
normalise	Logical. If TRUE (the default), the denominator of the estimator is data-dependent (equal to the sum of the reciprocal intensities at the points of type i), which reduces the sampling variability. If FALSE, the denominator is the length of the network.
sigma	Smoothing bandwidth passed to density.lpp for estimation of intensities when either lambdaI or lambdaJ is NULL.

Details

This is a counterpart of the function Kcross.inhom for a point pattern on a linear network (object of class "lpp").

The arguments i and j will be interpreted as levels of the factor marks(X). If i and j are missing, they default to the first and second level of the marks factor, respectively.

The argument r is the vector of values for the distance r at which $K_{ij}(r)$ should be evaluated. The values of r must be increasing nonnegative numbers and the maximum r value must not exceed the radius of the largest disc contained in the window.

If lambdaI or lambdaJ is missing or NULL, it will be estimated by kernel smoothing using density.lpp.

If lambdaI is a fitted point process model, the intensity of points of type i is computed from this model. If update=TRUE (the default), the model will first be updated by re-fitting it to the data:

- if `lambdaI` is a multitype point process, it is re-fitted to the entire dataset `X`.
- if `lambdaI` is an unmarked point process, it is re-fitted to the subset of `X` consisting of points of type `i` with the marks removed.

Then to compute the fitted intensity of points of type `i`,

- if `lambdaI` is a multitype point process, the predicted intensity of points of type `i` is computed
- if `lambdaI` is an unmarked point process, the predicted intensity of the model is computed.

Similarly for `lambdaJ`.

Value

An object of class `"fv"` (see `fv.object`).

Warnings

The arguments `i` and `j` are interpreted as levels of the factor `marks(X)`. Beware of the usual trap with factors: numerical values are not interpreted in the same way as character values.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

References

Baddeley, A, Jammalamadaka, A. and Nair, G. (2014) Multitype point process analysis of spines on the dendrite network of a neuron. *Applied Statistics* (Journal of the Royal Statistical Society, Series C), **63**, 673–694.

See Also

`linearKdot`, `linearK`.

Examples

```
lam <- table(marks(chicago))/(summary(chicago)$totlength)
lamI <- function(x,y,const=lam[["assault"]]){ rep(const, length(x)) }
lamJ <- function(x,y,const=lam[["robbery"]]){ rep(const, length(x)) }

K <- linearKcross.inhom(chicago, "assault", "robbery", lamI, lamJ)

# using fitted models for the intensity
# fit <- lppm(chicago ~marks + x)
# K <- linearKcross.inhom(chicago, "assault", "robbery", fit, fit)
```

`linearKdot` *Multitype K Function (Dot-type) for Linear Point Pattern*

Description

For a multitype point pattern on a linear network, estimate the multitype K function which counts the expected number of points (of any type) within a given distance of a point of type i.

Usage

```
linearKdot(X, i, r=NULL, ..., correction="Ang")
```

Arguments

`X`	The observed point pattern, from which an estimate of the dot type K function $K_{i\bullet}(r)$ will be computed. An object of class `"lpp"` which must be a multitype point pattern (a marked point pattern whose marks are a factor).
`i`	Number or character string identifying the type (mark value) of the points in `X` from which distances are measured. Defaults to the first level of `marks(X)`.
`r`	numeric vector. The values of the argument r at which the K-function $K_{i\bullet}(r)$ should be evaluated. There is a sensible default. First-time users are strongly advised not to specify this argument. See below for important conditions on r.
`correction`	Geometry correction. Either `"none"` or `"Ang"`. See Details.
`...`	Ignored.

Details

This is a counterpart of the function `Kdot` for a point pattern on a linear network (object of class `"lpp"`).

The argument `i` will be interpreted as levels of the factor `marks(X)`. If `i` is missing, it defaults to the first level of the marks factor.

The argument `r` is the vector of values for the distance r at which $K_{i\bullet}(r)$ should be evaluated. The values of r must be increasing nonnegative numbers and the maximum r value must not exceed the radius of the largest disc contained in the window.

Value

An object of class `"fv"` (see `fv.object`).

Warnings

The argument `i` is interpreted as a level of the factor `marks(X)`. Beware of the usual trap with factors: numerical values are not interpreted in the same way as character values.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

References

Baddeley, A, Jammalamadaka, A. and Nair, G. (2014) Multitype point process analysis of spines on the dendrite network of a neuron. *Applied Statistics* (Journal of the Royal Statistical Society, Series C), **63**, 673–694.

See Also

Kdot, linearKcross, linearK.

Examples

```
K <- linearKdot(chicago, "assault")
```

`linearKdot.inhom` *Inhomogeneous multitype K Function (Dot-type) for Linear Point Pattern*

Description

For a multitype point pattern on a linear network, estimate the inhomogeneous multitype K function which counts the expected number of points (of any type) within a given distance of a point of type i.

Usage

```
linearKdot.inhom(X, i, lambdaI=NULL, lambdadot=NULL, r=NULL, ...,
                 correction="Ang", normalise=TRUE, sigma=NULL)
```

Arguments

X	The observed point pattern, from which an estimate of the dot type K function $K_{i\bullet}(r)$ will be computed. An object of class "lpp" which must be a multitype point pattern (a marked point pattern whose marks are a factor).
i	Number or character string identifying the type (mark value) of the points in X from which distances are measured. Defaults to the first level of marks(X).
lambdaI	Intensity values for the points of type i. Either a numeric vector, a function, a pixel image (object of class "im" or "linim") or a fitted point process model (object of class "ppm" or "lppm") or NULL.
lambdadot	Intensity values for all points of X. Either a numeric vector, a function, a pixel image (object of class "im" or "linim") or a fitted point process model (object of class "ppm" or "lppm") or NULL.
r	numeric vector. The values of the argument r at which the K-function $K_{i\bullet}(r)$ should be evaluated. There is a sensible default. First-time users are strongly advised not to specify this argument. See below for important conditions on r.
correction	Geometry correction. Either "none" or "Ang". See Details.

...	Arguments passed to lambdaI and lambdadot if they are functions.
normalise	Logical. If TRUE (the default), the denominator of the estimator is data-dependent (equal to the sum of the reciprocal intensities at the points of type i), which reduces the sampling variability. If FALSE, the denominator is the length of the network.
sigma	Smoothing bandwidth passed to density.lpp for estimation of intensities when either lambdaI or lambdadot is NULL.

Details

This is a counterpart of the function Kdot.inhom for a point pattern on a linear network (object of class "lpp").

The argument i will be interpreted as levels of the factor marks(X). If i is missing, it defaults to the first level of the marks factor.

The argument r is the vector of values for the distance r at which $K_{i\bullet}(r)$ should be evaluated. The values of r must be increasing nonnegative numbers and the maximum r value must not exceed the radius of the largest disc contained in the window.

If lambdaI or lambdadot is missing, it will be estimated by kernel smoothing using density.lpp.

If lambdaI is a fitted point process model, the intensity of points of type i is computed from this model. If update=TRUE (the default), the model will first be updated by re-fitting it to the data:

- if lambdaI is a multitype point process, it is re-fitted to the entire dataset X.
- if lambdaI is an unmarked point process, it is re-fitted to the subset of X consisting of points of type i.

Then to compute the fitted intensity of points of type i,

- if lambdaI is a multitype point process, the predicted intensity of points of type i is computed
- if lambdaI is an unmarked point process, the predicted intensity of the model is computed.

If lambdadot is a fitted point process model, the marginal intensity (total intensity of points of any type) is computed from this model. If update=TRUE (the default), the model will first be updated by re-fitting it to the data:

- if lambdadot is a multitype point process, it is re-fitted to the entire dataset X.
- if lambdadot is an unmarked point process, it is re-fitted to unmark(X).

Then to compute the fitted marginal intensity,

- if lambdadot is a multitype point process, the predicted total intensity of points of any type is computed
- if lambdadot is an unmarked point process, the predicted intensity of the model is computed.

Value

An object of class "fv" (see fv.object).

Warnings

The argument `i` is interpreted as a level of the factor `marks(X)`. Beware of the usual trap with factors: numerical values are not interpreted in the same way as character values.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

References

Baddeley, A, Jammalamadaka, A. and Nair, G. (2014) Multitype point process analysis of spines on the dendrite network of a neuron. *Applied Statistics* (Journal of the Royal Statistical Society, Series C), **63**, 673–694.

See Also

`linearKdot`, `linearK`.

Examples

```
lam <- table(marks(chicago))/(summary(chicago)$totlength)
lamI <- function(x,y,const=lam[["assault"]]){ rep(const, length(x)) }
lam. <- function(x,y,const=sum(lam)){ rep(const, length(x)) }

K <- linearKdot.inhom(chicago, "assault", lamI, lam.)

# using fitted models for the intensity
# fit <- lppm(chicago ~marks + x)
# linearKdot.inhom(chicago, "assault", fit, fit)
```

---

linearKEuclid *Linear K Function Using Euclidean Distance*

Description

Computes an estimate of the linear K function based on Euclidean distances, for a point pattern on a linear network.

Usage

```
linearKEuclid(X, r = NULL, ...)
```

Arguments

`X`	Point pattern on linear network (object of class `"lpp"`).
`r`	Optional. Numeric vector of values of the function argument r. There is a sensible default.
`...`	Ignored.

Details

This command computes an estimate of the linear K function based on Euclidean distances between the points, as described by Rakshit, Nair and Baddeley (2017).

This is different from the linear K function based on shortest-path distances, which is computed by linearK.

The linear K function based on Euclidean distances is defined in equation (20) of Rakshit, Nair and Baddeley (2017). The estimate is computed from the point pattern as described in equation (25).

Value

Function value table (object of class "fv").

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

References

Rakshit. S., Nair, G. and Baddeley, A. (2017) Second-order analysis of point patterns on a network using any distance metric. *Spatial Statistics* **22** (1) 129–154.

See Also

linearpcfEuclid, linearKEuclidInhom.

See linearK for the corresponding function based on shortest-path distances.

Examples

```
X <- rpoislpp(5, simplenet)
K <- linearKEuclid(X)
```

---

linearKEuclidInhom *Inhomogeneous Linear K Function Based on Euclidean Distances*

Description

Computes an estimate of the inhomogeneous linear K function based on Euclidean distances, for a point pattern on a linear network.

Usage

```
linearKEuclidInhom(X, lambda = NULL, r = NULL, ...,
   normalise = TRUE, normpower = 2, update = TRUE,
   leaveoneout = TRUE, sigma=NULL)
```

Arguments

X	Point pattern on linear network (object of class "lpp").
lambda	Intensity values for the point pattern. Either a numeric vector, a function, a pixel image (object of class "im" or "linim") or a fitted point process model (object of class "ppm" or "lppm") or NULL.
r	Optional. Numeric vector of values of the function argument r. There is a sensible default.
...	Ignored.
normalise	Logical. If TRUE (the default), the denominator of the estimator is data-dependent (equal to the sum of the reciprocal intensities at the data points, raised to normpower), which reduces the sampling variability. If FALSE, the denominator is the length of the network.
normpower	Integer (usually either 1 or 2). Normalisation power. See Details.
update	Logical value indicating what to do when lambda is a fitted model (class "lppm" or "ppm"). If update=TRUE (the default), the model will first be refitted to the data X (using update.lppm or update.ppm) before the fitted intensity is computed. If update=FALSE, the fitted intensity of the model will be computed without re-fitting it to X.
leaveoneout	Logical value specifying whether to use a leave-one-out rule when calculating the intensity. See Details.
sigma	Smoothing bandwidth (passed to density.lpp) for kernel density estimation of the intensity when lambda=NULL.

Details

This command computes the inhomogeneous version of the linear K function based on *Euclidean* distances, for a point pattern on a linear network.

This is different from the inhomogeneous K function based on *shortest-path* distances, which is computed by linearKinhom.

The inhomogeneous K function based on *Euclidean* distances is defined in equation (23) of Rakshit, Nair and Baddeley (2017). Estimation is performed as described in equation (28).

The argument lambda should provide estimated values of the intensity of the point process at each point of X.

If lambda=NULL, the intensity will be estimated by kernel smoothing by calling density.lpp with the smoothing bandwidth sigma, and with any other relevant arguments that might be present in .... A leave-one-out kernel estimate will be computed if leaveoneout=TRUE.

If lambda is given, then it is expected to provide estimated values of the intensity of the point process at each point of X. The argument lambda may be a numeric vector (of length equal to the number of points in X), or a function(x,y) that will be evaluated at the points of X to yield numeric values, or a pixel image (object of class "im") or a fitted point process model (object of class "ppm" or "lppm").

If lambda is a fitted point process model, the default behaviour is to update the model by re-fitting it to the data, before computing the fitted intensity. This can be disabled by setting update=FALSE.

The intensity at data points will be computed by `fitted.lppm` or `fitted.ppm`. A leave-one-out estimate will be computed if `leaveoneout=TRUE` and `update=TRUE`.

If `normalise=TRUE` (the default), then the estimate is multiplied by $c^{\mathrm{normpower}}$ where $c = \mathrm{length}(L)/\sum(1/\lambda(x_i))$. This rescaling reduces the variability and bias of the estimate in small samples and in cases of very strong inhomogeneity. The default value of `normpower` is 1 (for consistency with previous versions of **spatstat**) but the most sensible value is 2, which would correspond to rescaling the `lambda` values so that $\sum(1/\lambda(x_i)) = \mathrm{area}(W)$.

Value

Function value table (object of class `"fv"`).

Warning

Older versions of `linearKEuclidInhom` interpreted `lambda=NULL` to mean that the homogeneous function `linearKEuclid` should be computed. This was changed to the current behaviour in version `3.1-0` of **spatstat.linnet**.

Author(s)

Adrian Baddeley `<Adrian.Baddeley@curtin.edu.au>`.

References

Rakshit. S., Nair, G. and Baddeley, A. (2017) Second-order analysis of point patterns on a network using any distance metric. *Spatial Statistics* **22** (1) 129–154.

See Also

`linearpcfEuclidInhom`, `linearKEuclid`.

See `linearKinhom` for the corresponding function based on shortest-path distances.

Examples

```
X <- rpoislpp(5, simplenet)
fit <- lppm(X ~x)
K <- linearKEuclidInhom(X, lambda=fit)
plot(K)
```

---

linearKinhom *Inhomogeneous Linear K Function*

Description

Computes an estimate of the inhomogeneous linear K function for a point pattern on a linear network.

Usage

```
linearKinhom(X, lambda=NULL, r=NULL, ..., correction="Ang",
             normalise=TRUE, normpower=1,
     update=TRUE, leaveoneout=TRUE, sigma=NULL, ratio=FALSE)
```

Arguments

X	Point pattern on linear network (object of class "lpp").
lambda	Intensity values for the point pattern. Either a numeric vector, a function, a pixel image (object of class "im" or "linim") or a fitted point process model (object of class "ppm" or "lppm") or NULL.
r	Optional. Numeric vector of values of the function argument r. There is a sensible default. Users are advised not to specify r in normal usage.
...	Ignored.
correction	Geometry correction. Either "none" or "Ang". See Details.
normalise	Logical. If TRUE (the default), the denominator of the estimator is data-dependent (equal to the sum of the reciprocal intensities at the data points, raised to normpower), which reduces the sampling variability. If FALSE, the denominator is the length of the network.
normpower	Integer (usually either 1 or 2). Normalisation power. See Details.
update	Logical value indicating what to do when lambda is a fitted model (class "lppm" or "ppm"). If update=TRUE (the default), the model will first be refitted to the data X (using update.lppm or update.ppm) before the fitted intensity is computed. If update=FALSE, the fitted intensity of the model will be computed without re-fitting it to X.
leaveoneout	Logical value specifying whether to use a leave-one-out rule when calculating the intensity. See Details.
sigma	Smoothing bandwidth (passed to density.lpp) for kernel density estimation of the intensity when lambda=NULL.
ratio	Logical. If TRUE, the numerator and denominator of the estimate will also be saved, for use in analysing replicated point patterns.

Details

This command computes the inhomogeneous version of the linear K function from point pattern data on a linear network.

The argument lambda should provide estimated values of the intensity of the point process at each point of X.

If lambda=NULL, the intensity will be estimated by kernel smoothing by calling density.lpp with the smoothing bandwidth sigma, and with any other relevant arguments that might be present in .... A leave-one-out kernel estimate will be computed if leaveoneout=TRUE.

If lambda is given, it may be a numeric vector (of length equal to the number of points in X), or a function(x,y) that will be evaluated at the points of X to yield numeric values, or a pixel image (object of class "im") or a fitted point process model (object of class "ppm" or "lppm").

If `lambda` is a fitted point process model, the default behaviour is to update the model by re-fitting it to the data, before computing the fitted intensity. This can be disabled by setting `update=FALSE`. The intensity at data points will be computed by `fitted.lppm` or `fitted.ppm`. A leave-one-out estimate will be computed if `leaveoneout=TRUE` and `update=TRUE`.

If `correction="none"`, the calculations do not include any correction for the geometry of the linear network. If `correction="Ang"`, the pair counts are weighted using Ang's correction (Ang, 2010).

Each estimate is initially computed as

$$\widehat{K}_{\mathrm{inhom}}(r) = \frac{1}{\mathrm{length}(L)} \sum_i \sum_j \frac{1\{d_{ij} \le r\} e(x_i, x_j)}{\lambda(x_i)\lambda(x_j)}$$

where `L` is the linear network, d_{ij} is the distance between points x_i and x_j, and $e(x_i, x_j)$ is a weight. If `correction="none"` then this weight is equal to 1, while if `correction="Ang"` the weight is $e(x_i, x_j, r) = 1/m(x_i, d_{ij})$ where $m(u, t)$ is the number of locations on the network that lie exactly t units distant from location u by the shortest path.

If `normalise=TRUE` (the default), then the estimates described above are multiplied by $c^{\mathrm{normpower}}$ where $c = \mathrm{length}(L)/\sum(1/\lambda(x_i))$. This rescaling reduces the variability and bias of the estimate in small samples and in cases of very strong inhomogeneity. The default value of `normpower` is 1 (for consistency with previous versions of **spatstat**) but the most sensible value is 2, which would correspond to rescaling the `lambda` values so that $\sum(1/\lambda(x_i)) = \mathrm{area}(W)$.

Value

Function value table (object of class `"fv"`).

Warning

Older versions of `linearKinhom` interpreted `lambda=NULL` to mean that the homogeneous function `linearK` should be computed. This was changed to the current behaviour in version `3.1-0` of **spatstat.linnet**.

Author(s)

Ang Qi Wei <aqw07398@hotmail.com> and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

References

Ang, Q.W. (2010) Statistical methodology for spatial point patterns on a linear network. MSc thesis, University of Western Australia.

Ang, Q.W., Baddeley, A. and Nair, G. (2012) Geometrically corrected second-order analysis of events on a linear network, with applications to ecology and criminology. *Scandinavian Journal of Statistics* **39**, 591–617.

See Also

`lpp`

Examples

```
X <- rpoislpp(5, simplenet)
fit <- lppm(X ~x)
K <- linearKinhom(X, lambda=fit)
plot(K)
Ke <- linearKinhom(X, sigma=bw.lppl)
plot(Ke)
```

`linearmarkconnect` *Mark Connection Function for Multitype Point Pattern on Linear Network*

Description

For a multitype point pattern on a linear network, estimate the mark connection function from points of type i to points of type j.

Usage

```
linearmarkconnect(X, i, j, r=NULL, ...)
```

Arguments

`X`	The observed point pattern, from which an estimate of the mark connection function $p_{ij}(r)$ will be computed. An object of class `"lpp"` which must be a multitype point pattern (a marked point pattern whose marks are a factor).
`i`	Number or character string identifying the type (mark value) of the points in `X` from which distances are measured. Defaults to the first level of `marks(X)`.
`j`	Number or character string identifying the type (mark value) of the points in `X` to which distances are measured. Defaults to the second level of `marks(X)`.
`r`	numeric vector. The values of the argument r at which the function $p_{ij}(r)$ should be evaluated. There is a sensible default. First-time users are strongly advised not to specify this argument. See below for important conditions on r.
`...`	Arguments passed to `linearpcfcross` and `linearpcf`.

Details

This is a counterpart of the function `markconnect` for a point pattern on a linear network (object of class `"lpp"`).

The argument `i` will be interpreted as levels of the factor `marks(X)`. If `i` is missing, it defaults to the first level of the marks factor.

The argument `r` is the vector of values for the distance r at which $p_{ij}(r)$ should be evaluated. The values of r must be increasing nonnegative numbers and the maximum r value must not exceed the radius of the largest disc contained in the window.

Value

An object of class "fv" (see fv.object).

Warnings

The argument i is interpreted as a level of the factor marks(X). Beware of the usual trap with factors: numerical values are not interpreted in the same way as character values.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

References

Baddeley, A, Jammalamadaka, A. and Nair, G. (2014) Multitype point process analysis of spines on the dendrite network of a neuron. *Applied Statistics* (Journal of the Royal Statistical Society, Series C), **63**, 673–694.

See Also

linearpcfcross, linearpcf, linearmarkequal, markconnect.

Examples

```
pab <- linearmarkconnect(chicago, "assault", "burglary")

# plot(alltypes(chicago, linearmarkconnect))
```

---

linearmarkequal *Mark Connection Function for Multitype Point Pattern on Linear Network*

Description

For a multitype point pattern on a linear network, estimate the mark connection function from points of type i to points of type j.

Usage

```
linearmarkequal(X, r=NULL, ...)
```

Arguments

X	The observed point pattern, from which an estimate of the mark connection function $p_{ij}(r)$ will be computed. An object of class "lpp" which must be a multitype point pattern (a marked point pattern whose marks are a factor).
r	numeric vector. The values of the argument r at which the function $p_{ij}(r)$ should be evaluated. There is a sensible default. First-time users are strongly advised not to specify this argument. See below for important conditions on r.
...	Arguments passed to linearpcfcross and linearpcf.

Details

This is the mark equality function for a point pattern on a linear network (object of class "lpp").

The argument r is the vector of values for the distance r at which $p_{ij}(r)$ should be evaluated. The values of r must be increasing nonnegative numbers and the maximum r value must not exceed the radius of the largest disc contained in the window.

Value

An object of class "fv" (see fv.object).

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

References

Baddeley, A, Jammalamadaka, A. and Nair, G. (2014) Multitype point process analysis of spines on the dendrite network of a neuron. *Applied Statistics* (Journal of the Royal Statistical Society, Series C), **63**, 673–694.

See Also

linearpcfcross, linearpcf, linearmarkconnect, markconnect.

Examples

```
if(interactive()) {
  X <- chicago
} else {
  m <- sample(factor(c("A","B")), 20, replace=TRUE)
  X <- runiflpp(20, simplenet) %mark% m
}
p <- linearmarkequal(X)
```

linearpcf *Linear Pair Correlation Function*

Description

Computes an estimate of the linear pair correlation function for a point pattern on a linear network.

Usage

```
linearpcf(X, r=NULL, ..., correction="Ang", ratio=FALSE)
```

Arguments

X	Point pattern on linear network (object of class "lpp").
r	Optional. Numeric vector of values of the function argument r. There is a sensible default.
...	Arguments passed to density.default to control the smoothing.
correction	Geometry correction. Either "none" or "Ang". See Details.
ratio	Logical. If TRUE, the numerator and denominator of each estimate will also be saved, for use in analysing replicated point patterns.

Details

This command computes the linear pair correlation function from point pattern data on a linear network.

The pair correlation function is estimated from the shortest-path distances between each pair of data points, using the fixed-bandwidth kernel smoother density.default, with a bias correction at each end of the interval of r values. To switch off the bias correction, set endcorrect=FALSE.

The bandwidth for smoothing the pairwise distances is determined by arguments ... passed to density.default, mainly the arguments bw and adjust. The default is to choose the bandwidth by Silverman's rule of thumb bw="nrd0" explained in density.default.

If correction="none", the calculations do not include any correction for the geometry of the linear network. The result is an estimate of the first derivative of the network K function defined by Okabe and Yamada (2001).

If correction="Ang", the pair counts are weighted using Ang's correction (Ang, 2010). The result is an estimate of the pair correlation function in the linear network.

Value

Function value table (object of class "fv").

If ratio=TRUE then the return value also has two attributes called "numerator" and "denominator" which are "fv" objects containing the numerators and denominators of each estimate of $g(r)$.

Author(s)

Ang Qi Wei <aqw07398@hotmail.com> and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

References

Ang, Q.W. (2010) Statistical methodology for spatial point patterns on a linear network. MSc thesis, University of Western Australia.

Ang, Q.W., Baddeley, A. and Nair, G. (2012) Geometrically corrected second-order analysis of events on a linear network, with applications to ecology and criminology. *Scandinavian Journal of Statistics* **39**, 591–617.

Okabe, A. and Yamada, I. (2001) The K-function method on a network and its computational implementation. *Geographical Analysis* **33**, 271-290.

See Also

linearK, linearpcfinhom, lpp

Examples

```
X <- rpoislpp(5, simplenet)
linearpcf(X)
linearpcf(X, correction="none")
```

---

linearpcfcross *Multitype Pair Correlation Function (Cross-type) for Linear Point Pattern*

Description

For a multitype point pattern on a linear network, estimate the multitype pair correlation function from points of type i to points of type j.

Usage

```
linearpcfcross(X, i, j, r=NULL, ..., correction="Ang")
```

Arguments

X	The observed point pattern, from which an estimate of the i-to-any pair correlation function $g_{ij}(r)$ will be computed. An object of class "lpp" which must be a multitype point pattern (a marked point pattern whose marks are a factor).
i	Number or character string identifying the type (mark value) of the points in X from which distances are measured. Defaults to the first level of marks(X).
j	Number or character string identifying the type (mark value) of the points in X to which distances are measured. Defaults to the second level of marks(X).

r	numeric vector. The values of the argument r at which the function $g_{ij}(r)$ should be evaluated. There is a sensible default. First-time users are strongly advised not to specify this argument. See below for important conditions on r.
correction	Geometry correction. Either "none" or "Ang". See Details.
...	Arguments passed to density.default to control the kernel smoothing.

Details

This is a counterpart of the function pcfcross for a point pattern on a linear network (object of class "lpp").

The argument i will be interpreted as levels of the factor marks(X). If i is missing, it defaults to the first level of the marks factor.

The argument r is the vector of values for the distance r at which $g_{ij}(r)$ should be evaluated. The values of r must be increasing nonnegative numbers and the maximum r value must not exceed the radius of the largest disc contained in the window.

Value

An object of class "fv" (see fv.object).

Warnings

The argument i is interpreted as a level of the factor marks(X). Beware of the usual trap with factors: numerical values are not interpreted in the same way as character values.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

References

Baddeley, A, Jammalamadaka, A. and Nair, G. (2014) Multitype point process analysis of spines on the dendrite network of a neuron. *Applied Statistics* (Journal of the Royal Statistical Society, Series C), **63**, 673–694.

See Also

linearpcfdot, linearpcf, pcfcross.

Examples

```
g <- linearpcfcross(chicago, "assault")
```

`linearpcfcross.inhom` *Inhomogeneous Multitype Pair Correlation Function (Cross-type) for Linear Point Pattern*

Description

For a multitype point pattern on a linear network, estimate the inhomogeneous multitype pair correlation function from points of type i to points of type j.

Usage

```
linearpcfcross.inhom(X, i, j, lambdaI, lambdaJ, r=NULL, ...,
                     correction="Ang", normalise=TRUE,
                     sigma=NULL, adjust.sigma=1,
                     bw="nrd0", adjust.bw=1)
```

Arguments

`X`	The observed point pattern, from which an estimate of the i-to-any pair correlation function $g_{ij}(r)$ will be computed. An object of class `"lpp"` which must be a multitype point pattern (a marked point pattern whose marks are a factor).
`i`	Number or character string identifying the type (mark value) of the points in `X` from which distances are measured. Defaults to the first level of `marks(X)`.
`j`	Number or character string identifying the type (mark value) of the points in `X` to which distances are measured. Defaults to the second level of `marks(X)`.
`lambdaI`	Intensity values for the points of type `i`. Either a numeric vector, a `function`, a pixel image (object of class `"im"` or `"linim"`) or a fitted point process model (object of class `"ppm"` or `"lppm"`).
`lambdaJ`	Intensity values for the points of type `j`. Either a numeric vector, a `function`, a pixel image (object of class `"im"` or `"linim"`) or a fitted point process model (object of class `"ppm"` or `"lppm"`).
`r`	numeric vector. The values of the argument r at which the function $g_{ij}(r)$ should be evaluated. There is a sensible default. First-time users are strongly advised not to specify this argument. See below for important conditions on r.
`correction`	Geometry correction. Either `"none"` or `"Ang"`. See Details.
`...`	Arguments passed to `density.default` to control the kernel smoothing.
`normalise`	Logical. If `TRUE` (the default), the denominator of the estimator is data-dependent (equal to the sum of the reciprocal intensities at the points of type `i`), which reduces the sampling variability. If `FALSE`, the denominator is the length of the network.
`sigma`	Smoothing bandwidth passed to `density.lpp` for estimation of intensities when either `lambdaI` or `lambdaJ` is `NULL`.
`adjust.sigma`	Numeric value. `sigma` will be multiplied by this value.

bw	Smoothing bandwidth (passed to density.default) for one-dimensional kernel smoothing of the pair correlation function. Either a numeric value, or a character string recognised by density.default.
adjust.bw	Numeric value. bw will be multiplied by this value.

Details

This is a counterpart of the function pcfcross.inhom for a point pattern on a linear network (object of class "lpp").

The argument i will be interpreted as levels of the factor marks(X). If i is missing, it defaults to the first level of the marks factor.

The argument r is the vector of values for the distance r at which $g_{ij}(r)$ should be evaluated. The values of r must be increasing nonnegative numbers and the maximum r value must not exceed the radius of the largest disc contained in the window.

If lambdaI or lambdaJ is missing or NULL, it will be estimated by kernel smoothing using density.lpp.

If lambdaI is a fitted point process model, the intensity of points of type i is computed from this model. If update=TRUE (the default), the model will first be updated by re-fitting it to the data:

- if lambdaI is a multitype point process, it is re-fitted to the entire dataset X.
- if lambdaI is an unmarked point process, it is re-fitted to the subset of X consisting of points of type i with the marks removed.

Then to compute the fitted intensity of points of type i,

- if lambdaI is a multitype point process, the predicted intensity of points of type i is computed
- if lambdaI is an unmarked point process, the predicted intensity of the model is computed.

Similarly for lambdaJ.

Value

An object of class "fv" (see fv.object).

Warnings

The argument i is interpreted as a level of the factor marks(X). Beware of the usual trap with factors: numerical values are not interpreted in the same way as character values.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

References

Baddeley, A, Jammalamadaka, A. and Nair, G. (2014) Multitype point process analysis of spines on the dendrite network of a neuron. *Applied Statistics* (Journal of the Royal Statistical Society, Series C), **63**, 673–694.

See Also

linearpcfdot, linearpcf, pcfcross.inhom.

Examples

```
lam <- table(marks(chicago))/(summary(chicago)$totlength)
lamI <- function(x,y,const=lam[["assault"]]){ rep(const, length(x)) }
lamJ <- function(x,y,const=lam[["robbery"]]){ rep(const, length(x)) }

g <- linearpcfcross.inhom(chicago, "assault", "robbery", lamI, lamJ)

# using fitted models for intensity
# fit <- lppm(chicago ~marks + x)
# linearpcfcross.inhom(chicago, "assault", "robbery", fit, fit)
```

---

linearpcfdot *Multitype Pair Correlation Function (Dot-type) for Linear Point Pattern*

Description

For a multitype point pattern on a linear network, estimate the multitype pair correlation function from points of type i to points of any type.

Usage

```
linearpcfdot(X, i, r=NULL, ..., correction="Ang")
```

Arguments

X	The observed point pattern, from which an estimate of the i-to-any pair correlation function $g_{i\bullet}(r)$ will be computed. An object of class "lpp" which must be a multitype point pattern (a marked point pattern whose marks are a factor).
i	Number or character string identifying the type (mark value) of the points in X from which distances are measured. Defaults to the first level of marks(X).
r	numeric vector. The values of the argument r at which the function $g_{i\bullet}(r)$ should be evaluated. There is a sensible default. First-time users are strongly advised not to specify this argument. See below for important conditions on r.
correction	Geometry correction. Either "none" or "Ang". See Details.
...	Arguments passed to density.default to control the kernel smoothing.

Details

This is a counterpart of the function pcfdot for a point pattern on a linear network (object of class "lpp").

The argument i will be interpreted as levels of the factor marks(X). If i is missing, it defaults to the first level of the marks factor.

The argument r is the vector of values for the distance r at which $g_{i\bullet}(r)$ should be evaluated. The values of r must be increasing nonnegative numbers and the maximum r value must not exceed the radius of the largest disc contained in the window.

Value

An object of class "fv" (see fv.object).

Warnings

The argument i is interpreted as a level of the factor marks(X). Beware of the usual trap with factors: numerical values are not interpreted in the same way as character values.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

References

Baddeley, A, Jammalamadaka, A. and Nair, G. (2014) Multitype point process analysis of spines on the dendrite network of a neuron. *Applied Statistics* (Journal of the Royal Statistical Society, Series C), **63**, 673–694.

See Also

linearpcfcross, linearpcf, pcfdot.

Examples

```
g <- linearpcfdot(chicago, "assault")
```

---

linearpcfdot.inhom *Inhomogeneous Multitype Pair Correlation Function (Dot-type) for Linear Point Pattern*

Description

For a multitype point pattern on a linear network, estimate the inhomogeneous multitype pair correlation function from points of type i to points of any type.

Usage

```
linearpcfdot.inhom(X, i, lambdaI, lambdadot, r=NULL, ...,
                   correction="Ang", normalise=TRUE,
                   sigma=NULL, adjust.sigma=1,
                   bw="nrd0", adjust.bw=1)
```

Arguments

X	The observed point pattern, from which an estimate of the i-to-any pair correlation function $g_{i\bullet}(r)$ will be computed. An object of class "lpp" which must be a multitype point pattern (a marked point pattern whose marks are a factor).
i	Number or character string identifying the type (mark value) of the points in X from which distances are measured. Defaults to the first level of marks(X).
lambdaI	Intensity values for the points of type i. Either a numeric vector, a function, a pixel image (object of class "im" or "linim") or a fitted point process model (object of class "ppm" or "lppm") or NULL.
lambdadot	Intensity values for all points of X. Either a numeric vector, a function, a pixel image (object of class "im" or "linim") or a fitted point process model (object of class "ppm" or "lppm") or NULL.
r	numeric vector. The values of the argument r at which the function $g_{i\bullet}(r)$ should be evaluated. There is a sensible default. First-time users are strongly advised not to specify this argument. See below for important conditions on r.
correction	Geometry correction. Either "none" or "Ang". See Details.
...	Arguments passed to density.default to control the kernel smoothing.
normalise	Logical. If TRUE (the default), the denominator of the estimator is data-dependent (equal to the sum of the reciprocal intensities at the points of type i), which reduces the sampling variability. If FALSE, the denominator is the length of the network.
sigma	Smoothing bandwidth passed to density.lpp for estimation of intensities when either lambdaI or lambdadot is NULL.
adjust.sigma	Numeric value. sigma will be multiplied by this value.
bw	Smoothing bandwidth (passed to density.default) for one-dimensional kernel smoothing of the pair correlation function. Either a numeric value, or a character string recognised by density.default.
adjust.bw	Numeric value. bw will be multiplied by this value.

Details

This is a counterpart of the function pcfdot.inhom for a point pattern on a linear network (object of class "lpp").

The argument i will be interpreted as levels of the factor marks(X). If i is missing, it defaults to the first level of the marks factor.

The argument r is the vector of values for the distance r at which $g_{i\bullet}(r)$ should be evaluated. The values of r must be increasing nonnegative numbers and the maximum r value must not exceed the radius of the largest disc contained in the window.

If lambdaI or lambdadot is missing or NULL, it will be estimated by kernel smoothing using density.lpp.

If lambdaI is a fitted point process model, the intensity of points of type i is computed from this model. If update=TRUE (the default), the model will first be updated by re-fitting it to the data:

- if lambdaI is a multitype point process, it is re-fitted to the entire dataset X.
- if lambdaI is an unmarked point process, it is re-fitted to the subset of X consisting of points of type i.

Then to compute the fitted intensity of points of type i,

- if lambdaI is a multitype point process, the predicted intensity of points of type i is computed
- if lambdaI is an unmarked point process, the predicted intensity of the model is computed.

If lambdadot is a fitted point process model, the marginal intensity (total intensity of points of any type) is computed from this model. If update=TRUE (the default), the model will first be updated by re-fitting it to the data:

- if lambdadot is a multitype point process, it is re-fitted to the entire dataset X.
- if lambdadot is an unmarked point process, it is re-fitted to unmark(X).

Then to compute the fitted marginal intensity,

- if lambdadot is a multitype point process, the predicted total intensity of points of any type is computed
- if lambdadot is an unmarked point process, the predicted intensity of the model is computed.

Value

An object of class "fv" (see fv.object).

Warnings

The argument i is interpreted as a level of the factor marks(X). Beware of the usual trap with factors: numerical values are not interpreted in the same way as character values.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

References

Baddeley, A, Jammalamadaka, A. and Nair, G. (2014) Multitype point process analysis of spines on the dendrite network of a neuron. *Applied Statistics* (Journal of the Royal Statistical Society, Series C), **63**, 673–694.

See Also

linearpcfcross.inhom, linearpcfdot, pcfdot.inhom.

Examples

```
lam <- table(marks(chicago))/(summary(chicago)$totlength)
lamI <- function(x,y,const=lam[["assault"]]){ rep(const, length(x)) }
lam. <- function(x,y,const=sum(lam)){ rep(const, length(x)) }

g <- linearpcfdot.inhom(chicago, "assault", lamI, lam.)

# using fitted models for the intensity
# fit <- lppm(chicago, ~marks + x)
# linearpcfdot.inhom(chicago, "assault", fit, fit)
```

`linearpcfEuclid` *Linear Pair Correlation Function Using Euclidean Distance*

Description

Computes an estimate of the pair correlation function based on Euclidean distances, for a point pattern on a linear network.

Usage

```
linearpcfEuclid(X, r = NULL, ...)
```

Arguments

`X`	Point pattern on linear network (object of class `"lpp"`).
`r`	Optional. Numeric vector of values of the function argument r. There is a sensible default.
`...`	Ignored.

Details

This command computes an estimate of the pair correlation function based on Euclidean distances between the points, as described by Rakshit, Nair and Baddeley (2017).

This is different from the linear pair correlation function based on shortest-path distances, which is computed by `linearpcf`.

The linear pair correlation function based on Euclidean distances is defined in equation (15) of Rakshit, Nair and Baddeley (2017). The estimate is computed from the point pattern as described in equation (31).

Value

Function value table (object of class `"fv"`).

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

References

Rakshit. S., Nair, G. and Baddeley, A. (2017) Second-order analysis of point patterns on a network using any distance metric. *Spatial Statistics* **22** (1) 129–154.

See Also

linearKEuclid, linearpcfEuclidInhom.

See linearpcf for the corresponding function based on shortest-path distances.

Examples

```
X <- rpoislpp(5, simplenet)
g <- linearpcfEuclid(X)
```

---

linearpcfEuclidInhom *Inhomogeneous Linear Pair Correlation Function Based on Euclidean Distances*

Description

Computes an estimate of the inhomogeneous pair correlation function based on Euclidean distances, for a point pattern on a linear network.

Usage

```
linearpcfEuclidInhom(X, lambda = NULL, r = NULL, ...,
   normalise = TRUE, normpower = 2,
   update = TRUE, leaveoneout = TRUE,
   sigma=NULL, adjust.sigma=1, bw="nrd0", adjust.bw=1)
```

Arguments

X	Point pattern on linear network (object of class "lpp").
lambda	Intensity values for the point pattern. Either a numeric vector, a function, a pixel image (object of class "im" or "linim") or a fitted point process model (object of class "ppm" or "lppm") or NULL.
r	Optional. Numeric vector of values of the function argument r. There is a sensible default.
...	Ignored.
normalise	Logical. If TRUE (the default), the denominator of the estimator is data-dependent (equal to the sum of the reciprocal intensities at the data points, raised to normpower), which reduces the sampling variability. If FALSE, the denominator is the length of the network.
normpower	Integer (usually either 1 or 2). Normalisation power. See Details.

update	Logical value indicating what to do when lambda is a fitted model (class "lppm" or "ppm"). If update=TRUE (the default), the model will first be refitted to the data X (using update.lppm or update.ppm) before the fitted intensity is computed. If update=FALSE, the fitted intensity of the model will be computed without re-fitting it to X.
leaveoneout	Logical value specifying whether to use a leave-one-out rule when calculating the intensity. See Details.
sigma	Smoothing bandwidth (passed to density.lpp) for kernel density estimation of the intensity when lambda=NULL.
adjust.sigma	Numeric value. sigma will be multiplied by this value.
bw	Smoothing bandwidth (passed to density.default) for one-dimensional kernel smoothing of the pair correlation function. Either a numeric value, or a character string recognised by density.default.
adjust.bw	Numeric value. bw will be multiplied by this value.

Details

This command computes the inhomogeneous version of the pair correlation function based on *Euclidean* distances, for a point pattern on a linear network.

This is different from the inhomogeneous pair correlation function based on *shortest-path* distances, which is computed by linearpcfinhom.

The inhomogeneous pair correlation function based on *Euclidean* distances is defined in equation (30) of Rakshit, Nair and Baddeley (2017). Estimation is performed as described in equation (34) of Rakshit, Nair and Baddeley (2017).

The argument lambda should provide estimated values of the intensity of the point process at each point of X.

If lambda=NULL, the intensity will be estimated by kernel smoothing by calling density.lpp with the smoothing bandwidth sigma, and with any other relevant arguments that might be present in .... A leave-one-out kernel estimate will be computed if leaveoneout=TRUE.

If lambda is given, then it may be a numeric vector (of length equal to the number of points in X), or a function(x,y) that will be evaluated at the points of X to yield numeric values, or a pixel image (object of class "im") or a fitted point process model (object of class "ppm" or "lppm").

If lambda is a fitted point process model, the default behaviour is to update the model by re-fitting it to the data, before computing the fitted intensity. This can be disabled by setting update=FALSE. The intensity at data points will be computed by fitted.lppm or fitted.ppm. A leave-one-out estimate will be computed if leaveoneout=TRUE and update=TRUE.

If normalise=TRUE (the default), then the estimate is multiplied by $c^{\mathrm{normpower}}$ where $c = \mathrm{length}(L)/\sum(1/\lambda(x_i))$. This rescaling reduces the variability and bias of the estimate in small samples and in cases of very strong inhomogeneity. The default value of normpower is 1 (for consistency with previous versions of **spatstat**) but the most sensible value is 2, which would correspond to rescaling the lambda values so that $\sum(1/\lambda(x_i)) = \mathrm{area}(W)$.

Value

Function value table (object of class "fv").

Warning

Older versions of linearpcfEuclidInhom interpreted lambda=NULL to mean that the homogeneous function linearpcfEuclid should be computed. This was changed to the current behaviour in version 3.1-0 of **spatstat.linnet**.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

References

Rakshit. S., Nair, G. and Baddeley, A. (2017) Second-order analysis of point patterns on a network using any distance metric. *Spatial Statistics* **22** (1) 129–154.

See Also

linearKEuclidInhom, linearpcfEuclid.

See linearpcfinhom for the corresponding function based on shortest-path distances.

Examples

```
X <- rpoislpp(5, simplenet)
fit <- lppm(X ~x)
g <- linearpcfEuclidInhom(X, lambda=fit)
plot(g)
```

---

linearpcfinhom *Inhomogeneous Linear Pair Correlation Function*

Description

Computes an estimate of the inhomogeneous linear pair correlation function for a point pattern on a linear network.

Usage

```
linearpcfinhom(X, lambda=NULL, r=NULL, ..., correction="Ang",
               normalise=TRUE, normpower=1,
       update = TRUE, leaveoneout = TRUE,
               sigma=NULL, adjust.sigma=1,
               bw="nrd0", adjust.bw=1,
       ratio = FALSE)
```

Arguments

X	Point pattern on linear network (object of class "lpp").
lambda	Intensity values for the point pattern. Either a numeric vector, a function, a pixel image (object of class "im") or a fitted point process model (object of class "ppm" or "lppm").
r	Optional. Numeric vector of values of the function argument r. There is a sensible default.
...	Arguments passed to density.default to control the smoothing of the estimates of pair correlation.
correction	Geometry correction. Either "none" or "Ang". See Details.
normalise	Logical. If TRUE (the default), the denominator of the estimator is data-dependent (equal to the sum of the reciprocal intensities at the data points, raised to normpower), which reduces the sampling variability. If FALSE, the denominator is the length of the network.
normpower	Integer (usually either 1 or 2). Normalisation power. See explanation in linearKinhom.
update	Logical value indicating what to do when lambda is a fitted model (class "lppm" or "ppm"). If update=TRUE (the default), the model will first be refitted to the data X (using update.lppm or update.ppm) before the fitted intensity is computed. If update=FALSE, the fitted intensity of the model will be computed without re-fitting it to X.
leaveoneout	Logical value specifying whether to use a leave-one-out rule when calculating the intensity. See Details.
sigma	Smoothing bandwidth (passed to density.lpp) for kernel density estimation of the intensity when lambda=NULL.
adjust.sigma	Numeric value. sigma will be multiplied by this value.
bw	Smoothing bandwidth (passed to density.default) for one-dimensional kernel smoothing of the pair correlation function. Either a numeric value, or a character string recognised by density.default.
adjust.bw	Numeric value. bw will be multiplied by this value.
ratio	Logical. If TRUE, the numerator and denominator of each estimate will also be saved, for use in analysing replicated point patterns.

Details

This command computes the inhomogeneous version of the linear pair correlation function from point pattern data on a linear network.

The argument lambda should provide estimated values of the intensity of the point process at each point of X.

If lambda=NULL, the intensity will be estimated by kernel smoothing by calling density.lpp with the smoothing bandwidth sigma, and with any other relevant arguments that might be present in .... A leave-one-out kernel estimate will be computed if leaveoneout=TRUE.

If lambda is given, it may be a numeric vector (of length equal to the number of points in X), or a function(x,y) that will be evaluated at the points of X to yield numeric values, or a pixel image (object of class "im") or a fitted point process model (object of class "ppm" or "lppm").

If lambda is a fitted point process model, the default behaviour is to update the model by re-fitting it to the data, before computing the fitted intensity. This can be disabled by setting update=FALSE. The intensity at data points will be computed by fitted.lppm or fitted.ppm. A leave-one-out estimate will be computed if leaveoneout=TRUE and update=TRUE.

If correction="none", the calculations do not include any correction for the geometry of the linear network. If correction="Ang", the pair counts are weighted using Ang's correction (Ang, 2010).

The bandwidth for smoothing the pairwise distances is determined by arguments ... passed to density.default, mainly the arguments bw and adjust. The default is to choose the bandwidth by Silverman's rule of thumb bw="nrd0" explained in density.default.

Value

Function value table (object of class "fv").

If ratio=TRUE then the return value also has two attributes called "numerator" and "denominator" which are "fv" objects containing the numerators and denominators of each estimate of $g(r)$.

Warning

Older versions of linearpcfinhom interpreted lambda=NULL to mean that the homogeneous function linearpcf should be computed. This was changed to the current behaviour in version 3.1-0 of **spatstat.linnet**.

Author(s)

Ang Qi Wei <aqw07398@hotmail.com> and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

References

Ang, Q.W. (2010) Statistical methodology for spatial point patterns on a linear network. MSc thesis, University of Western Australia.

Ang, Q.W., Baddeley, A. and Nair, G. (2012) Geometrically corrected second-order analysis of events on a linear network, with applications to ecology and criminology. *Scandinavian Journal of Statistics* **39**, 591–617.

Okabe, A. and Yamada, I. (2001) The K-function method on a network and its computational implementation. *Geographical Analysis* **33**, 271-290.

See Also

linearpcf, linearKinhom, lpp

Examples

```
X <- rpoislpp(5, simplenet)
fit <- lppm(X ~x)
g <- linearpcfinhom(X, lambda=fit, update=FALSE)
plot(g)
ge <- linearpcfinhom(X, sigma=bw.lppl)
```

lineartileindex *Determine Which Tile Contains Each Given Point on a Linear Network*

Description

Given a tessellation on a linear network, and a list of points on the network, determine which tile of the tessellation contains each of the given points.

Usage

```
lineartileindex(seg, tp, Z, method = c("encode", "C", "interpreted"))
```

Arguments

seg, tp	Vectors of local coordinates of the query points. See Details.
Z	A tessellation on a linear network (object of class "lintess").
method	Internal use only.

Details

This low-level function is the analogue of tileindex for linear networks. For a tessellation Z on a linear network, and a list of query points on the same network, the function determines which tile of the tessellation contains each query point.

Argument Z should be a tessellation on a linear network (object of class "lintess").

The vectors seg and tp specify the locations of the query points, on the same network, using local coordinates: seg contains integer values specifying which segment of the network contains each query point; tp contains numeric values between 0 and 1 specifying the fractional position along that segment.

The result is a factor, of the same length as seg and tp, indicating which tile contains each point. The levels of the factor are the names of the tiles of Z.

Value

A factor, of the same length as seg and tp, whose levels are the names of the tiles of Z.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>

See Also

lintess.

as.linfun.lintess to create a function whose value is the tile index.

cut.lpp for a neater way to classify the points of a point pattern on a linear network according to a tessellation on the network.

Examples

```
Z <- lineardirichlet(runiflpp(15, simplenet))
X <- runiflpp(10, simplenet)
coX <- coords(X)
ii <- lineartileindex(coX$seg, coX$tp, Z)
```

`linequad` *Quadrature Scheme on a Linear Network*

Description

Generates a quadrature scheme (an object of class `"quad"`) on a linear network.

Usage

```
linequad(X, Y, ..., eps = NULL, nd = 1000, random = FALSE)
```

Arguments

`X`	Data points. An object of class `"lpp"` or `"ppp"`.
`Y`	Line segments on which the points of `X` lie. An object of class `"psp"` or `"linnet"`. Required only when `X` is a `"ppp"` object.
`...`	Ignored.
`eps`	Optional. Spacing between successive dummy points along each segment. (This is the maximum spacing; some spacings will be shorter.)
`nd`	Optional. Total number of dummy locations to be generated. (Actual number may be larger.)
`random`	Logical value indicating whether the sequence of dummy points should start at a randomly-chosen position along each segment.

Details

This command generates a quadrature scheme (object of class `"quad"`) from a pattern of points on a linear network.

Normally the user does not need to call `linequad` explicitly. It is invoked by **spatstat** functions when needed. A quadrature scheme is required by `lppm` in order to fit point process models to point pattern data on a linear network. A quadrature scheme is also used by `rhohat.lpp` and other functions.

In order to create the quadrature scheme, dummy points are placed along each line segment of the network. The dummy points are evenly-spaced with spacing `eps`. The default is `eps = totlen/nd` where `totlen` is the total length of all line segments in the network.

Every line segment of the network will contain at least one dummy location. Consequently the actual number of dummy location generated will typically be greater than `nd`, especially when `nd` is small. If `eps` is specified, the number of dummy locations will be greater than `totlen/eps`, especially when `eps` is large.

If X is a multitype point pattern with m possible types, the dummy points will also be a marked point pattern. At each dummy location, m marked dummy points will be placed, one dummy point of each possible type. Additionally at each data location, a further $m-1$ dummy points will be placed, one dummy point of each possible type other than the type of the data point. The total number of dummy points will be $mk + (m-1)n = m(k+n) - n$ and the total number of quadrature points will be $m(k+n)$, where k is the number of dummy locations and n is the number of data points in X.

Value

A quadrature scheme (object of class "quad").

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Greg McSwiggan and Suman Rakshit.

See Also

lppm

---

linfun *Function on a Linear Network*

Description

Create a function on a linear network.

Usage

```
linfun(f, L)
```

Arguments

f	A function in the R language.
L	A linear network (object of class "linnet") on which f is defined.

Details

This creates an object of class "linfun". This is a simple mechanism for handling a function defined on a linear network, to make it easier to display and manipulate.

f should be a function in the R language, with formal arguments x,y,seg,tp (and optional additional arguments) where x,y are Cartesian coordinates of locations on the linear network, seg, tp are the local coordinates.

The function f should be vectorised: that is, if x,y,seg,tp are numeric vectors of the same length n, then v <- f(x,y,seg,tp) should be a vector of length n.

L should be a linear network (object of class "linnet") on which the function f is well-defined.

The result is a function g in the R language which belongs to the special class "linfun". There are several methods for this class including print, plot and as.linim.

This function can be called as g(X) where X is an "lpp" object, or called as g(x,y) or g(x,y,seg,tp) where x,y,seg,tp are coordinates. If the original function f had additional arguments, then these may be included in the call to g, and will be passed to f.

Value

A function in the R\ language. It also belongs to the class "linfun" which has methods for plot, print etc.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Rolf Turner <rolfturner@posteo.net>

See Also

methods.linfun for methods applicable to "linfun" objects.

distfun.lpp, nnfun.lpp.

Examples

```
f <- function(x,y,seg,tp) { x+y }
g <- linfun(f, simplenet)
plot(g)
X <- runiflpp(3, simplenet)
g(X)
Z <- as.linim(g)

f <- function(x,y,seg,tp, mul=1) { mul*(x+y) }
g <- linfun(f, simplenet)
plot(g)
plot(g, mul=10)
g(X, mul=10)
Z <- as.linim(g, mul=10)
```

---

linim *Create Pixel Image on Linear Network*

Description

Creates an object of class "linim" that represents a pixel image on a linear network.

Usage

```
linim(L, Z, ..., restrict=TRUE, df=NULL)
```

Arguments

L	Linear network (object of class "linnet").
Z	Pixel image (object of class "im").
...	Ignored.
restrict	Advanced use only. Logical value indicating whether to ensure that all pixels in Z which do not lie on the network L have pixel value NA. This condition must be satisfied, but if you set restrict=FALSE it will not be checked, and the code will run faster.
df	Advanced use only. Data frame giving full details of the mapping between the pixels of Z and the lines of L. See Details.

Details

This command creates an object of class "linim" that represents a pixel image defined on a linear network. Typically such objects are used to represent the result of smoothing or model-fitting on the network. Most users will not need to call linim directly.

The argument L is a linear network (object of class "linnet"). It gives the exact spatial locations of the line segments of the network, and their connectivity.

The argument Z is a pixel image object of class "im" that gives a pixellated approximation of the function values.

For increased efficiency, advanced users may specify the optional argument df. This is a data frame giving the precomputed mapping between the pixels of Z and the line segments of L. It should have columns named xc, yc containing the coordinates of the pixel centres, x,y containing the projections of these pixel centres onto the linear network, mapXY identifying the line segment on which each projected point lies, and tp giving the parametric position of (x,y) along the segment.

Value

Object of class "linim" that also inherits the class "im". There is a special method for plotting this class.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

References

Ang, Q.W. (2010) *Statistical methodology for events on a network*. Master's thesis, School of Mathematics and Statistics, University of Western Australia.

Ang, Q.W., Baddeley, A. and Nair, G. (2012) Geometrically corrected second-order analysis of events on a linear network, with applications to ecology and criminology. *Scandinavian Journal of Statistics* **39**, 591–617.

McSwiggan, G., Nair, M.G. and Baddeley, A. (2012) Fitting Poisson point process models to events on a linear network. Manuscript in preparation.

See Also

plot.linim, linnet, eval.linim, Math.linim, im.

Examples

```
Z <- as.im(function(x,y) {x-y}, Frame(simplenet))
X <- linim(simplenet, Z)
X
```

---

linim.apply *Apply Function Pixelwise to List of Images on a Network*

Description

Returns a pixel image obtained by applying a given function to corresponding pixels in a list of several pixel images on a linear network.

Usage

```
linim.apply(X, FUN, ..., fun.handles.na=FALSE, check=TRUE, verbose=TRUE)
```

Arguments

X	A list of pixel images on the same network (objects of class "linim").
FUN	A function that can be applied to vectors, or a character string giving the name of such a function.
...	Additional arguments to FUN.
fun.handles.na	Logical value specifying what to do when the data include NA values. See Details.
check	Logical value specifying whether to check that the images in X are compatible (for example that they have the same grid of pixel locations) and to convert them to compatible images if necessary.
verbose	Logical value specifying whether to print informative messages.

Details

The argument X should be a list of pixel images on a network (objects of class "linim"). They should all be defined on the same network. If the images do not have identical pixel grids, they will be converted to a common grid using harmonise.linim.

At each pixel location, the values of the images in X at that pixel will be extracted as a vector; the function FUN will be applied to this vector; and the return value of FUN will become the pixel value of the resulting image. For example linim.apply(X, mean) will return a pixel image in which the value of each pixel is the average of the corresponding pixel values in the images in X.

If the result of FUN is a vector, then the result of linim.apply will be a list of images. For example linim.apply(X, range) will return a list of two images containing the pixelwise minimum and pixelwise maximum, respectively, of the input images in X.

The argument fun.handles.na specifies what to do when some of the pixel values are NA.

- If fun.handles.na=FALSE (the default), the function FUN is never applied to data that include NA values; the result is defined to be NA whenever the data contain NA.
- If fun.handles.na=TRUE, the function FUN will be applied to all pixel data, including those which contain NA values.

Value

A pixel image on a network (object of class "linim") or a list of pixel images on the same network.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

eval.linim for algebraic operations with images.

Examples

```
# list of two pixel images
X <- runiflpp(5, simplenet, nsim=2)
Y <- solapply(lapply(X, distfun), as.linim)
plot(Y)
linim.apply(Y, max)
linim.apply(Y, sum)
linim.apply(Y, range)
```

---

linnet *Create a Linear Network*

Description

Creates an object of class "linnet" representing a network of line segments.

Usage

```
linnet(vertices, m, edges, sparse=FALSE, warn=TRUE)
```

Arguments

vertices	Point pattern (object of class "ppp") specifying the vertices of the network.
m	Adjacency matrix. A matrix or sparse matrix of logical values equal to TRUE when the corresponding vertices are joined by a line. (Specify either m or edges.)
edges	Edge list. A two-column matrix of integers, specifying all pairs of vertices that should be joined by an edge. (Specify either m or edges.)
sparse	Optional. Logical value indicating whether to use a sparse matrix representation of the network. See Details.
warn	Logical value indicating whether to issue a warning if the resulting network is not connected.

Details

An object of class "linnet" represents a network of straight line segments in two dimensions. The function linnet creates such an object from the minimal information: the spatial location of each vertex (endpoint, crossing point or meeting point of lines) and information about which vertices are joined by an edge.

If sparse=FALSE (the default), the algorithm will compute and store various properties of the network, including the adjacency matrix m and a matrix giving the shortest-path distances between each pair of vertices in the network. This is more efficient for small datasets. However it can require large amounts of memory and can take a long time to execute.

If sparse=TRUE, then the shortest-path distances will not be computed, and the network adjacency matrix m will be stored as a sparse matrix. This saves a lot of time and memory when creating the linear network.

If the argument edges is given, then it will also determine the *ordering* of the line segments when they are stored or extracted. For example, edges[i,] corresponds to as.psp(L)[i].

Value

Object of class "linnet" representing the linear network.

Author(s)

Ang Qi Wei <aqw07398@hotmail.com> and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

See Also

simplenet for an example of a linear network.

methods.linnet for methods applicable to linnet objects.

Special tools: thinNetwork, insertVertices, joinVertices, connected.linnet, lixellate.

delaunayNetwork for the Delaunay triangulation as a network.

ppp, psp.

Examples

```
# letter 'A' specified by adjacency matrix
v <- ppp(x=(-2):2, y=3*c(0,1,2,1,0), c(-3,3), c(-1,7))
m <- matrix(FALSE, 5,5)
for(i in 1:4) m[i,i+1] <- TRUE
m[2,4] <- TRUE
m <- m | t(m)
letterA <- linnet(v, m)
plot(letterA)

# letter 'A' specified by edge list
edg <- cbind(1:4, 2:5)
edg <- rbind(edg, c(2,4))
letterA <- linnet(v, edges=edg)
```

lintess *Tessellation on a Linear Network*

Description

Create a tessellation on a linear network.

Usage

```
lintess(L, df, marks=NULL)
```

Arguments

L	Linear network (object of class "linnet").
df	Data frame of local coordinates for the pieces that make up the tiles of the tessellation. See Details.
marks	Vector or data frame of marks associated with the tiles of the tessellation.

Details

A tessellation on a linear network L is a partition of the network into non-overlapping pieces (tiles). Each tile consists of one or more line segments which are subsets of the line segments making up the network. A tile can consist of several disjoint pieces.

The data frame df should have columns named seg, t0, t1 and tile. Any additional columns will be ignored.

Each row of the data frame specifies one sub-segment of the network and allocates it to a particular tile.

The seg column specifies which line segment of the network contains the sub-segment. Values of seg are integer indices for the segments in as.psp(L).

The t0 and t1 columns specify the start and end points of the sub-segment. They should be numeric values between 0 and 1 inclusive, where the values 0 and 1 representing the network vertices that are joined by this network segment.

The tile column specifies which tile of the tessellation includes this sub-segment. It will be coerced to a factor and its levels will be the names of the tiles.

If df is missing or NULL, the result is a tessellation with only one tile, consisting of the entire network L.

Additional data called *marks* may be associated with each tile of the tessellation. The argument marks should be a vector with one entry for each tile (that is, one entry for each level of df$tile) or a data frame with one row for each tile. In general df and marks will have different numbers of rows.

Value

An object of class "lintess". There are methods for print, plot and summary for this object.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Greg McSwiggan.

See Also

linnet for linear networks.

plot.lintess for plotting.

divide.linnet to make a tessellation demarcated by given points.

chop.linnet to make a tessellation demarcated by infinite lines.

lineardirichlet to create the Dirichlet-Voronoi tessellation from a point pattern on a linear network.

as.linfun.lintess, as.linnet.lintess and as.linim to convert to other classes.

tile.lengths to compute the length of each tile in the tessellation.

lineartileindex and identify.lintess to identify which tile of the tessellation contains a given location on the network.

The undocumented methods Window.lintess and as.owin.lintess extract the spatial window.

Examples

```
# tessellation consisting of one tile for each existing segment
ns <- nsegments(simplenet)
df <- data.frame(seg=1:ns, t0=0, t1=1, tile=letters[1:ns])
u <- lintess(simplenet, df)
u
plot(u)
S <- as.psp(simplenet)
marks(u) <- data.frame(len=lengths_psp(S), ang=angles.psp(S))
u
plot(u)
```

---

lixellate *Subdivide Segments of a Network*

Description

Each line segment of a linear network will be divided into several shorter segments (line elements or lixels).

Usage

```
lixellate(X, ..., nsplit, eps, sparse = TRUE)
```

Arguments

X	A linear network (object of class "linnet") or a point pattern on a linear network (object of class "lpp").
...	Ignored.
nsplit	Number of pieces into which *each* line segment of X should be divided. Either a single integer, or an integer vector with one entry for each line segment in X. Incompatible with eps.
eps	Maximum length of the resulting pieces of line segment. A single numeric value. Incompatible with nsplit.
sparse	Optional. Logical value specifying whether the resulting linear network should be represented using a sparse matrix. If sparse=NULL, then the representation will be the same as in X.

Details

Each line segment in X will be subdivided into equal pieces. The result is an object of the same kind as X, representing the same data as X except that the segments have been subdivided.

Splitting is controlled by the arguments nsplit and eps, exactly one of which should be given.

If nsplit is given, it specifies the number of pieces into which *each* line segment of X should be divided. It should be either a single integer, or an integer vector of length equal to the number of line segments in X.

If eps is given, it specifies the maximum length of any resulting piece of line segment.

It is strongly advisable to use sparse=TRUE (the default) to limit the computation time.

If X is a point pattern (class "lpp") then the spatial coordinates and marks of each data point are unchanged, but the local coordinates will change, because they are adjusted to map them to the new subdivided network.

Value

Object of the same kind as X.

Author(s)

Greg McSwiggan, Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

linnet, lpp.

Examples

```
A <- lixellate(simplenet, nsplit=4)
plot(A, main="lixellate(simplenet, nsplit=4)")
points(vertices(A), pch=16)

spiders
lixellate(spiders, nsplit=3)
```

lpp *Create Point Pattern on Linear Network*

Description

Creates an object of class "lpp" that represents a point pattern on a linear network.

Usage

```
lpp(X, L, ...)
```

Arguments

X	Locations of the points. A matrix or data frame of coordinates, or a point pattern object (of class "ppp") or other data acceptable to as.ppp.
L	Linear network (object of class "linnet").
...	Ignored.

Details

This command creates an object of class "lpp" that represents a point pattern on a linear network.

Normally X is a point pattern. The points of X should lie on the lines of L.

Alternatively X may be a matrix or data frame containing at least two columns.

- Usually the first two columns of X will be interpreted as spatial coordinates, and any remaining columns as marks.
- An exception occurs if X is a data frame with columns named x, y, seg and tp. Then x and y will be interpreted as spatial coordinates, and seg and tp as local coordinates, with seg indicating which line segment of L the point lies on, and tp indicating how far along the segment the point lies (normalised to 1). Any remaining columns will be interpreted as marks.
- Another exception occurs if X is a data frame with columns named seg and tp. Then seg and tp will be interpreted as local coordinates, as above, and the spatial coordinates x,y will be computed from them. Any remaining columns will be interpreted as marks.

If X is missing or NULL, the result is an empty point pattern (i.e. containing no points).

Value

An object of class "lpp". Also inherits the class "ppx".

Note on changed format

The internal format of "lpp" objects was changed in **spatstat** version 1.28-0. Objects in the old format are still handled correctly, but computations are faster in the new format. To convert an object X from the old format to the new format, use X <- lpp(as.ppp(X), as.linnet(X)).

Author(s)

Ang Qi Wei <aqw07398@hotmail.com> and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

See Also

Installed datasets which are "lpp" objects: chicago, dendrite, spiders.

See as.lpp for converting data to an lpp object.

See methods.lpp and methods.ppx for other methods applicable to lpp objects.

Calculations on an lpp object: intensity.lpp, distfun.lpp, nndist.lpp, nnwhich.lpp, nncross.lpp, nnfun.lpp.

Summary functions: linearK, linearKinhom, linearpcf, linearKdot, linearKcross, linearmarkconnect, etc.

Random point patterns on a linear network can be generated by rpoislpp or runiflpp.

See linnet for linear networks.

Examples

```
# letter 'A'
v <- ppp(x=(-2):2, y=3*c(0,1,2,1,0), c(-3,3), c(-1,7))
edg <- cbind(1:4, 2:5)
edg <- rbind(edg, c(2,4))
letterA <- linnet(v, edges=edg)

# points on letter A
xx <- list(x=c(-1.5,0,0.5,1.5), y=c(1.5,3,4.5,1.5))
X <- lpp(xx, letterA)

plot(X)
X
summary(X)

# empty pattern
lpp(L=letterA)
```

---

lppm *Fit Point Process Model to Point Pattern on Linear Network*

Description

Fit a point process model to a point pattern dataset on a linear network

Usage

```
lppm(X, ...)

## S3 method for class 'formula'
lppm(X, interaction=NULL, ..., data=NULL)

## S3 method for class 'lpp'
lppm(X, ..., eps=NULL, nd=1000, random=FALSE)
```

Arguments

X	Either an object of class "lpp" specifying a point pattern on a linear network, or a formula specifying the point process model.
...	Arguments passed to ppm.
interaction	An object of class "interact" describing the point process interaction structure, or NULL indicating that a Poisson process (stationary or nonstationary) should be fitted.
data	Optional. The values of spatial covariates (other than the Cartesian coordinates) required by the model. A list whose entries are images, functions, windows, tessellations or single numbers.
eps	Optional. Spacing between dummy points along each segment of the network.
nd	Optional. Total number of dummy points placed on the network. Ignored if eps is given.
random	Logical value indicating whether the grid of dummy points should be placed at a randomised starting position.

Details

This function fits a point process model to data that specify a point pattern on a linear network. It is a counterpart of the model-fitting function ppm designed to work with objects of class "lpp" instead of "ppp".

The function lppm is generic, with methods for the classes formula and lppp.

In lppm.lpp the first argument X should be an object of class "lpp" (created by the command lpp) specifying a point pattern on a linear network.

In lppm.formula, the first argument is a formula in the R language describing the spatial trend model to be fitted. It has the general form pattern ~ trend where the left hand side pattern is usually the name of a point pattern on a linear network (object of class "lpp") to which the model should be fitted, or an expression which evaluates to such a point pattern; and the right hand side trend is an expression specifying the spatial trend of the model. Variable names which appear in the trend can be

- the name of an object in the current environment
- the name of an entry in the list covariates
- one of the reserved names x, y, seg, tp representing respectively the spatial coordinates x and y, and the local coordinates seg (line segment index) and tp (relative position along the segment).

Covariates which are objects in the environment or entries in the list `covariates` may have any of the following formats:

a pixel image, giving the values of a spatial covariate at a fine grid of locations. It should be an object of class `"im"`, see `im.object`, or class `"linim"`, see `linim`.

a function, which can be evaluated at any location on the network to obtain the value of the spatial covariate. This may be a function of class `"linfun"` (function on a network) or `"funxy"` (function in two dimensional space). Alternatively it may be any function in the R language: the first two arguments of the function should be the Cartesian coordinates x and y. The function may have additional arguments include `seg`, `tp` and `marks` and other arguments.

a window, interpreted as a logical variable which is `TRUE` inside the window and `FALSE` outside it. This should be an object of class `"owin"`.

a tessellation, interpreted as a factor covariate. For each spatial location, the factor value indicates which tile of the tessellation it belongs to. This should be an object of class `"tess"` or `"lintess"`.

a single number, indicating a covariate that is constant in this dataset.

Other arguments `...` are passed from `lppm.formula` to `lppm.lpp` and from `lppm.lpp` to `ppm`.

Value

An object of class `"lppm"` representing the fitted model. There are methods for `print`, `predict`, `coef` and similar functions.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Greg McSwiggan.

References

McSwiggan, G. (2019) Spatial point process methods for linear networks with applications to road accident analysis. PhD thesis, University of Western Australia.

See Also

`methods.lppm`, `predict.lppm`, `ppm`, `lpp`.

Examples

```
X <- runiflpp(15, simplenet)
lppm(X ~1)
lppm(X ~x)
marks(X) <- factor(rep(letters[1:3], 5))
lppm(X ~ marks)
lppm(X ~ marks * x)
```

lurking.lppm *Lurking Variable Plot on a Linear Network*

Description

Plot point process residuals against a covariate, for a point process model on a linear network, or a point pattern on a linear network.

Usage

```
 ## S3 method for class 'lppm'
lurking(object, covariate,
                    type="raw",
                    cumulative=TRUE,
                    ...,
                    plot.it = TRUE,
                    plot.sd = is.poisson(object),
                    clipwindow=NULL,
                    rv = NULL,
                    envelope=FALSE, nsim=39, nrank=1,
                    typename,
                    covname,
                    oldstyle=FALSE,
                    check=TRUE,
                    verbose=TRUE,
                    nx=128,
                    splineargs=list(spar=0.5),
                    internal=NULL)

 ## S3 method for class 'lpp'
lurking(object, covariate,
                    type="raw",
                    cumulative=TRUE,
                    ...,
                    plot.it = TRUE,
                    plot.sd = is.poisson(object),
                    clipwindow=NULL,
                    rv = NULL,
                    envelope=FALSE, nsim=39, nrank=1,
                    typename,
                    covname,
                    oldstyle=FALSE,
                    check=TRUE,
                    verbose=TRUE,
                    nx=128,
                    splineargs=list(spar=0.5),
                    internal=NULL)
```

Arguments

object	The fitted point process model on a linear network (an object of class "lppm") for which diagnostics should be produced. This object is usually obtained from lppm. Alternatively, object may be a point pattern on a linear network (object of class "lpp").
covariate	The covariate against which residuals should be plotted. Either a numeric vector, a pixel image, a function(x,y), an expression, or one of the strings "x", "y" or "tp". See *Details* below.
type	String indicating the type of residuals or weights to be computed. Choices include "eem", "raw", "inverse" and "pearson".
cumulative	Logical value indicating whether to plot a cumulative sum of marks (cumulative=TRUE, the default) or the derivative of this sum, a marginal density of the smoothed residual field (cumulative=FALSE).
...	Arguments passed to plot.default and lines to control the plot behaviour.
plot.it	Logical value indicating whether plots should be shown. If plot.it=FALSE, only the computed coordinates for the plots are returned. See *Value*.
plot.sd	Logical value indicating whether error bounds should be added to plot. The default is TRUE for Poisson models and FALSE for non-Poisson models. See Details.
clipwindow	If not NULL this argument indicates that residuals shall only be computed inside a subregion of the window containing the original point pattern data. Then clipwindow should be a window object of class "owin".
rv	Usually absent. If this argument is present, the point process residuals will not be calculated from the fitted model object, but will instead be taken directly from rv.
envelope	Logical value indicating whether to compute simulation envelopes for the plot. Alternatively envelope may be a list of point patterns to use for computing the simulation envelopes, or an object of class "envelope" containing simulated point patterns.
nsim	Number of simulated point patterns to be generated to produce the simulation envelope, if envelope=TRUE.
nrank	Integer. Rank of the envelope value amongst the nsim simulated values. A rank of 1 means that the minimum and maximum simulated values will be used.
typename	Usually absent. If this argument is present, it should be a string, and will be used (in the axis labels of plots) to describe the type of residuals.
covname	A string name for the covariate, to be used in axis labels of plots.
oldstyle	Logical flag indicating whether error bounds should be plotted using the approximation given in the original paper (oldstyle=TRUE), or using the correct asymptotic formula (oldstyle=FALSE).
check	Logical flag indicating whether the integrity of the data structure in object should be checked.
verbose	Logical value indicating whether to print progress reports during Monte Carlo simulation.

nx	Integer. Number of covariate values to be used in the plot.
splineargs	A list of arguments passed to smooth.spline for the estimation of the derivatives in the case cumulative=FALSE.
internal	Internal use only.

Details

This function generates a 'lurking variable' plot for a fitted point process model on a linear network. Residuals from the model represented by object are plotted against the covariate specified by covariate. This plot can be used to reveal departures from the fitted model, in particular, to reveal that the point pattern depends on the covariate.

The function lurking is generic, with methods for lppm and lpp documented here.

The argument object would usually be a fitted point process model on a network, obtained from the model-fitting algorithm lppm). If object is a point pattern on a network (object of class "lpp") then the model is taken to be the uniform Poisson process on the network (Complete Spatial Randomness on the Network).

First the residuals from the fitted model (Baddeley et al, 2004) are computed at each pixel, or alternatively the 'exponential energy marks' (Stoyan and Grabarnik, 1991) are computed at each data point. The argument type selects the type of residual or weight. See diagnose.ppm for options and explanation.

A lurking variable plot for point processes (Baddeley et al, 2004) displays either the cumulative sum of residuals/weights (if cumulative = TRUE) or a kernel-weighted average of the residuals/weights (if cumulative = FALSE) plotted against the covariate. The empirical plot (solid lines) is shown together with its expected value assuming the model is true (dashed lines) and optionally also the pointwise two-standard-deviation limits (grey shading).

To be more precise, let $Z(u)$ denote the value of the covariate at a spatial location u on the network.

- If cumulative=TRUE then we plot $H(z)$ against z, where $H(z)$ is the sum of the residuals over all quadrature points where the covariate takes a value less than or equal to z, or the sum of the exponential energy weights over all data points where the covariate takes a value less than or equal to z.
- If cumulative=FALSE then we plot $h(z)$ against z, where $h(z)$ is the derivative of $H(z)$, computed approximately by spline smoothing.

For the point process residuals $E(H(z)) = 0$, while for the exponential energy weights $E(H(z)) =$ length of the subset of the network satisfying $Z(u) <= z$.

If the empirical and theoretical curves deviate substantially from one another, the interpretation is that the fitted model does not correctly account for dependence on the covariate. The correct form (of the spatial trend part of the model) may be suggested by the shape of the plot.

If plot.sd = TRUE, then superimposed on the lurking variable plot are the pointwise two-standard-deviation error limits for $H(x)$ calculated for the inhomogeneous Poisson process. The default is plot.sd = TRUE for Poisson models and plot.sd = FALSE for non-Poisson models.

By default, the two-standard-deviation limits are calculated from the exact formula for the asymptotic variance of the residuals under the asymptotic normal approximation, equation (37) of Baddeley et al (2006). However, for compatibility with the original paper of Baddeley et al (2005), if

oldstyle=TRUE, the two-standard-deviation limits are calculated using the innovation variance, an over-estimate of the true variance of the residuals.

The argument covariate is either:

- a numeric vector, containing the values of the covariate for each of the quadrature points in the fitted model.
- a pixel image, containing the values of the covariate at each location in the window. The values of this image at the quadrature points will be extracted.
- a function(x,y). The values of this function at the quadrature points will be evaluated.
- an expression in the R language. The expression will be evaluated in the same environment as the model formula used in fitting the model object. It must yield a vector of the same length as the number of quadrature points. The expression may contain the terms x and y representing the cartesian coordinates, and may also contain other variables that were available when the model was fitted. Certain variable names are reserved words; see lppm.
- one of the strings "x" or "y" representing the cartesian coordinates.
- the string "tp" representing the local coordinate tp which measures relative position along the network segment.

Lurking variable plots for the x and y coordinates are also generated by diagnose.lppm, amongst other types of diagnostic plots. The function lurking is more general, in that it enables the user to plot the residuals against any chosen covariate that may have been present.

Value

The (invisible) return value is an object belonging to the class "lurk", for which there are methods for plot and print.

This object is a list containing two dataframes empirical and theoretical. The first dataframe empirical contains columns covariate and value giving the coordinates of the lurking variable plot. The second dataframe theoretical contains columns covariate, mean and sd giving the coordinates of the plot of the theoretical mean and standard deviation.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

References

Baddeley, A., Turner, R., Møller, J. and Hazelton, M. (2005) Residual analysis for spatial point processes. *Journal of the Royal Statistical Society, Series B* **67**, 617–666.

Baddeley, A., Møller, J. and Pakes, A.G. (2006) Properties of residuals for spatial point processes. *Annals of the Institute of Statistical Mathematics* **60**, 627–649.

Stoyan, D. and Grabarnik, P. (1991) Second-order characteristics for stochastic structures connected with Gibbs point processes. *Mathematische Nachrichten*, 151:95–100.

See Also

lppm, lurking

Examples

```
fit <- lppm(spiders ~ y)
(b <- lurking(fit, expression(x), type="raw"))
lurking(fit, "x", type="raw", cumulative=FALSE)
```

`marks.linnet` *Marks of a Network*

Description

Extract or change the marks attached to vertices or segments of a linear network.

Usage

```
## S3 method for class 'linnet'
marks(x, of=c("segments", "vertices"), ...)

## S3 replacement method for class 'linnet'
marks(x, of=c("segments", "vertices"), ...) <- value

## S3 method for class 'linnet'
unmark(X)
```

Arguments

`x`, `X`	Linear network (object of class `"linnet"`).
`of`	Character string (partially matched) specifying whether the marks are attached to the vertices of the network (`of="vertices"`) or to the line segments of the network (`of="segments"`, the default).
`...`	Ignored.
`value`	Vector or data frame of mark values, or `NULL`.

Details

These functions extract or change the marks attached to the network `x`. They are methods for the generic functions `marks`, `marks<-` and `unmark` for the class `"linnet"` of linear networks.

A linear network may include a set of marks attached to the line segments, and a separate set of marks attached to the vertices. Each set of marks can be a vector, a factor, or a data frame.

The expression `marks(x, of)` extracts the marks from `x`. The assignment `marks(x, of) <- value` assigns new marks to the dataset `x`, and updates the dataset `x` in the current environment. The argument `of` specifies whether we are referring to the segments or the vertices.

For the assignment `marks(x, "segments") <- value`, the `value` should be a vector or factor of length equal to the number of segments in `x`, or a data frame with as many rows as there are segments in `x`. If `value` is a single value, or a data frame with one row, then it will be replicated so that the

same marks will be attached to each segment. Similarly for `marks(x, "vertices") <- value` the number of marks must match the number of vertices.

To remove marks, use `unmark(x)` to remove all marks, or `marks(x, of) <- NULL` to remove the specified kind of marks.

To extract the vertices (including their marks) as a point pattern, use `vertices(x)`. To extract the segments (including their marks) as a line segment pattern, use `as.psp(x)`.

Value

For `marks(x)`, the result is a vector, factor or data frame, containing the mark values attached to the vertices or the segments of `x`. If there are no marks, the result is `NULL`.

For `marks(x) <- value`, the result is the updated network `x` (with the side-effect that the dataset `x` is updated in the current environment).

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

`linnet`, `marks`, `marks<-`

Examples

```
L <- simplenet
marks(L, "vertices") <- letters[1:nvertices(L)]
marks(L, "segments") <- runif(nsegments(L))
L
marks(L, "v")
marks(L, "s")
unmark(L)
```

---

marks.lintess *Marks of a Tessellation on a Network*

Description

Extract or change the marks attached to the tiles of a tessellation on a linear network.

Usage

```
## S3 method for class 'lintess'
marks(x, ...)

## S3 replacement method for class 'lintess'
marks(x, ...) <- value
```

```
## S3 method for class 'lintess'
unmark(X)
```

Arguments

x, X	Tessellation on a linear network (object of class "lintess").
...	Ignored.
value	Vector or data frame of mark values, or NULL.

Details

These functions extract or change the marks attached to each of the tiles in the tessellation x. They are methods for the generic functions marks, marks<- and unmark for the class "lintess" of tessellations on a network.

The expression marks(x) extracts the marks of x. The assignment marks(x) <- value assigns new marks to the dataset x, and updates the dataset x in the current environment.

The marks can be a vector, a factor, or a data frame.

For the assignment marks(x) <- value, the value should be a vector or factor of length equal to the number of tiles in x, or a data frame with as many rows as there are tiles in x. If value is a single value, or a data frame with one row, then it will be replicated so that the same marks will be attached to each tile.

To remove marks, use marks(x) <- NULL or unmark(x).

Value

For marks(x), the result is a vector, factor or data frame, containing the mark values attached to the tiles of x. If there are no marks, the result is NULL.

For unmark(x), the result is the tessellation without marks.

For marks(x) <- value, the result is the updated tessellation x (with the side-effect that the dataset x is updated in the current environment).

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

lintess, marks, marks<-

Examples

```
B <- lineardirichlet(runiflpp(5, simplenet))
marks(B) <- letters[1:5]
```

Math.linim *S3 Group Generic Methods for Images on a Linear Network*

Description

These are group generic methods for images of class "linim", which allows for usual mathematical functions and operators to be applied directly to pixel images on a linear network. See Details for a list of implemented functions.

Usage

```
## S3 methods for group generics have prototypes:
Math(x, ...)
Ops(e1, e2)
Complex(z)
Summary(..., na.rm = FALSE)
```

Arguments

x, z, e1, e2	objects of class "linim".
...	further arguments passed to methods.
na.rm	logical: should missing values be removed?

Details

An object of class "linim" represents a pixel image on a linear network. See linim.

Below is a list of mathematical functions and operators which are defined for these images. Not all functions will make sense for all types of images. For example, none of the functions in the "Math" group make sense for character-valued images. Note that the "Ops" group methods are implemented using eval.linim.

1. Group "Math":
   - abs, sign, sqrt,
     floor, ceiling, trunc,
     round, signif
   - exp, log, expm1, log1p,
     cos, sin, tan,
     cospi, sinpi, tanpi,
     acos, asin, atan
     cosh, sinh, tanh,
     acosh, asinh, atanh
   - lgamma, gamma, digamma, trigamma
   - cumsum, cumprod, cummax, cummin
2. Group "Ops":
   - "+", "-", "*", "/", "^", "%%", "%/%"

- "&", "|", "!"
- "==", "!=", "<", "<=", ">=", ">"

3. Group "Summary":
   - all, any
   - sum, prod
   - min, max
   - range
4. Group "Complex":
   - Arg, Conj, Im, Mod, Re

Value

The return value is another object of class "linim", except in the following cases: all and any return a single logical value; sum, prod, min and max return a single numerical value; range returns a vector of two numerical values.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

eval.linim for evaluating expressions involving images.

Examples

```
fx <- function(x,y,seg,tp) { (x - y)^2 }
fL <- linfun(fx, simplenet)
Z <- as.linim(fL)
A <- Z+2
A <- -Z
A <- sqrt(Z)
A <- !(Z > 0.1)
```

---

mean.linim *Mean, Median, Quantiles of Pixel Values on a Linear Network*

Description

Calculates the mean, median, or quantiles of the pixel values in a pixel image on a linear network.

Usage

```
  ## S3 method for class 'linim'
mean(x, ...)

  ## S3 method for class 'linim'
median(x, ...)

  ## S3 method for class 'linim'
quantile(x, probs=seq(0,1,0.25), ...)

  ## S3 method for class 'linim'
quantilefun(x, ..., type=1)
```

Arguments

x	A pixel image on a linear network (object of class "linim").
probs	Vector of probabilities for which quantiles should be calculated.
...	Arguments passed to other methods.
type	Integer specifying the type of quantiles, as explained in quantile.default. Only types 1 and 2 are currently implemented.

Details

These functions calculate the mean, median and quantiles of the pixel values in the image x on a linear network.

An object of class "linim" describes a pixel image on a linear network. See linim.

The functions described here are methods for the generic mean, median and quantile for the class "linim".

Value

For mean and median, a single number. For quantile, a numeric vector of the same length as probs. For quantilefun, a function.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

mean, median, quantile,

mean.im, quantile.im, quantilefun

Examples

```
M <- psp2mask(as.psp(simplenet))
Z <- as.im(function(x,y) {x-y}, W=M)
X <- linim(simplenet, Z)
X
mean(X)
median(X)
quantile(X)
f <- quantilefun(X)
```

`mergeTiles.lintess` *Merge Groups of Tiles in a Tessellation on a Network*

Description

Given a tessellation on a linear network, and a factor which classifies the tiles of the tessellation into groups, form the set union of each group of tiles, and construct the tessellation based on these merged tiles.

Usage

```
 ## S3 method for class 'lintess'
mergeTiles(x, group, ...)
```

Arguments

`x`	A tessellation on a network (object of class `"lintess"`).
`group`	A `factor`, with one entry for each tile of `x`, which classifies the tiles into groups.
`...`	Other arguments, currently ignored.

Value

A tessellation on a network (object of class `"lintess"`).

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

See Also

`mergeTiles`

Examples

```
A <- as.lintess(simplenet)
A
g <- sample(letters[1:3], nobjects(A), replace=TRUE)
g
mergeTiles(A, g)
```

`methods.linfun` *Methods for Functions on Linear Network*

Description

Methods for the class `"linfun"` of functions on a linear network.

Usage

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

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

  ## S3 method for class 'linfun'
plot(x, ..., L=NULL, main)

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

  ## S3 method for class 'linfun'
as.owin(W, ...)

  ## S3 method for class 'linfun'
as.function(x, ...)
```

Arguments

`x`, `object`, `W`	A function on a linear network (object of class `"linfun"`).
`L`	A linear network
`...`	Extra arguments passed to `as.linim`, `plot.linim`, `plot.im` or `print.default`, or arguments passed to `x` if it is a function.
`main`	Main title for plot.

Details

These are methods for the generic functions `plot`, `print`, `summary` `as.data.frame` and `as.function`, and for the **spatstat** generic function `as.owin`.

An object of class `"linfun"` represents a mathematical function that could be evaluated at any location on a linear network. It is essentially an R `function` with some extra attributes.

The method `as.owin.linfun` extracts the two-dimensional spatial window containing the linear network.

The method `plot.linfun` first converts the function to a pixel image using `as.linim.linfun`, then plots the image using `plot.linim`.

Note that a linfun function may have additional arguments, other than those which specify the location on the network (see linfun). These additional arguments may be passed to plot.linfun.

Value

For print.linfun and summary.linfun the result is NULL.

For plot.linfun the result is the same as for plot.linim.

For the conversion methods, the result is an object of the required type: as.owin.linfun returns an object of class "owin", and so on.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>

Examples

```
X <- runiflpp(3, simplenet)
f <- nnfun(X)
f
plot(f)
as.function(f)
as.owin(f)
head(as.data.frame(f))
```

---

methods.linim *Methods for Images on a Linear Network*

Description

Methods for the class "linim" of functions on a linear network.

Usage

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

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

  ## S3 method for class 'linim'
as.im(X, ...)

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

  ## S3 method for class 'linim'
```

```
shift(X, ...)

  ## S3 method for class 'linim'
scalardilate(X, f, ..., origin=NULL)

  ## S3 method for class 'linim'
affine(X, mat=diag(c(1,1)), vec=c(0,0), ...)
```

Arguments

X, x, object	A pixel image on a linear network (object of class "linim").
...	Extra arguments passed to other methods.
f	Numeric. Scalar dilation factor.
mat	Numeric matrix representing the linear transformation.
vec	Numeric vector of length 2 specifying the shift vector.
origin	Character string determining a location that will be shifted to the origin. Options are "centroid", "midpoint" and "bottomleft". Partially matched.

Details

These are methods for the generic functions print, summary and as.data.frame, and the **spatstat** generic functions as.im, shift, scalardilate and affine.

An object of class "linfun" represents a pixel image defined on a linear network.

The method as.im.linim extracts the pixel values and returns a pixel image of class "im".

The method as.data.frame.linim returns a data frame giving spatial locations (in cartesian and network coordinates) and corresponding function values.

The methods shift.linim, scalardilate.linim and affine.linim apply geometric transformations to the pixels and the underlying linear network, without changing the pixel values.

Value

For print.linim the result is NULL.

The function summary.linim returns an object of class "summary.linim". In normal usage this summary is automatically printed by print.summary.linim.

For as.im.linim the result is an object of class "im".

For the geometric transformations shift.linim, scalardilate.linim and affine.linim, the result is another object of class "linim".

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>

Examples

```
M <- psp2mask(as.psp(simplenet))
Z <- as.im(function(x,y) {x-y}, W=M)
X <- linim(simplenet, Z)
## ............  print basic details ........................
X
## ............  print gory details  ........................
summary(X)
## ..........................................................
shift(X, c(1,1))
scalardilate(X, 2)
head(as.data.frame(X))
```

`methods.linnet` *Methods for Linear Networks*

Description

These are methods for the class `"linnet"` of linear networks.

Usage

```
as.linnet(X, ...)

## S3 method for class 'linnet'
as.linnet(X, ..., sparse, maxsize=30000)

## S3 method for class 'linnet'
as.owin(W, ...)

## S3 method for class 'linnet'
as.psp(x, ..., fatal=TRUE)

## S3 method for class 'linnet'
nsegments(x)

## S3 method for class 'linnet'
nvertices(x, ...)

## S3 method for class 'linnet'
pixellate(x, ...)

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

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

```
## S3 method for class 'linnet'
unitname(x)

## S3 replacement method for class 'linnet'
unitname(x) <- value

vertexdegree(x)

## S3 method for class 'linnet'
vertices(w)

## S3 method for class 'linnet'
volume(x)

## S3 method for class 'linnet'
Window(X, ...)
```

Arguments

x, X, object, w, W	An object of class "linnet" representing a linear network.
...	Arguments passed to other methods.
value	A valid name for the unit of length for x. See unitname.
fatal	Logical value indicating whether data in the wrong format should lead to an error (fatal=TRUE) or a warning (fatal=FALSE).
sparse	Logical value indicating whether to use a sparse matrix representation, as explained in linnet. Default is to keep the same representation as in X.
maxsize	Maximum permitted number of network vertices (to prevent a system crash due to lack of memory) when creating a network with sparse=FALSE.

Details

The function as.linnet is generic. It converts data from some other format into an object of class "linnet". The method as.linnet.lpp extracts the linear network information from an lpp object. The method as.linnet.linnet converts a linear network into another linear network with the required format.

The other functions are methods for the generic commands as.owin, as.psp, nsegments, nvertices, pixellate, print, summary, unitname, unitname<-, vertices, volume and Window for the class "linnet".

The methods as.owin.linnet and Window.linnet extract the window containing the linear network, and return it as an object of class "owin".

The method as.psp.linnet extracts the lines of the linear network as a line segment pattern (object of class "psp") while nsegments.linnet simply counts the number of line segments.

The method vertices.linnet extracts the vertices (nodes) of the linear network and nvertices.linnet simply counts the vertices. The function vertexdegree calculates the topological degree of each vertex (the number of lines emanating from that vertex) and returns these values as an integer vector.

The method pixellate.linnet applies as.psp.linnet to convert the network to a collection of line segments, then invokes pixellate.psp.

Value

For as.linnet the value is an object of class "linnet". For other functions, see the help file for the corresponding generic function.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

See Also

linnet.

Generic functions: as.owin, as.psp, nsegments, nvertices, pixellate, print, summary, unitname, unitname<-, vertices, volume and Window.

Special tools: thinNetwork, insertVertices, joinVertices, connected.linnet.

lixellate for dividing segments into shorter segments.

Examples

```
simplenet
summary(simplenet)
nsegments(simplenet)
nvertices(simplenet)
pixellate(simplenet)
volume(simplenet)
unitname(simplenet) <- c("cubit", "cubits")
Window(simplenet)
v <- vertices(simplenet)
d <- vertexdegree(simplenet)
plot(simplenet); text(v, labels=d, cex=2)
```

---

methods.lpp *Methods for Point Patterns on a Linear Network*

Description

These are methods specifically for the class "lpp" of point patterns on linear networks.

Usage

```
## S3 method for class 'lpp'
as.ppp(X, ..., fatal=TRUE)

## S3 method for class 'lpp'
as.psp(x, ..., fatal=TRUE)
```

```
## S3 replacement method for class 'lpp'
marks(x, ...) <- value

## S3 method for class 'lpp'
nsegments(x)

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

## S3 method for class 'summary.lpp'
print(x, ...)

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

## S3 method for class 'lpp'
unitname(x)

## S3 replacement method for class 'lpp'
unitname(x) <- value

## S3 method for class 'lpp'
unmark(X)
```

Arguments

x, X, object	An object of class "lpp" representing a point pattern on a linear network.
...	Arguments passed to other methods.
value	Replacement value for the marks or unitname of x. See Details.
fatal	Logical value indicating whether data in the wrong format should lead to an error (fatal=TRUE) or a warning (fatal=FALSE).

Details

These are methods for the generic functions as.ppp, as.psp, marks<-, nsegments, print, summary, unitname, unitname<- and unmark for objects of the class "lpp".

For "marks<-.lpp" the replacement value should be either NULL, or a vector of length equal to the number of points in x, or a data frame with one row for each point in x.

For "unitname<-.lpp" the replacement value should be a valid name for the unit of length, as described in unitname.

Value

See the documentation on the corresponding generic function.

Other methods

An object of class "lpp" also inherits the class "ppx" for which many other methods are available. See methods.ppx.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

See Also

lpp, intensity.lpp, methods.ppx

Examples

```
X <- runiflpp(10, simplenet)
unitname(X) <- c("furlong", "furlongs")
X
summary(X)
summary(chicago)
nsegments(X)
Y <- as.ppp(X)
```

---

methods.lppm *Methods for Fitted Point Process Models on a Linear Network*

Description

These are methods for the class "lppm" of fitted point process models on a linear network.

Usage

```
  ## S3 method for class 'lppm'
coef(object, ...)

  ## S3 method for class 'lppm'
emend(object, ...)

  ## S3 method for class 'lppm'
extractAIC(fit, ...)

  ## S3 method for class 'lppm'
formula(x, ...)

  ## S3 method for class 'lppm'
logLik(object, ...)

  ## S3 method for class 'lppm'
deviance(object, ...)
```

```
  ## S3 method for class 'lppm'
nobs(object, ...)

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

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

  ## S3 method for class 'lppm'
terms(x, ...)

  ## S3 method for class 'lppm'
update(object, ...)

  ## S3 method for class 'lppm'
valid(object, ...)

  ## S3 method for class 'lppm'
vcov(object, ...)

  ## S3 method for class 'lppm'
as.linnet(X, ...)

  ## S3 method for class 'lppm'
response(object)
```

Arguments

`object`, `fit`, `x`, `X`	An object of class `"lppm"` representing a fitted point process model on a linear network.
`...`	Arguments passed to other methods, usually the method for the class `"ppm"`.

Details

These are methods for the R generic commands `coef`, `extractAIC`, `formula`, `logLik`, `deviance`, `nobs`, `print`, `summary`, `terms`, `update` and `vcov`, and the **spatstat** generic commands `as.linnet`, `emend`, `response` and `valid`, for the class `"lppm"`.

Value

For `as.linnet.lppm` a linear network (object of class `"linnet"`). For `emend.lppm` another fitted model of the same class `"lppm"`. For `response.lppm` a spatial point pattern on a linear network (object of class `"lpp"`). For `valid.lppm` a logical value.

For the other methods, see the help for the default methods.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

lppm, plot.lppm.

Examples

```
X <- runiflpp(15, simplenet)
fit <- lppm(X ~ x)
print(fit)
coef(fit)
formula(fit)
terms(fit)
logLik(fit)
deviance(fit)
nobs(fit)
extractAIC(fit)
update(fit, ~1)
valid(fit)
vcov(fit)
response(fit)
```

---

model.frame.lppm *Extract the Variables in a Point Process Model on a Network*

Description

Given a fitted point process model on a network, this function returns a data frame containing all the variables needed to fit the model using the Berman-Turner device.

Usage

```
 ## S3 method for class 'lppm'
model.frame(formula, ...)
```

Arguments

formula	A fitted point process model on a linear network. An object of class "lppm".
...	Additional arguments passed to model.frame.glm.

Details

The function model.frame is generic. This function is a method for model.frame for fitted point process models on a linear network (objects of class "lppm").

The first argument should be a fitted point process model; it has to be named formula for consistency with the generic function.

The result is a data frame containing all the variables used in fitting the model. The data frame has one row for each quadrature point used in fitting the model. The quadrature scheme can be extracted using quad.ppm.

Value

A data.frame containing all the variables used in the fitted model, plus additional variables specified in .... It has an additional attribute "terms" containing information about the model formula. For details see model.frame.glm.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

References

Baddeley, A. and Turner, R. (2000) Practical maximum pseudolikelihood for spatial point patterns. *Australian and New Zealand Journal of Statistics* **42**, 283–322.

See Also

lppm, model.frame, model.matrix.ppm

Examples

```
fit <- lppm(spiders ~ x)
mf <- model.frame(fit)
```

---

model.images.lppm *Compute Images of Constructed Covariates*

Description

For a point process model fitted to spatial point pattern data on a linear network, this function computes pixel images of the covariates in the design matrix.

Usage

```
## S3 method for class 'lppm'
model.images(object, L = as.linnet(object), ...)
```

Arguments

object	Fitted point process model on a linear network. An object of class "lppm".
L	A linear network (object of class "linnet") in which the images should be computed. Defaults to the network in which the model was fitted.
...	Other arguments (such as na.action) passed to model.matrix.lm.

Details

This command is similar to model.matrix.lppm except that it computes pixel images of the covariates, instead of computing the covariate values at certain points only.

The object must be a fitted spatial point process model on a linear network (object of class "lppm" produced by the model-fitting function lppm).

The spatial covariates required by the model-fitting procedure are computed at every location on the network L.

Note that the spatial covariates computed here are not necessarily the original covariates that were supplied when fitting the model. Rather, they are the canonical covariates, the covariates that appear in the loglinear representation of the (conditional) intensity and in the columns of the design matrix. For example, they might include dummy or indicator variables for different levels of a factor, depending on the contrasts that are in force.

The format of the result depends on whether the original point pattern data were marked or unmarked.

- If the original dataset was unmarked, the result is a named list of pixel images on the network (objects of class "linim") containing the values of the spatial covariates. The names of the list elements are the names of the covariates determined by model.matrix.lm. The result is also of class "solist" so that it can be plotted immediately.
- If the original dataset was a multitype point pattern, the result is a hyperframe with one column for each possible type of points. Each column is a named list of pixel images on the network (objects of class "linim") containing the values of the spatial covariates. The row names of the hyperframe are the names of the covariates determined by model.matrix.lm.

The pixel resolution is determined by the arguments ... and spatstat.options.

Value

A list (of class "solist") or array (of class "hyperframe") containing pixel images on the network (objects of class "linim").

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

model.matrix.ppm, model.matrix, lppm.

Examples

```
fit <- lppm(spiders ~ x + polynom(y, 2))
model.images(fit)
```

`model.matrix.lppm` *Extract Design Matrix from Point Process Model on a Network*

Description

Given a point process model that has been fitted to spatial point pattern data on a linear network, this function extracts the design matrix of the model.

Usage

```
   ## S3 method for class 'lppm'
model.matrix(object,
                              data=model.frame(object, na.action=NULL),
                              ...,
                              keepNA=TRUE)
```

Arguments

`object`	The fitted point process model. An object of class `"lppm"`.
`data`	A model frame, containing the data required for the Berman-Turner device.
`keepNA`	Logical. Determines whether rows containing NA values will be deleted or retained.
`...`	Other arguments (such as `na.action`) passed to `model.matrix.lm`.

Details

This is a method for the generic function `model.matrix`. It extracts the design matrix of a spatial point process model on a linear network (object of class `"lppm"`).

More precisely, this command extracts the design matrix of the generalised linear model associated with a spatial point process model.

The `object` must be a fitted point process model on a network (object of class `"lppm"`) produced by the model-fitting function `lppm`. The method `model.matrix.lppm` extracts the model matrix for the GLM.

The result is a matrix, with one row for every quadrature point in the fitting procedure, and one column for every canonical covariate in the design matrix.

If there are `NA` values in the covariates, the argument `keepNA` determines whether to retain or delete the corresponding rows of the model matrix. The default `keepNA=TRUE` is to retain them. Note that this differs from the default behaviour of many other methods for `model.matrix`, which typically delete rows containing `NA`.

Value

A matrix. Columns of the matrix are canonical covariates in the model. Rows of the matrix correspond to quadrature points in the fitting procedure (provided keepNA=TRUE).

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

model.matrix, model.images.lppm, lppm

Examples

```
fit <- lppm(spiders ~ x + y)
head(model.matrix(fit))
```

---

nncross.lpp *Nearest Neighbours on a Linear Network*

Description

Given two point patterns X and Y on a linear network, finds the nearest neighbour in Y of each point of X using the shortest path in the network.

Usage

```
  ## S3 method for class 'lpp'
nncross(X, Y,
          iX=NULL, iY=NULL,
          what = c("dist", "which"),
          ...,
          k = 1,
          method="C")
```

Arguments

X, Y	Point patterns on a linear network (objects of class "lpp"). They must lie on the *same* linear network.
iX, iY	Optional identifiers, used to determine whether a point in X is identical to a point in Y. See Details.
what	Character string specifying what information should be returned. Either the nearest neighbour distance ("dist"), the identifier of the nearest neighbour ("which"), or both.
...	Ignored.

k	Integer, or integer vector. The algorithm will compute the distance to the kth nearest neighbour, for each value of k.
method	Internal use only.

Details

Given two point patterns X and Y on the same linear network, this function finds, for each point of X, the nearest point of Y, measuring distance by the shortest path in the network. The distance between these points is also computed.

The return value is a data frame, with rows corresponding to the points of X. The first column gives the nearest neighbour distances (i.e. the ith entry is the distance from the ith point of X to the nearest element of Y). The second column gives the indices of the nearest neighbours (i.e.\ the ith entry is the index of the nearest element in Y.) If what="dist" then only the vector of distances is returned. If what="which" then only the vector of indices is returned.

Note that this function is not symmetric in X and Y. To find the nearest neighbour in X of each point in Y, use nncross(Y,X).

The arguments iX and iY are used when the two point patterns X and Y have some points in common. In this situation nncross(X, Y) would return some zero distances. To avoid this, attach a unique integer identifier to each point, such that two points are identical if their identifying numbers are equal. Let iX be the vector of identifier values for the points in X, and iY the vector of identifiers for points in Y. Then the code will only compare two points if they have different values of the identifier. See the Examples.

The kth nearest neighbour may be undefined, for example if there are fewer than k+1 points in the dataset, or if the linear network is not connected. In this case, the kth nearest neighbour distance is infinite.

Value

By default (if what=c("dist", "which") and k=1) a data frame with two columns:

dist	Nearest neighbour distance
which	Nearest neighbour index in Y

If what="dist", a vector of nearest neighbour distances.

If what="which", a vector of nearest neighbour indices.

If k is a vector of integers, the result is a matrix with one row for each point in X, giving the distances and/or indices of the kth nearest neighbours in Y.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>

See Also

nndist.lpp for nearest neighbour distances in a single point pattern.

nnwhich.lpp to identify which points are nearest neighbours in a single point pattern.

Examples

```
# two different point patterns
X <- runiflpp(3, simplenet)
Y <- runiflpp(5, simplenet)
nn <- nncross(X,Y)
nn
plot(simplenet, main="nncross")
plot(X, add=TRUE, cols="red")
plot(Y, add=TRUE, cols="blue", pch=16)
XX <- as.ppp(X)
YY <- as.ppp(Y)
i <- nn$which
arrows(XX$x, XX$y, YY[i]$x, YY[i]$y, length=0.15)

# nearest and second-nearest neighbours
nncross(X, Y, k=1:2)

# two patterns with some points in common
X <- Y[1:2]
iX <- 1:2
iY <- 1:5
nncross(X,Y, iX, iY)
```

`nndist.lpp` *Nearest neighbour distances on a linear network*

Description

Given a pattern of points on a linear network, compute the nearest-neighbour distances, measured by the shortest path in the network.

Usage

```
## S3 method for class 'lpp'
nndist(X, ..., k=1, by=NULL, method="C")
```

Arguments

`X`	Point pattern on linear network (object of class `"lpp"`).
`k`	Integer, or integer vector. The algorithm will compute the distance to the `k`th nearest neighbour.
`by`	Optional. A factor, which separates `X` into groups. The algorithm will compute the distance to the nearest point in each group.
`method`	Optional string determining the method of calculation. Either `"interpreted"` or `"C"`.
`...`	Ignored.

Details

Given a pattern of points on a linear network, this function computes the nearest neighbour distance for each point (i.e. the distance from each point to the nearest other point), measuring distance by the shortest path in the network.

If `method="C"` the distances are computed using code in the C language. If `method="interpreted"` then the computation is performed using interpreted R code. The R code is much slower, but is provided for checking purposes.

The kth nearest neighbour distance is infinite if the kth nearest neighbour does not exist. This can occur if there are fewer than `k+1` points in the dataset, or if the linear network is not connected.

If the argument by is given, it should be a `factor`, of length equal to the number of points in `X`. This factor effectively partitions `X` into subsets, each subset associated with one of the levels of `X`. The algorithm will then compute, for each point of `X`, the distance to the nearest neighbour *in each subset*.

Value

A numeric vector, of length equal to the number of points in `X`, or a matrix, with one row for each point in `X` and one column for each entry of `k`. Entries are nonnegative numbers or infinity (`Inf`).

Distance values

The values returned by `nndist(X)` are distances, expressed as multiples of the unit of length of the spatial coordinates in `X`. The unit of length is given by `unitname(X)`.

Note that, if the unit of length in `X` is a composite expression such as '2 microns', then the values of `nndist(X)` are expressed as multiples of 2 microns, rather than being expressed in microns.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

See Also

`lpp`

Examples

```
X <- runiflpp(12, simplenet)
nndist(X)
nndist(X, k=2)

marks(X) <- factor(rep(letters[1:3], 4))
nndist(X, by=marks(X))
```

nnfromvertex *Nearest Data Point From Each Vertex in a Network*

Description

Given a point pattern on a linear network, for each vertex of the network find the nearest data point.

Usage

```
nnfromvertex(X, what = c("dist", "which"), k = 1)
```

Arguments

X	Point pattern on a linear network (object of class "lpp").
what	Character string specifying whether to return the nearest-neighbour distances, nearest-neighbour identifiers, or both.
k	Integer, or integer vector, specifying that the kth nearest neighbour should be returned.

Details

For each vertex (node) of the linear network, this algorithm finds the nearest data point to the vertex, and returns either the distance from the vertex to its nearest neighbour in X, or the serial number of the nearest neighbour in X, or both.

If k is an integer, then the k-th nearest neighbour is found instead.

If k is an integer vector, this is repeated for each integer in k.

Value

A numeric vector, matrix, or data frame.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

See Also

nndist.lpp

Examples

```
X <- runiflpp(5, simplenet)
nnfromvertex(X)
nnfromvertex(X, k=1:3)
```

nnfun.lpp *Nearest Neighbour Map on Linear Network*

Description

Compute the nearest neighbour function of a point pattern on a linear network.

Usage

```
  ## S3 method for class 'lpp'
nnfun(X, ..., k=1, value=c("index", "mark"))
```

Arguments

X	A point pattern on a linear network (object of class "lpp").
k	Integer. The algorithm finds the kth nearest neighbour in X from any spatial location.
value	String (partially matched) specifying whether to return the index of the neighbour (value="index", the default) or the mark value of the neighbour (value="mark").
...	Other arguments are ignored.

Details

The (geodesic) *nearest neighbour function* of a point pattern X on a linear network L tells us which point of X is closest to any given location.

If X is a point pattern on a linear network L, the *nearest neighbour function* of X is the mathematical function f defined for any location s on the network by f(s) = i, where X[i] is the closest point of X to the location s measured by the shortest path. In other words the value of f(s) is the identifier or serial number of the closest point of X.

The command nnfun.lpp is a method for the generic command nnfun for the class "lpp" of point patterns on a linear network.

If X is a point pattern on a linear network, f <- nnfun(X) returns a *function* in the R language, with arguments x,y, ..., that represents the nearest neighbour function of X. Evaluating the function f in the form v <- f(x,y), where x and y are any numeric vectors of equal length containing coordinates of spatial locations, yields a vector of identifiers or serial numbers of the data points closest to these spatial locations. More efficiently f can take the arguments x, y, seg, tp where seg and tp are the local coordinates on the network.

The result of f <- nnfun(X) also belongs to the class "linfun". It can be printed and plotted immediately as shown in the Examples. It can be converted to a pixel image using as.linim.

Value

A function in the R language, with arguments x,y and optional arguments seg,tp. It also belongs to the class "linfun" which has methods for plot, print etc.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>

See Also

linfun, methods.linfun.

To compute the *distance* to the nearest neighbour, see distfun.lpp.

Examples

```
X <- runiflpp(3, simplenet)
f <- nnfun(X)
f
plot(f)
plot(nnfun(chicago, value="m"))
```

---

nnwhich.lpp *Identify Nearest Neighbours on a Linear Network*

Description

Given a pattern of points on a linear network, identify the nearest neighbour for each point, measured by the shortest path in the network.

Usage

```
## S3 method for class 'lpp'
nnwhich(X, ..., k=1, method="C")
```

Arguments

X	Point pattern on linear network (object of class "lpp").
method	Optional string determining the method of calculation. Either "interpreted" or "C".
k	Integer, or integer vector. The algorithm will find the kth nearest neighbour.
...	Ignored.

Details

Given a pattern of points on a linear network, this function finds the nearest neighbour of each point (i.e. for each point it identifies the nearest other point) measuring distance by the shortest path in the network.

If method="C" the task is performed using code in the C language. If method="interpreted" then the computation is performed using interpreted R code. The R code is much slower, but is provided for checking purposes.

The result is NA if the kth nearest neighbour does not exist. This can occur if there are fewer than k+1 points in the dataset, or if the linear network is not connected.

Value

An integer vector, of length equal to the number of points in X, identifying the nearest neighbour of each point. If nnwhich(X)[2] = 4 then the nearest neighbour of point 2 is point 4.

Alternatively a matrix with one row for each point in X and one column for each entry of k.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

See Also

lpp

Examples

```
X <- runiflpp(10, simplenet)
nnwhich(X)
nnwhich(X, k=2)
```

---

pairdist.lpp *Pairwise shortest-path distances between points on a linear network*

Description

Given a pattern of points on a linear network, compute the matrix of distances between all pairs of points, measuring distance by the shortest path in the network.

Usage

```
## S3 method for class 'lpp'
pairdist(X, ..., method="C")
```

Arguments

X	Point pattern on linear network (object of class "lpp").
method	Optional string determining the method of calculation. Either "interpreted" or "C".
...	Ignored.

Details

Given a pattern of points on a linear network, this function computes the matrix of distances between all pairs of points, measuring distance by the shortest path in the network.

If two points cannot be joined by a path, the distance between them is infinite (Inf).

The argument method is not normally used. It is retained only for developers to check the validity of the software.

Value

A symmetric matrix, whose values are nonnegative numbers or infinity (`Inf`).

Algorithms and accuracy

Distances are accurate within the numerical tolerance of the network, `summary(X)$toler`.

For network data stored in the non-sparse representation described in `linnet`, then pairwise distances are computed using the matrix of path distances between vertices of the network, using R code if `method = "interpreted"`, or using C code if `method="C"` (the default).

For networks stored in the sparse representation, the argument `method` has no effect, and the distances are computed using an efficient C algorithm.

Distance values

The values returned by `pairdist(X)` are distances, expressed as multiples of the unit of length of the spatial coordinates in `X`. The unit of length is given by `unitname(X)`.

Note that, if the unit of length in `X` is a composite expression such as '2 microns', then the values of `pairdist(X)` are expressed as multiples of 2 microns, rather than being expressed in microns.

Author(s)

Ang Qi Wei <aqw07398@hotmail.com> and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

See Also

`lpp`

Examples

```
X <- runiflpp(12, simplenet)
d <- pairdist(X)
d[1:3, 1:3]
```

`pairs.linim` *Scatterplot Matrix for Pixel Images on a Linear Network*

Description

Produces a scatterplot matrix of the pixel values in two or more pixel images on a linear network.

Usage

```
## S3 method for class 'linim'
pairs(..., plot=TRUE, eps=NULL)
```

Arguments

...	Any number of arguments, each of which is either a pixel image on a linear network (object of class "linim"), a pixel image (object of class "im"), or a named argument to be passed to pairs.default.
plot	Logical. If TRUE, the scatterplot matrix is plotted.
eps	Optional. Spacing between sample points on the network. A positive number.

Details

This is a method for the generic function pairs for the class of pixel images on a linear network.

It produces a square array of plot panels, in which each panel shows a scatterplot of the pixel values of one image against the corresponding pixel values of another image.

At least two of the arguments ... should be a pixel image on a linear network (object of class "linim"). They should be defined on the **same** linear network, but may have different pixel resolutions.

First the pixel values of each image are extracted at a set of sample points equally-spaced across the network. Then pairs.default is called to plot the scatterplot matrix.

Any arguments in ... which are not pixel images will be passed to pairs.default to control the plot.

Value

Invisible. A data.frame containing the corresponding pixel values for each image. The return value also belongs to the class plotpairsim which has a plot method, so that it can be re-plotted.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>

See Also

pairs.default, pairs.im

Examples

```
fit <- lppm(chicago ~ marks * (x+y))
lam <- predict(fit)
do.call(pairs, lam)
```

parres.lppm *Partial Residuals for Point Process Model on a Linear Network*

Description

Computes the smoothed partial residuals, a diagnostic for transformation of a covariate in a Poisson point process model on a linear network.

Usage

```
## S3 method for class 'lppm'
parres(model, covariate, ...,
       smooth.effect=FALSE, subregion=NULL,
       bw = "nrd0", adjust=1, from = NULL, to = NULL, n = 512,
       bw.input = c("points", "quad"), bw.restrict=FALSE, covname)
```

Arguments

model	Fitted point process model on a linear network (object of class "lppm").
covariate	The covariate of interest. Either a character string matching the name of one of the canonical covariates in the model, or one of the names "x" or "y" referring to the Cartesian coordinates, or one of the names of the covariates given when model was fitted, or a pixel image (object of class "im") or function(x,y) supplying the values of a covariate at any location. If the model depends on only one covariate, then this covariate is the default; otherwise a covariate must be specified.
smooth.effect	Logical. Determines the choice of algorithm. See Details.
subregion	Optional. A window (object of class "owin") specifying a subset of the spatial domain of the data. The calculation will be confined to the data in this subregion.
bw	Smoothing bandwidth or bandwidth rule (passed to density.default).
adjust	Smoothing bandwidth adjustment factor (passed to density.default).
n, from, to	Arguments passed to density.default to control the number and range of values at which the function will be estimated.
...	Additional arguments passed to density.default.
bw.input	Character string specifying the input data used for automatic bandwidth selection.
bw.restrict	Logical value, specifying whether bandwidth selection is performed using data from the entire spatial domain or from the subregion.
covname	Optional. Character string to use as the name of the covariate.

Details

This command computes the smoothed partial residual diagnostic (Baddeley, Chang, Song and Turner, 2012) for the transformation of a covariate in a Poisson point process model.

The function parres is generic, with methods for different classes of point process models. This page documents the method parres.lppm. The argument model must be a fitted point process model on a linear network.

The diagnostic works in two different ways:

Canonical covariate: The argument covariate may be a character string which is the name of one of the *canonical covariates* in the model. The canonical covariates are the functions Z_j that appear in the expression for the Poisson point process intensity

$$\lambda(u) = \exp(\beta_1 Z_1(u) + \ldots + \beta_p Z_p(u))$$

at spatial location u. Type names(coef(model)) to see the names of the canonical covariates in model. If the selected covariate is Z_j, then the diagnostic plot concerns the model term $\beta_j Z_j(u)$. The plot shows a smooth estimate of a function $h(z)$ that should replace this linear term, that is, $\beta_j Z_j(u)$ should be replaced by $h(Z_j(u))$. The linear function is also plotted as a dotted line.

New covariate: If the argument covariate is a pixel image (object of class "im") or a function(x,y), it is assumed to provide the values of a covariate that is not present in the model. Alternatively covariate can be the name of a covariate that was supplied when the model was fitted (i.e. in the call to ppm) but which does not feature in the model formula. In either case we speak of a new covariate $Z(u)$. If the fitted model intensity is $\lambda(u)$ then we consider modifying this to $\lambda(u)\exp(h(Z(u)))$ where $h(z)$ is some function. The diagnostic plot shows an estimate of $h(z)$. **Warning: in this case the diagnostic is not theoretically justified. This option is provided for research purposes.**

Alternatively covariate can be one of the character strings "x" or "y" signifying the Cartesian coordinates. The behaviour here depends on whether the coordinate was one of the canonical covariates in the model.

If there is more than one canonical covariate in the model that depends on the specified covariate, then the covariate effect is computed using all these canonical covariates. For example in a log-quadratic model which includes the terms x and I(x^2), the quadratic effect involving both these terms will be computed.

There are two choices for the algorithm. If smooth.effect=TRUE, the fitted covariate effect (according to model) is added to the point process residuals, then smoothing is applied to these values. If smooth.effect=FALSE, the point process residuals are smoothed first, and then the fitted covariate effect is added to the result.

The smoothing bandwidth is controlled by the arguments bw, adjust, bw.input and bw.restrict. If bw is a numeric value, then the bandwidth is taken to be adjust * bw. If bw is a string representing a bandwidth selection rule (recognised by density.default) then the bandwidth is selected by this rule.

The data used for automatic bandwidth selection are specified by bw.input and bw.restrict. If bw.input="points" (the default) then bandwidth selection is based on the covariate values at the points of the original point pattern dataset to which the model was fitted. If bw.input="quad" then bandwidth selection is based on the covariate values at every quadrature point used to fit the model.

If bw.restrict=TRUE then the bandwidth selection is performed using only data from inside the subregion.

Value

A function value table (object of class "fv") containing the values of the smoothed partial residual, the estimated variance, and the fitted effect of the covariate. Also belongs to the class "parres" which has methods for print and plot.

Variance estimation and confidence bands

If the fitted model is a Poisson point process, the variance of the partial residual will also be calculated, and 95 percent confidence bands will be derived from this. The default plot of the result will show the confidence bands in grey shading.

Slow computation

In a large dataset, computation can be very slow if the default settings are used, because the smoothing bandwidth is selected automatically. To avoid this, specify a numerical value for the bandwidth bw. One strategy is to use a coarser subset of the data to select bw automatically. The selected bandwidth can be read off the print output for parres.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net>, Ya-Mei Chang and Yong Song.

References

Baddeley, A., Chang, Y.-M., Song, Y. and Turner, R. (2013) Residual diagnostics for covariate effects in spatial point process models. *Journal of Computational and Graphical Statistics*, **22**, 886–905.

See Also

addvar, rhohat, rho2hat

Examples

```
X <-  rpoispp(function(x,y){exp(3+x+2*x^2)})
model <- ppm(X ~x+y)
tra <- parres(model, "x")
plot(tra)
tra
plot(parres(model, "x", subregion=square(0.5)))
model2 <- ppm(X ~x+I(x^2)+y)
plot(parres(model2, "x"))
Z <- setcov(owin())
plot(parres(model2, Z))

#' when the model involves only one covariate
```

```
modelb <- ppm(bei ~ elev + I(elev^2), data=bei.extra)
plot(parres(modelb))
```

`persp.linfun` *Perspective View of Function on a Linear Network*

Description

Given a function on a linear network, generate a perspective view.

Usage

```
 ## S3 method for class 'linfun'
persp(x, ..., main, eps = NULL, dimyx = NULL, xy = NULL)
```

Arguments

`x`	The function to be plotted. An object of class `"linfun"`.
`...`	Arguments passed to `persp.linim` controlling the appearance of the plot.
`main`	Main title for the plot.
`eps, dimyx, xy`	Arguments passed to `as.linim` determining the spatial resolution when the function is converted to an image.

Details

The function `x` is converted to a pixel image on the linear network using `as.linim`. Then `persp.linim` is invoked to generate the perspective plot.

This style of plot is often attributed to Okabe and Sugihara (2012).

Value

(Invisibly) the perspective transformation matrix, as described in the help for `persp.default`.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Greg McSwiggan.

References

Okabe, A. and Sugihara, K. (2012) *Spatial Analysis Along Networks*. John Wiley and Sons, New York.

See Also

`persp.linim`

Examples

```
f <- linfun(function(x,y,seg,tp) { abs(sin(25*x)) + abs(sin(15*y)) }, simplenet)
persp(f, phi=20)
```

`persp.linim` *Perspective View of Pixel Image on a Linear Network*

Description

Given a pixel image on a linear network, generate a perspective view.

Usage

```
 ## S3 method for class 'linim'
persp(x, ..., main,
                      grid = TRUE, ngrid = 10,
                      col.grid = "grey", col.base = "white",
                      neg.args=list(), warncross=FALSE,
                      zadjust=1,
                      extrapolate=c("linear", "constant"))
```

Arguments

`x`	Pixel image on a linear network (object of class `"linim"`).
`...`	Arguments passed to `persp.default` to control the perspective view, or passed to `segments` or `polygon` to control the appearance of the vertical panes.
`main`	Main title for the plot.
`grid`	Logical value indicating whether to draw a rectangular grid on the base plane (at height zero), to assist the perception of perspective.
`ngrid`	Number of grid lines to draw, if `grid=TRUE`.
`col.grid`	Colour of grid lines, if `grid=TRUE`.
`col.base`	Colour of base plane. A single colour value, or a pixel image.
`neg.args`	Optional list of arguments passed to `polygon` when displaying negative values of the function.
`warncross`	Logical value indicating whether to issue a warning if two segments of the network cross each other (which causes difficulty for the algorithm).
`zadjust`	Adjustment factor for vertical scale, relative to the default scale.
`extrapolate`	Character string (partially matched) specifying how to extrapolate the value at the endpoint of each segment.

Details

The pixel values are interpreted as the spatially-varying height of a vertical surface erected on each segment of the linear network. These surfaces are drawn in perspective view. This style of plot is often attributed to Okabe and Sugihara (2012).

1. The horizontal plane at height zero is drawn, in perspective view, in the colour specified by `col.base`.

   If `col.base` is a pixel image, it will be rendered as a colour image shown in perspective view on the horizontal plane. The argument `colmap` controls the mapping from pixel values of `col.base` to physical colours.
2. A grid of lines on the horizontal plane is drawn if `grid=TRUE` (the default).
3. For each segment of the network, a vertical polygon is constructed, with a straight lower edge aligned with the network segment, and a crooked upper edge whose height is proportional to values of `x`. The polygon linearly interpolates between the values of pixels that lie along the segment. At each end of the segment,
   - If `extrapolate="linear"` (the default), the polygon height at the end of the segment is determined by linearly extrapolating from the two nearest pixel values.
   - If `extrapolate="constant"`, the polygon height at the end of the segment is defined to be equal to the nearest pixel value.

   The vertical polygons are drawn in the colour and style specified by the additional arguments `...`, for example, `col` for colour.

If `x` contains negative values, they will be represented as polygons extending downwards below the horizontal plane. These would be obscured if `col.base` is an opaque colour other than white, or if `col.base` is a pixel image. A transparent colour for `col.base` can be used if it is supported by the graphics device.

Like all spatial plots in the **spatstat** family, `persp.linim` does not independently rescale the x and y coordinates. A long narrow window will be represented as a long narrow window in the perspective view. To override this and allow the coordinates to be independently rescaled, use the argument `scale=TRUE` which will be passed to `persp.default`.

Value

(Invisibly) the perspective transformation matrix, as described in the help for `persp.default`.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Greg McSwiggan.

References

Okabe, A. and Sugihara, K. (2012) *Spatial Analysis Along Networks*. John Wiley and Sons, New York.

See Also

`persp.linfun`

Examples

```
if(interactive()) {
  Z <- density(chicago, 100)
} else {
  X <- runiflpp(10, simplenet)
  Z <- density(X, 0.1)
}
persp(Z, theta=30, phi=20)
```

---

plot.linim *Plot Pixel Image on Linear Network*

Description

Given a pixel image on a linear network, the pixel values are displayed either as colours or as line widths.

Usage

```
## S3 method for class 'linim'
plot(x, ..., style = c("colour", "width"),
             scale, adjust = 1, fatten = 0,
             negative.args = list(col=2),
             legend=TRUE,
             leg.side=c("right", "left", "bottom", "top"),
             leg.sep=0.1,
             leg.wid=0.1,
             leg.args=list(),
             leg.scale=1,
             zlim,
             box=FALSE,
             do.plot=TRUE)
```

Arguments

x	The pixel image to be plotted. An object of class "linim".
...	Extra graphical parameters, passed to plot.im if style="colour", or to polygon if style="width".
style	Character string (partially matched) specifying the type of plot. See Details.
scale	Physical scale factor for representing the pixel values as line widths.
adjust	Adjustment factor for the conversion of pixel value to line width, when style="width".
fatten	Distance by which the line segments should be thickened, when style="colour".
negative.args	A list of arguments to be passed to polygon specifying how to plot negative values of x when style="width".
legend	Logical value indicating whether to plot a legend (colour ribbon or scale bar).

leg.side	Character string (partially matched) indicating where to display the legend relative to the main image.
leg.sep	Factor controlling the space between the legend and the image.
leg.wid	Factor controlling the width of the legend.
leg.scale	Rescaling factor for annotations on the legend. The values on the numerical scale printed beside the legend will be multiplied by this rescaling factor.
leg.args	List of additional arguments passed to image.default, axis or text.default to control the display of the legend. These may override the ... arguments.
zlim	The range of numerical values that should be mapped. A numeric vector of length 2. Defaults to the range of values of x.
box	Logical value indicating whether to draw a bounding box.
do.plot	Logical value indicating whether to actually perform the plot.

Details

This is the plot method for objects of class "linim". Such an object represents a pixel image defined on a linear network.

If style="colour" (the default) then the pixel values of x are plotted as colours, using plot.im. The mapping from pixel values to colours is determined by any additional arguments ... which are passed to plot.im.

If style="width" then the pixel values of x are used to determine the widths of thick lines centred on the line segments of the linear network. This style of plot is often attributed to Xie and Yan (2008). The mapping from pixel values to line widths is determined by the arguments scale and adjust. The plotting of colours and borders of the lines is controlled by the additional arguments ... which are passed to polygon. A different set of colours and borders can be assigned to negative pixel values by passing a list of arguments in negative.args as shown in the Examples.

A legend is displayed alongside the plot if legend=TRUE (the default). The legend displays the relationship between pixel values and colours (if style="colour") or between pixel values and line widths (if style="width").

The plotting of the legend itself is controlled by the arguments leg.side, leg.sep, leg.wid, leg.scale and the list of arguments leg.args, which are described above. If style="colour", these arguments are mapped to the arguments ribside, ribsep, ribwid, ribscale and ribargs respectively, which are passed to plot.im.

Value

If style="colour", the result is an object of class "colourmap" specifying the colour map used. If style="width", the result is a numeric value v giving the physical scale: one unit of pixel value is represented as v physical units on the plot.

The result also has an attribute "bbox" giving a bounding box for the plot. The bounding box includes the ribbon or scale bar, if present, but not the main title.

Thin lines

When `style="colour"` it often appears that the lines are drawn too thin. This occurs because `x` is a pixel image, in which the only pixels that have a defined value are those which lie directly over the network. To make the lines appear thicker in the plot, use the argument `fatten`. The domain of the image will be expanded by a distance equal to `fatten/2` in every direction using `dilation.owin`; the pixel values will be extrapolated to this expanded domain using `nearestValue`. This may improve the visual appearance of the plot.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

References

Ang, Q.W., Baddeley, A. and Nair, G. (2012) Geometrically corrected second-order analysis of events on a linear network, with applications to ecology and criminology. *Scandinavian Journal of Statistics* **39**, 591–617.

Xie, Z. and Yan, J. (2008) Kernel Density Estimation of traffic accidents in a network space. *Computers, Environment and Urban Systems* **32**, 396–406.

See Also

`linim`, `plot.im`, `polygon`, `default.image.colours`

Examples

```
X <- linfun(function(x,y,seg,tp){y^2+x}, simplenet)
X <- as.linim(X)

plot(X, main="Colour represents function value")
plot(X, fatten=0.02, main="fattened")

plot(X, style="width", main="Width proportional to function value")

# signed values
f <- linfun(function(x,y,seg,tp){y-x}, simplenet)
plot(f, style="w", main="Negative values in red")

plot(f, style="w", negative.args=list(density=10),
     main="Negative values are hatched")
```

---

plot.linnet *Plot a linear network*

Description

Plots a linear network

Usage

```
 ## S3 method for class 'linnet'
plot(x, ..., main=NULL, add=FALSE,
                                do.plot=TRUE,
                                show.vertices=FALSE, show.window=FALSE,
                                args.vertices=list(), args.segments=list())
```

Arguments

x	Linear network (object of class "linnet").
...	Graphics arguments passed to plot.psp and plot.ppp.
main	Main title for plot. Use main="" to suppress it.
add	Logical. If TRUE, superimpose the graphics over the current plot. If FALSE, generate a new plot.
do.plot	Logical value specifying whether to actually perform the plot.
show.vertices	Logical value specifying whether to plot the vertices as well.
show.window	Logical value specifying whether to plot the window containing the linear network.
args.segments	Optional list of arguments passed to plot.psp when plotting the line segments of the network. These arguments override any arguments in ....
args.vertices	Optional list of arguments passed to plot.ppp when plotting the vertices of the network (only when vertices=TRUE). These arguments override any arguments in ....

Details

This is the plot method for class "linnet".

The line segments of the network x are plotted using plot.psp. If show.vertices=TRUE, the vertices of the network will also be plotted, using plot.ppp. If show.window=TRUE, the window surrounding the network will also be plotted.

If the vertices or line segments of x are marked, the marks are not displayed by default. To plot the marks, set use.marks=TRUE. To plot the marks and plot the associated legends, set use.marks=TRUE, legend=TRUE. To plot only the marks of the segments and not the marks of the vertices, set args.segments=list(use.marks and so on.

Value

An (invisible) list with two elements, segments and vertices describing the representation of the marks. The element segments contains the result of plot.psp (either a colourmap, a numeric value or an owin). The element vertices contains the result of plot.ppp (a symbolmap) or NULL.

The result also has attribute "bbox" giving the bounding box for the plot.

Author(s)

Ang Qi Wei <aqw07398@hotmail.com> and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

See Also

linnet

Examples

```
plot(simplenet)

L <- simplenet
marks(L, "vertices") <- letters[1:nvertices(L)]
marks(L, "segments") <- runif(nsegments(L))
plot(L, show.vertices=TRUE, use.marks=TRUE, legend=TRUE)
```

---

plot.lintess *Plot a Tessellation on a Linear Network*

Description

Plot a tessellation or division of a linear network into tiles.

Usage

```
## S3 method for class 'lintess'
plot(x, ...,
        main, add = FALSE,
        style = c("colour", "width", "image"),
        col = NULL, values=marks(x),
        ribbon=TRUE, ribargs=list(), multiplot=TRUE, do.plot=TRUE)
```

Arguments

x	Tessellation on a linear network (object of class "lintess").
...	Arguments passed to segments (if style="segments") or to plot.im (if style="image") to control the plot.
main	Optional main title for the plot.
add	Logical value indicating whether the plot is to be added to an existing plot.
style	Character string (partially matched) specifying the type of plot. If style="colour" (the default), tiles are plotted using segments using colours to distinguish the different tiles or values. If style="width", tiles are plotted using segments using different segment widths to distinguish the different tiles or values. If style="image", the tessellation is converted to a pixel image and plotted by plot.im.
col	Vector of colours, or colour map, determining the colours used to plot the different tiles of the tessellation.
values	Values associated with each tile of the tessellation, used to determine the colours or widths. A vector with one entry for each tile, or a data frame with one row for each tile. The default is marks(x), or if that is null, then tilenames(x).

ribbon	Logical value specifying whether to print an explanatory legend for the colour map or width map.
ribargs	Arguments passed to plot.colourmap controlling the display of the colour map legend.
multiplot	Logical value determining what should happen if marks(x) has more than one column. If multiplot=TRUE (the default), several plot panels will be generated, one panel for each column of marks. If multiplot=FALSE, the first column of marks will be selected.
do.plot	Logical value specifying whether to actually generate the plot (do.plot=TRUE, the default) or just to compute the colour map and return it (do.plot=FALSE).

Details

A tessellation on a linear network L is a partition of the network into non-overlapping pieces (tiles). Each tile consists of one or more line segments which are subsets of the line segments making up the network. A tile can consist of several disjoint pieces.

This function plots the tessellation on the current device. It is a method for the generic plot.

If style="colour", each tile is plotted using segments, drawing segments of different colours.

If style="width", each tile is plotted using segments, drawing segments of different widths.

If style="image", the tessellation is converted to a pixel image, and plotted as a colour image using plot.im.

The colours or widths are determined by the values associated with each tile of the tessellation. If values is missing, the default is to use the marks of the tessellation, or if there are no marks, the names of the tiles.

Value

(Invisible) colour map.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

See Also

lintess

Examples

```
X <- runiflpp(7, simplenet)
Z <- divide.linnet(X)
plot(Z, main="tessellation on network")
points(as.ppp(X))
plot(Z, main="tessellation on network",
        values=1:nobjects(Z), style="w")
```

plot.lpp *Plot Point Pattern on Linear Network*

Description

Plots a point pattern on a linear network. Plot method for the class "lpp" of point patterns on a linear network.

Usage

```
## S3 method for class 'lpp'
plot(x, ..., main, add = FALSE,
     type = c("p", "n"),
     use.marks=TRUE, which.marks=NULL,
     legend=TRUE,
     leg.side=c("left", "bottom", "top", "right"),
     leg.args=list(),
     show.all = !add, show.window=FALSE, show.network=TRUE,
     do.plot = TRUE, multiplot=TRUE)
```

Arguments

x	Point pattern on a linear network (object of class "lpp").
...	Additional arguments passed to plot.linnet or plot.ppp.
main	Main title for plot.
add	Logical value indicating whether the plot is to be added to the existing plot (add=TRUE) or whether a new plot should be initialised (add=FALSE, the default).
type	Type of plot: either "p" or "n". If type="p" (the default), both the points and the observation window are plotted. If type="n", only the window is plotted.
use.marks	logical flag; if TRUE, plot points using a different plotting symbol for each mark; if FALSE, only the locations of the points will be plotted, using points().
which.marks	Index determining which column of marks to use, if the marks of x are a data frame. A character or integer vector identifying one or more columns of marks. If add=FALSE then the default is to plot all columns of marks, in a series of separate plots. If add=TRUE then only one column of marks can be plotted, and the default is which.marks=1 indicating the first column of marks.
legend	Logical value indicating whether to add a legend showing the mapping between mark values and graphical symbols (for a marked point pattern).
leg.side	Position of legend relative to main plot.
leg.args	List of additional arguments passed to plot.symbolmap or symbolmap to control the legend. In addition to arguments documented under plot.symbolmap, and graphical arguments recognised by symbolmap, the list may also include the argument sep giving the separation between the main plot and the legend, or sep.frac giving the separation as a fraction of the relevant dimension (width or height) of the main plot.

show.all	Logical value indicating whether to plot everything including the main title and the window containing the network.
show.window	Logical value indicating whether to plot the window containing the network. Overrides show.all.
show.network	Logical value indicating whether to plot the network.
do.plot	Logical value determining whether to actually perform the plotting.
multiplot	Logical value giving permission to display multiple plots.

Details

The linear network is plotted by plot.linnet, then the points are plotted using code equivalent to plot.ppp.

Commonly-used arguments include:

- col and lwd for the colour and width of lines in the linear network
- cols for the colour or colours of the points
- chars for the plot characters representing different types of points
- shape to control the shape of the symbol (this argument takes precedence over chars).

These are documented in the help file for plot.ppp.

If shape="crossticks", the points are drawn as short line segments perpendicular to the network.

Note that the linear network will be plotted even when add=TRUE, unless show.network=FALSE.

Value

(Invisible) object of class "symbolmap" giving the correspondence between mark values and plotting characters.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

lpp.

See plot.ppp for options for representing the points.

See also points.lpp, text.lpp.

Examples

```
plot(chicago, cols=1:7)
plot(dendrite, shape="crossticks", cols=2:4, size=8,
               leg.side="bottom", leg.args=list(lwd=3))
```

plot.lppm *Plot a Fitted Point Process Model on a Linear Network*

Description

Plots the fitted intensity of a point process model on a linear network.

Usage

```
  ## S3 method for class 'lppm'
plot(x, ..., type="trend")
```

Arguments

x	An object of class "lppm" representing a fitted point process model on a linear network.
...	Arguments passed to plot.linim to control the plot.
type	Character string (either "trend" or "cif") determining whether to plot the fitted first order trend or the conditional intensity.

Details

This function is the plot method for the class "lppm". It computes the fitted intensity of the point process model, and displays it using plot.linim.

The default is to display intensity values as colours. Alternatively if the argument style="width" is given, intensity values are displayed as the widths of thick lines drawn over the network.

Value

Null.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

See Also

lppm, plot.linim, methods.lppm, predict.lppm.

Examples

```
X <- runiflpp(10, simplenet)
fit <- lppm(X ~x)
plot(fit)
plot(fit, style="width")
```

points.lpp *Draw Points on Existing Plot*

Description

For a point pattern on a linear network, this function draws the coordinates of the points only, on the existing plot display.

Usage

```
## S3 method for class 'lpp'
points(x, ...)
```

Arguments

x	A point pattern on a linear network (object of class "lpp").
...	Additional arguments passed to points.default.

Details

This is a method for the generic function points for the class "lpp" of point patterns on a linear network.

If x is a point pattern on a linear network, then points(x) plots the spatial coordinates of the points only, on the existing plot display, without plotting the underlying network. It is an error to call this function if a plot has not yet been initialised.

The spatial coordinates are extracted and passed to points.default along with any extra arguments. Arguments controlling the colours and the plot symbols are interpreted by points.default. For example, if the argument col is a vector, then the ith point is drawn in the colour col[i].

Value

Null.

Difference from plot method

The more usual way to plot the points is using plot.lpp. For example plot(x) would plot both the points and the underlying network, while plot(x, add=TRUE) would plot only the points. The interpretation of arguments controlling the colours and plot symbols is different here: they determine a symbol map, as explained in the help for plot.ppp.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

plot.lpp, points.default

Examples

```
plot(Frame(spiders), main="Spiders on a Brick Wall")
points(spiders)
```

`predict.lppm` *Predict Point Process Model on Linear Network*

Description

Given a fitted point process model on a linear network, compute the fitted intensity or conditional intensity of the model.

Usage

```
## S3 method for class 'lppm'
predict(object, ..., type = "trend",
                      locations = NULL, covariates = NULL,
                      se = FALSE,
                      new.coef=NULL)
```

Arguments

`object`	The fitted model. An object of class `"lppm"`, see `lppm`.
`type`	Type of values to be computed. Either `"trend"` or `"cif"`. Currently ignored.
`locations`	Optional. Locations at which predictions should be computed. Either a point pattern (class `"lpp"` or `"ppp"`), a data frame containing spatial coordinates, or a binary image mask, or a pixel image.
`covariates`	Values of external covariates required by the model. Either a data frame, or a list of images and/or functions.
`se`	Logical value indicating whether to calculate standard errors as well.
`new.coef`	Optional. Numeric vector of model coefficients, to be used instead of the fitted coefficients `coef(object)` when calculating the prediction.
`...`	Optional arguments passed to `as.mask` to determine the pixel resolution (if `locations` is missing).

Details

This function computes the fitted point process intensity, optionally with standard errors, for a point process model on a linear network. It is a method for the generic `predict` for the class `"lppm"`.

The argument `object` should be an object of class `"lppm"` (produced by `lppm`) representing a point process model on a linear network.

Currently the argument `type` has no effect. The fitted intensity is computed in all cases. This occurs because currently all fitted models of class `"lppm"` are Poisson point processes, where the trend, intensity, and conditional intensity are the same.

Predicted values are computed at the locations given by the argument `locations`. If this argument is missing, then predicted values are computed at a fine grid of points on the linear network.

- If `locations` is missing or `NULL` (the default), the return value is a pixel image (object of class `"linim"` and `"im"`) corresponding to a discretisation of the linear network, with numeric pixel values giving the predicted values at each location on the linear network. (If the model is multitype, the result is a list of such pixel images, one for each possible type of point.)
- If `locations` is a data frame containing spatial coordinates `x` and `y`, and/or local coordinates `seg` and `tp`, the result is a numeric vector of predicted values at the locations specified by the data frame.
- If `locations` is a binary mask or pixel image, the result is a pixel image with predicted values computed at the pixels of the mask. (If the model is multitype, the result is a list of such pixel images, one for each possible type of point.)

If `se=TRUE`, standard errors are also computed. The result is a list of two elements, each following the format described above; the first element contains the fitted estimates, and the second element contains the standard errors.

Value

If `se=FALSE` (the default), the result is a pixel image (object of class `"linim"` and `"im"`) or a list of pixel images, or a numeric vector, depending on the argument `locations`. See Details.

If `se=TRUE`, the result is a list of two elements, each with the format described above.

Author(s)

Adrian Baddeley `<Adrian.Baddeley@curtin.edu.au>`

References

Ang, Q.W. (2010) *Statistical methodology for events on a network*. Master's thesis, School of Mathematics and Statistics, University of Western Australia.

Ang, Q.W., Baddeley, A. and Nair, G. (2012) Geometrically corrected second-order analysis of events on a linear network, with applications to ecology and criminology. *Scandinavian Journal of Statistics* **39**, 591–617.

Rakshit, S., McSwiggan, G., Nair, G. and Baddeley, A. (2021) Variable selection using penalised likelihoods for point patterns on a linear network. *Australian and New Zealand Journal of Statistics* **63**. DOI 10.1111/anzs.12341.

Baddeley, A., Nair, G., Rakshit, S., McSwiggan, G. and Davies, T.M. (2021) Analysing point patterns on networks — a review. *Spatial Statistics* **42**, 100435.

See Also

`lpp`, `linim`

Examples

```
X <- runiflpp(12, simplenet)
fit <- lppm(X ~ x)
v <- predict(fit, type="trend")
plot(v)
```

`pseudoR2.lppm` *Calculate Pseudo-R-Squared for Point Process Model on Linear Network*

Description

Given a fitted point process model on a linear network, calculate the pseudo-R-squared value, which measures the fraction of variation in the data that is explained by the model.

Usage

```
  ## S3 method for class 'lppm'
pseudoR2(object, ..., keepoffset=TRUE)
```

Arguments

`object`	Fitted point process model on a linear network. An object of class `"lppm"`.
`keepoffset`	Logical value indicating whether to retain offset terms in the model when computing the deviance difference. See Details.
`...`	Additional arguments passed to `deviance.lppm`.

Details

The function `pseudoR2` is generic, with methods for fitted point process models of class `"ppm"` and `"lppm"`.

This function computes McFadden's pseudo-Rsquared

$$R^2 = 1 - \frac{D}{D_0}$$

where D is the deviance of the fitted model `object`, and D_0 is the deviance of the null model. Deviance is defined as twice the negative log-likelihood or log-pseudolikelihood.

The null model is usually obtained by re-fitting the model using the trend formula `~1`. However if the original model formula included `offset` terms, and if `keepoffset=TRUE` (the default), then the null model formula consists of these offset terms. This ensures that the `pseudoR2` value is non-negative.

Value

A single numeric value.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

pseudoR2, deviance.lppm.

Examples

```
X <- rpoislpp(10, simplenet)
fit <- lppm(X ~ y)
pseudoR2(fit)
```

---

qqplot.lppm *Q-Q Plot of Residuals from Fitted Point Process Model on a Linear Network*

Description

Given a point process model fitted to a point pattern on a linear network, produce a Q-Q plot based on residuals from the model.

Usage

```
qqplot.lppm(fit, nsim=100, expr=NULL, ..., type="raw",
            style="mean", fast=TRUE, verbose=TRUE, plot.it=TRUE,
            probs=NULL,
            saveall=FALSE,
            monochrome=FALSE,
            limcol=if(monochrome) "black" else "red",
            maxerr=max(100, ceiling(nsim/10)),
            envir.expr)
```

Arguments

fit	The fitted point process model on a network, which is to be assessed using the Q-Q plot. An object of class "lppm". Smoothed residuals obtained from this fitted model will provide the "data" quantiles for the Q-Q plot.
nsim	The number of simulations from the "reference" point process model.
expr	Determines the simulation mechanism which provides the "theoretical" quantiles for the Q-Q plot. See Details.
...	Arguments passed to diagnose.lppm influencing the computation of residuals.
type	String indicating the type of residuals or weights to be used. Current options are "eem" for the Stoyan-Grabarnik exponential energy weights, "raw" for the raw residuals, "inverse" for the inverse-lambda residuals, and "pearson" for the Pearson residuals. A partial match is adequate.
style	Character string controlling the type of Q-Q plot. Options are "classical" and "mean". See Details.
fast	Logical flag controlling the speed and accuracy of computation. Use fast=TRUE for interactive use and fast=FALSE for publication standard plots. See Details.

verbose	Logical value controlling whether the algorithm prints progress reports during long computations.
plot.it	Logical value controlling whether the function produces a plot or simply returns a value (silently).
probs	Probabilities for which the quantiles should be calculated and plotted. A numeric vector of values between 0 and 1.
saveall	Logical flag indicating whether to save all the intermediate calculations.
monochrome	Logical flag indicating whether the plot should be in black and white (monochrome=TRUE), or in colour (monochrome=FALSE).
limcol	String. The colour to be used when plotting the 95% limit curves.
maxerr	Maximum number of failures tolerated while generating simulated realisations. See Details.
envir.expr	Optional. An environment in which the expression expr should be evaluated.

Details

This function generates a Q-Q plot of the residuals from a fitted point process model on a linear network. It is an addendum to the suite of diagnostic plots produced by the function diagnose.lppm, kept separate because it is computationally intensive. The quantiles of the theoretical distribution are estimated by simulation.

In classical statistics, a Q-Q plot of residuals is a useful diagnostic for checking the distributional assumptions. Analogously, in spatial statistics, a Q-Q plot of the (smoothed) residuals from a fitted point process model is a useful way to check the interpoint interaction part of the model (Baddeley et al, 2005). The systematic part of the model (spatial trend, covariate effects, etc) is assessed using other plots made by diagnose.lppm.

The argument fit represents the fitted point process model. It must be an object of class "lppm" (typically produced by the maximum pseudolikelihood fitting algorithm lppm). Residuals will be computed for this fitted model using residuals.lppm, and the residuals will be kernel-smoothed to produce a "residual field". The values of this residual field will provide the "data" quantiles for the Q-Q plot.

The argument expr is not usually specified. It provides a way to modify the "theoretical" or "reference" quantiles for the Q-Q plot.

In normal usage we set expr=NULL. The default is to generate nsim simulated realisations of the fitted model fit using simulate.lppm, re-fit this model to each of the simulated patterns, evaluate the residuals from these fitted models, and use the kernel-smoothed residual field from these fitted models as a sample from the reference distribution for the Q-Q plot.

In advanced use, expr may be an expression. It will be re-evaluated nsim times, and should include random computations so that the results are not identical each time. The result of evaluating expr should be either a point pattern on a network (object of class "lpp") or a fitted point process model on a network (object of class "lppm"). If the value is a point pattern, then the original fitted model fit will be re-fitted to this new point pattern using update.lppm, to yield another fitted model. Smoothed residuals obtained from these nsim fitted models will yield the "theoretical" quantiles for the Q-Q plot.

Alternatively expr can be a list of point patterns, or an envelope object that contains a list of point patterns (typically generated by calling envelope.lpp or envelope.lppm with savepatterns=TRUE). These point patterns will be used as the simulated patterns.

The argument type selects the type of residual or weight that will be computed. For options, see diagnose.lppm.

The argument style determines the type of Q-Q plot. It is highly recommended to use the default, style="mean".

style="classical" The quantiles of the residual field for the data (on the y axis) are plotted against the quantiles of the **pooled** simulations (on the x axis). This plot is biased, and therefore difficult to interpret, because of strong autocorrelations in the residual field and the large differences in sample size.

style="mean" Quantiles of the residual field for the original data are plotted against the sample means, over the nsim simulations, of the corresponding quantiles of the residual field for the simulated datasets. Dotted lines show the 2.5 and 97.5 percentiles, over the nsim simulations, of each of these quantiles.

The argument fast is a simple way to control the accuracy and speed of computation. If fast=FALSE, the residual field is computed on a fine grid of pixels (by default 100 by 100 pixels, see below) and the Q-Q plot is based on the complete set of order statistics (up to 10,000 quantiles). If fast=TRUE, the residual field is computed on a coarse grid (at most 40 by 40 pixels) and the Q-Q plot is based on the *percentiles* only. This is about 7 times faster. It is recommended to use fast=TRUE for interactive data analysis and fast=FALSE for definitive plots for publication.

Since the computation is so time-consuming, qqplot.lppm returns a list containing all the data necessary to re-display the Q-Q plot. It is advisable to assign the result of qqplot.lppm to something (or use .Last.value if you forgot to.) The return value is an object of class "qqlppm". There are methods for plot and print. See the Examples.

The argument saveall is usually set to FALSE. If saveall=TRUE, then the intermediate results of calculation for each simulated realisation are saved and returned. The return value includes a 3-dimensional array sim containing the smoothed residual field images for each of the nsim realisations. When saveall=TRUE, the return value is an object of very large size, and should not be saved on disk.

Errors may occur during the simulation process, because random data are generated. For example:

- one of the simulated patterns may be empty.
- one of the simulated patterns may cause an error in the code that fits the point process model.
- the user-supplied argument expr may have a bug.

Empty point patterns do not cause a problem for the code, but they are reported. Other problems that would lead to a crash are trapped; the offending simulated data are discarded, and the simulation is retried. The argument maxerr determines the maximum number of times that such errors will be tolerated (mainly as a safeguard against an infinite loop).

Value

An object of class "qqlppm" containing the information needed to reproduce the Q-Q plot. Entries x and y are numeric vectors containing quantiles of the simulations and of the data, respectively.

Side Effects

Produces a Q-Q plot if plot.it=TRUE (the default).

Warning messages

A warning message will be issued if any of the simulations trapped an error (a potential crash).

A warning message will be issued if all, or many, of the simulated point patterns are empty. This usually indicates a problem with the simulation procedure.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

References

Baddeley, A., Turner, R., Møller, J. and Hazelton, M. (2005) Residual analysis for spatial point processes. *Journal of the Royal Statistical Society, Series B* **67**, 617–666.

Stoyan, D. and Grabarnik, P. (1991) Second-order characteristics for stochastic structures connected with Gibbs point processes. *Mathematische Nachrichten*, 151:95–100.

See Also

diagnose.lppm, lurking.lppm, residuals.lppm, lppm

Examples

```
if(online <- interactive()) {
  X <- unmark(chicago)
  fit <- lppm(X ~ x + y)
  ns <- 100
} else {
  X <- runiflpp(20, simplenet)
  fit <- lppm(X ~ y)
  ns <- 4
}

qqplot.lppm(fit, nsim=ns)
qqplot.lppm(fit, nsim=ns, type="pearson")


  # capture the plot coordinates
  mypreciousdata <- qqplot.lppm(fit, ns, type="pearson")
  ## or use the idiom .Last.value if you forgot to assign them
  qqplot.lppm(fit, ns, type="pearson")
  mypreciousdata <- .Last.value
  plot(mypreciousdata)
```

quadrat.test.lpp *Dispersion Test for Point Pattern on a Network Based on Quadrat Counts*

Description

Performs a test of Complete Spatial Randomness for a given point pattern on a linear network, based on quadrat counts. Alternatively performs a goodness-of-fit test of a fitted inhomogeneous Poisson model on a network. By default performs chi-squared tests; can also perform power-divergence tests and Monte Carlo tests.

Usage

```
## S3 method for class 'lpp'
quadrat.test(X, ...,
                          tess=NULL,
                          nx=5, ny=nx,
                          xbreaks=NULL, ybreaks=NULL,
                          alternative=c("two.sided", "regular", "clustered"),
                          method=c("Chisq", "MonteCarlo"),
                          conditional=TRUE, CR=1,
                          lambda=NULL, df.est=NULL,
                          nsim=1999)
## S3 method for class 'lppm'
quadrat.test(X,...,
                          tess=NULL,
                          nx=5, ny=nx,
                          xbreaks=NULL, ybreaks=NULL,
                          alternative=c("two.sided", "regular", "clustered"),
                          method=c("Chisq", "MonteCarlo"),
                          conditional=TRUE, CR=1, df.est=NULL,
                          nsim=1999)
## S3 method for class 'linearquadratcount'
quadrat.test(X, ...,
                          alternative=c("two.sided", "regular", "clustered"),
                          method=c("Chisq", "MonteCarlo"),
                          conditional=TRUE, CR=1,
                          lambda=NULL, df.est=NULL,
                          nsim=1999)
```

Arguments

X	A point pattern on a network (object of class "lpp") to be subjected to the goodness-of-fit test. Alternatively a fitted point process model on a network (object of class "lppm") to be tested. Alternatively X can be the result of applying quadratcount to a point pattern on a network.

tess	Tessellation (object of class "tess" or "lintess") determining the quadrats. Incompatible with nx,ny,xbreaks,ybreaks.
nx, ny	Numbers of quadrats in the x and y directions. Incompatible with xbreaks and ybreaks.
xbreaks	Optional. Numeric vector giving the x coordinates of the boundaries of the quadrats. Incompatible with nx.
ybreaks	Optional. Numeric vector giving the y coordinates of the boundaries of the quadrats. Incompatible with ny.
alternative	Character string (partially matched) specifying the alternative hypothesis.
method	Character string (partially matched) specifying the test to use: either method="Chisq" for the chi-squared test (the default), or method="MonteCarlo" for a Monte Carlo test.
conditional	Logical. Should the Monte Carlo test be conducted conditionally upon the observed number of points of the pattern? Ignored if method="Chisq".
CR	Optional. Numerical value. The exponent for the Cressie-Read test statistic. See Details.
lambda	Optional. Pixel image (object of class "im" or "linim") or function (class "funxy") giving the predicted intensity of the point process.
df.est	Optional. Advanced use only. The number of fitted parameters, or the number of degrees of freedom lost by estimation of parameters.
...	Ignored.
nsim	The number of simulated samples to generate when method="MonteCarlo".

Details

These functions perform χ^2 tests or Monte Carlo tests of goodness-of-fit for a point process model on a linear network, based on quadrat counts.

The function quadrat.test is generic, with methods for many classes. This page documents the methods for data on a linear network.

- if X is a point pattern on a network (object of class "lpp"), we test the null hypothesis that the data pattern is a realisation of Complete Spatial Randomness (the uniform Poisson point process) on the network. Marks in the point pattern are ignored. (If lambda is given then the null hypothesis is the Poisson process with intensity lambda.)
- If X is a fitted point process model on a network (object of class "lppm"), then it should be a Poisson point process model. The data to which this model was fitted are extracted from the model object, and are treated as the data point pattern for the test. We test the null hypothesis that the data pattern is a realisation of the (inhomogeneous) Poisson point process specified by X.

First the network is divided into pieces to form a tessellation (object of class "lintess") as follows:

- By default, if none of the arguments nx, ny, xbreaks, ybreaks, tess is given, every segment of the network is taken as a separate piece. The number of points in each segment of the network is counted.

- If nx, ny are given, the window containing the point pattern X is divided into an nx * ny grid of rectangular tiles or 'quadrats'. These tiles are then intersected with the network on which X is defined. The number of points falling in each rectangle is counted.
- If xbreaks is given, the window containing the point pattern X will be divided into rectangles, with xbreaks and ybreaks giving the x and y coordinates of the rectangle boundaries, respectively. The lengths of xbreaks and ybreaks may be different.
- The argument tess can be a tessellation on the network (object of class "lintess") whose tiles will serve as the quadrats.
- Alternatively tess can be a two-dimensional tessellation (object of class "tess") which will be intersected with the network to determine the tessellation of the network.

Next the number of data points in each tile of the tessellation is counted.

The expected number of points in each quadrat is also calculated, as determined by CSR (in the first case) or by the fitted model (in the second case).

Then the Pearson X^2 statistic

$$X^2 = sum((observed - expected)^2/expected)$$

is computed.

If method="Chisq" then a χ^2 test of goodness-of-fit is performed by comparing the test statistic to the χ^2 distribution with $m - k$ degrees of freedom, where m is the number of quadrats and k is the number of fitted parameters (equal to 1 for quadrat.test.ppp). The default is to compute the *two-sided* p-value, so that the test will be declared significant if X^2 is either very large or very small. One-sided p-values can be obtained by specifying the alternative. An important requirement of the χ^2 test is that the expected counts in each quadrat be greater than 5.

If method="MonteCarlo" then a Monte Carlo test is performed, obviating the need for all expected counts to be at least 5. In the Monte Carlo test, nsim random point patterns are generated from the null hypothesis (either CSR or the fitted point process model). The Pearson X^2 statistic is computed as above. The p-value is determined by comparing the X^2 statistic for the observed point pattern, with the values obtained from the simulations. Again the default is to compute the *two-sided* p-value.

If conditional is TRUE then the simulated samples are generated from the multinomial distribution with the number of "trials" equal to the number of observed points and the vector of probabilities equal to the expected counts divided by the sum of the expected counts. Otherwise the simulated samples are independent Poisson counts, with means equal to the expected counts.

If the argument CR is given, then instead of the Pearson X^2 statistic, the Cressie-Read (1984) power divergence test statistic

$$2nI = \frac{2}{CR(CR+1)} \sum_i \left[\left(\frac{X_i}{E_i} \right)^C R - 1 \right]$$

is computed, where X_i is the ith observed count and E_i is the corresponding expected count. The value CR=1 gives the Pearson X^2 statistic; CR=0 gives the likelihood ratio test statistic G^2; CR=-1/2 gives the Freeman-Tukey statistic T^2; CR=-1 gives the modified likelihood ratio test statistic GM^2; and CR=-2 gives Neyman's modified statistic NM^2. In all cases the asymptotic distribution of this test statistic is the same χ^2 distribution as above.

The return value is an object of class "htest". Printing the object gives comprehensible output about the outcome of the test.

The return value also belongs to the special class "quadrat.test". Plotting the object will display the quadrats, annotated by their observed and expected counts and the Pearson residuals. See the examples.

Value

An object of class "htest". See chisq.test for explanation.

The return value is also an object of the special class "quadrattest", and there is a plot method for this class. See the examples.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

References

Cressie, N. and Read, T.R.C. (1984) Multinomial goodness-of-fit tests. *Journal of the Royal Statistical Society, Series B* **46**, 440–464.

See Also

quadrat.test, quadratcount.lpp, lintess.

Examples

```
X <- runiflpp(100, simplenet)

quadrat.test(X)

quadrat.test(X, nx=2)
```

---

quadratcount *Quadrat counting for a point pattern on a linear network*

Description

Given a point pattern on a linear network, divide the network into tiles, and count the numbers of points in each file.

Usage

```
  ## S3 method for class 'lpp'
quadratcount(X, ..., nx=5, ny=nx,
               xbreaks=NULL, ybreaks=NULL, left.open=TRUE,
               tess=NULL)
```

Arguments

X	A point pattern on a linear network (object of class "lpp").
nx, ny	Numbers of rectangular quadrats in the x and y directions. Incompatible with xbreaks and ybreaks.
...	Additional arguments are ignored.
xbreaks	Numeric vector giving the x coordinates of the boundaries of the rectangular quadrats. Incompatible with nx.
ybreaks	Numeric vector giving the y coordinates of the boundaries of the rectangular quadrats. Incompatible with ny.
tess	Tessellation (object of class "tess" or "lintess") determining the quadrats. Incompatible with nx,ny,xbreaks,ybreaks.
left.open	Logical value specifying whether rectangular quadrats are left-open and right-closed (left.open=TRUE, the default) or left-closed and right-open (left.open=FALSE).

Details

Quadrat counting is an elementary technique for analysing spatial point patterns. See Diggle (2003).

The function quadratcount is generic. This page documents the method quadratcount.lpp for the class "lpp" of point patterns on a linear network.

First the network is divided into pieces, as described below. Then the number of points of X falling in each piece of the network is counted. These numbers are returned as a contingency table.

- By default, if none of the arguments nx, ny, xbreaks, ybreaks, tess is given, every segment of the network is taken as a separate piece. The number of points in each segment of the network is counted.
- If nx, ny are given, the window containing the point pattern X is divided into an nx * ny grid of rectangular tiles or 'quadrats'. These tiles are then intersected with the network on which X is defined. The number of points falling in each rectangle is counted.
- If xbreaks is given, the window containing the point pattern X will be divided into rectangles, with xbreaks and ybreaks giving the x and y coordinates of the rectangle boundaries, respectively. The lengths of xbreaks and ybreaks may be different.
- The argument tess can be a tessellation on the network (object of class "lintess") whose tiles will serve as the quadrats.
- Alternatively tess can be a two-dimensional tessellation (object of class "tess") which will be intersected with the network to determine the tessellation of the network.

The algorithm counts the number of points of X falling in each tile of the tessellation, and returns these counts as a contingency table.

The return value is a table which can be printed neatly. The return value is also a member of the special class "linearquadratcount". Plotting the object will display the quadrats, annotated by their counts. See the examples.

To calculate an estimate of intensity based on the quadrat counts, use intensity.linearquadratcount.

To extract the quadrats used in a linearquadratcount object, use as.lintess.

Marks attached to the points are ignored by quadratcount.lpp. To obtain a separate contingency table for each type of point in a multitype point pattern, first separate the different points using split.ppx, then apply quadratcount.lpp to each pattern.

Value

Contingency table containing the number of points counted in each tile. The table is also an object of the special class "linearquadratcount" and there is a plot method for this class.

Treament of data points on the boundary

The treatment of points which lie on the boundary of two quadrats is undefined, and may depend on the hardware.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

References

Diggle, P.J. *Statistical analysis of spatial point patterns*. Academic Press, 2003.

Stoyan, D. and Stoyan, H. (1994) *Fractals, random shapes and point fields: methods of geometrical statistics.* John Wiley and Sons.

See Also

lintess.

Examples

```
X <- runiflpp(40, simplenet)
A <- quadratcount(X)
A
plot(A)
B <- quadratcount(X, nx=2)
B
plot(B)
```

---

rcelllpp *Simulate Cell Process on Linear Network*

Description

Generate a realisation of the cell process on a linear network.

Usage

```
rcelllpp(L, lambda, rnumgen = NULL, ..., saveid=FALSE)
```

Arguments

L	Either a linear network (object of class "linnet") or a tessellation on a linear network (object of class "lintess").
lambda	Intensity of the process (expected number of points per unit length),
rnumgen	Optional. Random number generator for the number of points in each cell.
...	Additional arguments to rnumgen.
saveid	Logical value indicating whether to save information about cell membership.

Details

This function generates simulated realisations of a cell point process on a network, as described in Baddeley et al (2017). This is the analogue on a linear network of the two-dimensional cell point process of Baddeley and Silverman (1988).

The argument L should be a tessellation on a linear network. Alternatively if L is a linear network, it is converted to a tessellation by treating each network segment as a tile in the tessellation.

The cell process generates a point process by generating independent point processes inside each tile of the tessellation. Within each tile, given the number of random points in the tile, the points are independent and uniformly distributed within the tile.

By default (when rnumgen is not given), the number of points in a tile of length t is a random variable with mean and variance equal to lambda * t, generated by calling rcellnumber.

If rnumgen is given, it should be a function with arguments rnumgen(n, mu, ...) where n is the number of random integers to be generated, mu is the mean value of the distribution, and ... are additional arguments, if needed. It will be called in the form rnumgen(1, lambda * t, ...) to determine the number of random points falling in each tile of length t.

Value

Point pattern on a linear network (object of class "lpp"). If saveid=TRUE, the result has an attribute "cellid" which is a factor specifying the cell that contains each point.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

References

Baddeley, A.J. and Silverman, B.W. (1984) A cautionary example on the use of second-order methods for analyzing point patterns. *Biometrics* **40**, 1089-1094.

Baddeley, A., Nair, G., Rakshit, S. and McSwiggan, G. (2017) 'Stationary' point processes are uncommon on linear networks. *STAT* **6**, 68–78.

See Also

rSwitzerlpp

Examples

```
X <- rcelllpp(domain(spiders), 0.01)
plot(X)
plot(linearK(X))
```

`relrisk.lpp` *Nonparametric Estimate of Spatially-Varying Relative Risk on a Network*

Description

Given a multitype point pattern on a linear network, this function estimates the spatially-varying probability of each type of point, or the ratios of such probabilities, using kernel smoothing.

Usage

```
## S3 method for class 'lpp'
relrisk(X, sigma, ...,
           at = c("pixels", "points"),
           relative=FALSE,
           adjust=1,
           casecontrol=TRUE, control=1, case,
           finespacing=FALSE)
```

Arguments

`X`	A multitype point pattern (object of class `"lpp"` which has factor valued marks).
`sigma`	The numeric value of the smoothing bandwidth (the standard deviation of Gaussian smoothing kernel) passed to `density.lpp`. Alternatively `sigma` may be a function which can be used to select the bandwidth. See Details.
`...`	Arguments passed to `density.lpp` to control the pixel resolution.
`at`	Character string specifying whether to compute the probability values at a grid of pixel locations (`at="pixels"`) or only at the points of `X` (`at="points"`).
`relative`	Logical. If `FALSE` (the default) the algorithm computes the probabilities of each type of point. If `TRUE`, it computes the *relative risk*, the ratio of probabilities of each type relative to the probability of a control.
`adjust`	Optional. Adjustment factor for the bandwidth `sigma`.
`casecontrol`	Logical. Whether to treat a bivariate point pattern as consisting of cases and controls, and return only the probability or relative risk of a case. Ignored if there are more than 2 types of points. See Details.
`control`	Integer, or character string, identifying which mark value corresponds to a control.
`case`	Integer, or character string, identifying which mark value corresponds to a case (rather than a control) in a bivariate point pattern. This is an alternative to the argument `control` in a bivariate point pattern. Ignored if there are more than 2 types of points.

finespacing Logical value specifying whether to use a finer spatial resolution (with longer computation time but higher accuracy).

Details

The command relrisk is generic and can be used to estimate relative risk in different ways.

This function relrisk.lpp is the method for point patterns on a linear network (objects of class "lpp"). It computes *nonparametric* estimates of relative risk by kernel smoothing.

If X is a bivariate point pattern (a multitype point pattern consisting of two types of points) then by default, the points of the first type (the first level of marks(X)) are treated as controls or non-events, and points of the second type are treated as cases or events. Then by default this command computes the spatially-varying *probability* of a case, i.e. the probability $p(u)$ that a point at location u on the network will be a case. If relative=TRUE, it computes the spatially-varying *relative risk* of a case relative to a control, $r(u) = p(u)/(1 - p(u))$.

If X is a multitype point pattern with $m > 2$ types, or if X is a bivariate point pattern and casecontrol=FALSE, then by default this command computes, for each type j, a nonparametric estimate of the spatially-varying *probability* of an event of type j. This is the probability $p_j(u)$ that a point at location u on the network will belong to type j. If relative=TRUE, the command computes the *relative risk* of an event of type j relative to a control, $r_j(u) = p_j(u)/p_k(u)$, where events of type k are treated as controls. The argument control determines which type k is treated as a control.

If at = "pixels" the calculation is performed for every location u on a fine pixel grid over the network, and the result is a pixel image on the network representing the function $p(u)$, or a list of pixel images representing the functions $p_j(u)$ or $r_j(u)$ for $j = 1, \ldots, m$. An infinite value of relative risk (arising because the probability of a control is zero) will be returned as NA.

If at = "points" the calculation is performed only at the data points x_i. By default the result is a vector of values $p(x_i)$ giving the estimated probability of a case at each data point, or a matrix of values $p_j(x_i)$ giving the estimated probability of each possible type j at each data point. If relative=TRUE then the relative risks $r(x_i)$ or $r_j(x_i)$ are returned. An infinite value of relative risk (arising because the probability of a control is zero) will be returned as Inf.

Estimation is performed by a Nadaraja-Watson type kernel smoother (McSwiggan et al., 2019).

The smoothing bandwidth sigma should be a single numeric value, giving the standard deviation of the isotropic Gaussian kernel. If adjust is given, the smoothing bandwidth will be adjust * sigma before the computation of relative risk.

Alternatively, sigma may be a function that can be applied to the point pattern X to select a bandwidth; the function must return a single numerical value; examples include the functions bw.relrisk.lpp and bw.scott.iso.

Accuracy depends on the spatial resolution of the density computations. If the arguments dx and dt are present, they are passed to density.lpp to determine the spatial resolution. Otherwise, the spatial resolution is determined by a default rule that depends on finespacing and sigma. If finespacing=FALSE (the default), the spatial resolution is equal to the default resolution for pixel images. If finespacing=TRUE, the spatial resolution is much finer and is determined by a rule which guarantees higher accuracy, but takes a longer time.

Value

If X consists of only two types of points, and if casecontrol=TRUE, the result is a pixel image on the network (if at="pixels") or a vector (if at="points"). The pixel values or vector values are

the probabilities of a case if `relative=FALSE`, or the relative risk of a case (probability of a case divided by the probability of a control) if `relative=TRUE`.

If `X` consists of more than two types of points, or if `casecontrol=FALSE`, the result is:

- (if `at="pixels"`) a list of pixel images on the network, with one image for each possible type of point. The result also belongs to the class `"solist"` so that it can be printed and plotted.
- (if `at="points"`) a matrix of probabilities, with rows corresponding to data points x_i, and columns corresponding to types j.

The pixel values or matrix entries are the probabilities of each type of point if `relative=FALSE`, or the relative risk of each type (probability of each type divided by the probability of a control) if `relative=TRUE`.

If `relative=FALSE`, the resulting values always lie between 0 and 1. If `relative=TRUE`, the results are either non-negative numbers, or the values `Inf` or `NA`.

Author(s)

Greg McSwiggan and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

References

McSwiggan, G., Baddeley, A. and Nair, G. (2019) Estimation of relative risk for events on a linear network. *Statistics and Computing* **30** (2) 469–484.

See Also

relrisk

Examples

```
## case-control data: 2 types of points
set.seed(2020)
X <- superimpose(A=runiflpp(20, simplenet),
                 B=runifpointOnLines(20, as.psp(simplenet)[5]))
plot(X)
plot(relrisk(X, 0.1))
plot(relrisk(X, 0.1, case="B"))
head(relrisk(X, 0.1, at="points"))
## cross-validated bandwidth selection
if(human <- interactive()) {
  plot(relrisk(X, bw.relrisk.lpp, hmax=0.3, allow.infinite=FALSE))
} else {
  a <- relrisk(X, bw.relrisk.lpp, hmax=0.2, nh=3, allow.infinite=FALSE)
}
## more than 2 types
if(human) {
  U <- chicago
  sig <- 170
} else {
  U <- do.call(superimpose,
               split(chicago)[c("theft", "cartheft", "burglary")])
```

```
  sig <- 40
}
plot(relrisk(U, sig))
head(relrisk(U, sig, at="points"))
plot(relrisk(U, sig, relative=TRUE, control="theft"))
```

---

repairNetwork *Repair Internal Data in a Linear Network*

Description

Detect and repair inconsistencies or duplication in the internal data of a network object.

Usage

```
repairNetwork(X)
```

Arguments

X	A linear network (object of class "linnet") or a point pattern on a linear network (object of class "lpp").

Details

This function detects and repairs inconsistencies in the internal data of X. Currently it does the following:

- checks that different ways of calculating the number of edges give the same answer
- removes any duplicated edges of the network
- ensures that each edge is recorded as a pair of vertex indices (from, to) with from < to.

Value

An object of the same kind as X.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

See Also

thinNetwork

`Replace.linim` *Reset Values in Subset of Image on Linear Network*

Description

Reset the values in a subset of a pixel image on a linear network.

Usage

```
  ## S3 replacement method for class 'linim'
x[i, j] <- value
```

Arguments

`x`	A pixel image on a linear network. An object of class `"linim"`.
`i`	Object defining the subregion or subset to be replaced. Either a spatial window (an object of class `"owin"`), or a pixel image with logical values, or a point pattern (an object of class `"ppp"`), or any type of index that applies to a matrix, or something that can be converted to a point pattern by `as.ppp` (using the window of `x`).
`j`	An integer or logical vector serving as the column index if matrix indexing is being used. Ignored if `i` is appropriate to some sort of replacement *other than* matrix indexing.
`value`	Vector, matrix, factor or pixel image containing the replacement values. Short vectors will be recycled.

Details

This function changes some of the pixel values in a pixel image. The image `x` must be an object of class `"linim"` representing a pixel image on a linear network.

The pixel values are replaced according to the rules described in the help for `[<-.im`. Then the auxiliary data are updated.

Value

The image `x` with the values replaced.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

`[<-.im`.

Examples

```
# make a function
Y <- as.linim(distfun(runiflpp(5, simplenet)))
# replace some values
B <- square(c(0.25, 0.55))
Y[B] <- 2
plot(Y, main="")
plot(B, add=TRUE, lty=3)
X <- runiflpp(4, simplenet)
Y[X] <- 5
```

---

residuals.lppm *Residuals for Fitted Point Process Model on a Network*

Description

Given a point process model fitted to a point pattern on a linear network, compute residuals of the fitted model.

Usage

```
  ## S3 method for class 'lppm'
residuals(object, type="raw", ...)
```

Arguments

object	The fitted point process model (an object of class "ppm") for which residuals should be calculated.
type	String indicating the type of residuals to be calculated. Current options are "raw", "inverse", "pearson" and "score". A partial match is adequate.
...	Other arguments are currently ignored.

Details

This function computes several kinds of residuals for the fit of a point process model to a spatial point pattern on a linear network. It is an extension of the method of Baddeley et al (2005) to point process models on a network. Use plot.msr to plot the residuals directly.

The argument object must be a fitted point process model on a network (object of class "lppm"). Such objects are produced by the model-fitting algorithm lppm. This fitted model object contains complete information about the original data pattern.

Residuals are attached both to the data points and to some other points in the window of observation (namely, to the dummy points of the quadrature scheme used to fit the model). If the fitted model is correct, then the sum of the residuals over all (data and dummy) points in a spatial region B has mean zero. For further explanation, see Baddeley et al (2005).

The type of residual is chosen by the argument type. Current options are

`"raw"`: the raw residuals

$$r_j = z_j - w_j \lambda_j$$

at the quadrature points u_j, where z_j is the indicator equal to 1 if u_j is a data point and 0 if u_j is a dummy point; w_j is the quadrature weight attached to u_j; and

$$\lambda_j = \hat{\lambda}(u_j, x)$$

is the conditional intensity of the fitted model at u_j. These are the spatial analogue of the martingale residuals of a one-dimensional counting process.

`"inverse"`: the 'inverse-lambda' residuals (Baddeley et al, 2005)

$$r_j^{(I)} = \frac{r_j}{\lambda_j} = \frac{z_j}{\lambda_j} - w_j$$

obtained by dividing the raw residuals by the fitted conditional intensity. These are a counterpart of the exponential energy marks (see `eem`).

`"pearson"`: the Pearson residuals (Baddeley et al, 2005)

$$r_j^{(P)} = \frac{r_j}{\sqrt{\lambda_j}} = \frac{z_j}{\sqrt{\lambda_j}} - w_j \sqrt{\lambda_j}$$

obtained by dividing the raw residuals by the square root of the fitted conditional intensity. The Pearson residuals are standardised, in the sense that if the model (true and fitted) is Poisson, then the sum of the Pearson residuals in a spatial region B has variance equal to the area of B.

`"score"`: the score residuals (Baddeley et al, 2005)

$$r_j = (z_j - w_j \lambda_j) x_j$$

obtained by multiplying the raw residuals r_j by the covariates x_j for quadrature point j. The score residuals always sum to zero.

The result of `residuals.ppm` is a measure (object of class `"msr"`). Use `plot.msr` to plot the residuals directly. Use `integral.msr` to compute the total residual.

Value

An object of class `"msr"` representing a signed measure or vector-valued measure (see `msr`). This object can be plotted.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

References

Baddeley, A., Turner, R., Møller, J. and Hazelton, M. (2005) Residual analysis for spatial point processes. *Journal of the Royal Statistical Society, Series B* **67**, 617–666.

See Also

`lppm`, `msr`, `residuals.ppm`.

Examples

```
fit <- lppm(unmark(chicago) ~ x + y)

# raw residuals
rr <- residuals(fit)
rr

# Pearson residuals
rp <- residuals(fit, type="pe")
rp
plot(rp, main="Pearson residuals")

## multitype data
fitm <- lppm(chicago ~ (x+y) * marks, eps=100)
rpm <- residuals(fitm, type="pe")
## plot(rpm) would display 7 panels, one for each crime type
## Select residuals for crime type = Assault
plot(split(rpm)[["assault"]], markscale=2)
```

---

rhohat.lpp *Nonparametric Estimate of Intensity as Function of a Covariate*

Description

Computes a nonparametric estimate of the intensity of a point process on a linear network, as a function of a (continuous) spatial covariate.

Usage

```
## S3 method for class 'lpp'
rhohat(object, covariate, ...,
       weights=NULL,
       method=c("ratio", "reweight", "transform"),
       horvitz=FALSE,
       smoother=c("kernel", "local", "decreasing", "increasing",
                  "mountain", "valley", "piecewise"),
       subset=NULL,
       do.CI=TRUE,
       jitter=TRUE, jitterfactor=1, interpolate=TRUE,
       nd=1000, eps=NULL, random=TRUE,
       n = 512, bw = "nrd0", adjust=1, from = NULL, to = NULL,
       bwref=bw,
       covname, confidence=0.95, positiveCI, breaks=NULL, delta=NULL)

## S3 method for class 'lppm'
rhohat(object, covariate, ...,
       weights=NULL,
       method=c("ratio", "reweight", "transform"),
```

```
horvitz=FALSE,
smoother=c("kernel", "local", "decreasing", "increasing",
           "mountain", "valley", "piecewise"),
subset=NULL,
do.CI=TRUE,
jitter=TRUE, jitterfactor=1, interpolate=TRUE,
nd=1000, eps=NULL, random=TRUE,
n = 512, bw = "nrd0", adjust=1, from = NULL, to = NULL,
bwref=bw,
covname, confidence=0.95, positiveCI, breaks=NULL, delta=NULL)
```

Arguments

object	A point pattern on a linear network (object of class "lpp"), or a fitted point process model on a linear network (object of class "lppm").
covariate	Either a function(x,y) or a pixel image (object of class "im" or "linim") providing the values of the covariate at any location. Alternatively one of the strings "x" or "y" signifying the Cartesian coordinates.
weights	Optional weights attached to the data points. Either a numeric vector of weights for each data point, or a pixel image (object of class "im") or a function(x,y) providing the weights.
method	Character string determining the estimation method. See Details.
horvitz	Logical value indicating whether to use Horvitz-Thompson weights. See Details.
smoother	Character string determining the smoothing algorithm and the type of curve that will be estimated. See Details.
subset	Optional. A spatial window (object of class "owin") specifying a subset of the data, from which the estimate should be calculated.
do.CI	Logical value specifying whether to calculate standard errors and confidence bands.
jitter	Logical value. If jitter=TRUE (the default), the values of the covariate at the data points will be jittered (randomly perturbed by adding a small amount of noise) using the function jitter. If jitter=FALSE, the covariate values at the data points will not be altered. See the section on *Randomisation and discretisation*.
jitterfactor	Numeric value controlling the scale of jittering. Passed to jitter as the argument factor.
interpolate	Logical value specifying whether to use spatial interpolation to obtain the values of the covariate at the data points, when the covariate is a pixel image (object of class "im" or "linim"). If interpolate=FALSE, the covariate value for each data point is simply the value of the covariate image at the pixel centre that is nearest to the data point. If interpolate=TRUE, the covariate value for each data point is obtained by interpolating the nearest pixel values using interp.im.
eps, nd, random	Arguments controlling the pixel resolution at which the covariate will be evaluated. See Details.

bw	Smoothing bandwidth or bandwidth rule (passed to density.default).
adjust	Smoothing bandwidth adjustment factor (passed to density.default).
n, from, to	Arguments passed to density.default to control the number and range of values at which the function will be estimated.
bwref	Optional. An alternative value of bw to use when smoothing the reference density (the density of the covariate values observed at all locations in the window).
...	Additional arguments passed to density.default or locfit::locfit.
covname	Optional. Character string to use as the name of the covariate.
confidence	Confidence level for confidence intervals. A number between 0 and 1.
positiveCI	Logical value. If TRUE, confidence limits are always positive numbers; if FALSE, the lower limit of the confidence interval may sometimes be negative. Default is FALSE if smoother="kernel" and TRUE if smoother="local". See Details.
breaks	Breakpoints for the piecewise-constant function computed when smoother='piecewise'. Either a vector of numeric values specifying the breakpoints, or a single integer specifying the number of equally-spaced breakpoints. There is a sensible default. Incompatible with delta.
delta	Spacing between breakpoints for the piecewise-constant function computed when smoother='piecewise'. A single positive number. Incompatible with breaks.

Details

This command estimates the relationship between point process intensity and a given spatial covariate. Such a relationship is sometimes called a *resource selection function* (if the points are organisms and the covariate is a descriptor of habitat) or a *prospectivity index* (if the points are mineral deposits and the covariate is a geological variable). This command uses nonparametric methods which do not assume a particular form for the relationship.

If object is a point pattern, and baseline is missing or null, this command assumes that object is a realisation of a point process with intensity function $\lambda(u)$ of the form

$$\lambda(u) = \rho(Z(u))$$

where Z is the spatial covariate function given by covariate, and $\rho(z)$ is the resource selection function or prospectivity index. A nonparametric estimator of the function $\rho(z)$ is computed.

If object is a point pattern, and baseline is given, then the intensity function is assumed to be

$$\lambda(u) = \rho(Z(u))B(u)$$

where $B(u)$ is the baseline intensity at location u. A nonparametric estimator of the relative intensity $\rho(z)$ is computed.

If object is a fitted point process model, suppose X is the original data point pattern to which the model was fitted. Then this command assumes X is a realisation of a Poisson point process with intensity function of the form

$$\lambda(u) = \rho(Z(u))\kappa(u)$$

where $\kappa(u)$ is the intensity of the fitted model object. A nonparametric estimator of the relative intensity $\rho(z)$ is computed.

The nonparametric estimation procedure is controlled by the arguments `smoother`, `method` and `horvitz`.

The argument `smoother` selects the type of estimation technique.

- If `smoother="kernel"` (the default), the nonparametric estimator is a *kernel smoothing estimator* of $\rho(z)$ (Guan, 2008; Baddeley et al, 2012). The estimated function $\rho(z)$ will be a smooth function of z which takes nonnegative values. If `do.CI=TRUE` (the default), confidence bands are also computed, assuming a Poisson point process. See the section on *Smooth estimates*.
- If `smoother="local"`, the nonparametric estimator is a *local regression estimator* of $\rho(z)$ (Baddeley et al, 2012) obtained using local likelihood. The estimated function $\rho(z)$ will be a smooth function of z. If `do.CI=TRUE` (the default), confidence bands are also computed, assuming a Poisson point process. See the section on *Smooth estimates*.
- If `smoother="increasing"`, we assume that $\rho(z)$ is an increasing function of z, and use the *nonparametric maximum likelihood estimator* of $\rho(z)$ described by Sager (1982). The estimated function will be a step function, that is increasing as a function of z. Confidence bands are not computed. See the section on *Monotone estimates*.
- If `smoother="decreasing"`, we assume that $\rho(z)$ is a decreasing function of z, and use the *nonparametric maximum likelihood estimator* of $\rho(z)$ described by Sager (1982). The estimated function will be a step function, that is decreasing as a function of z. Confidence bands are not computed. See the section on *Monotone estimates*.
- If `smoother="mountain"`, we assume that $\rho(z)$ is a function with an inverted U shape, with a single peak at a value z_0, so that $\rho(z)$ is an increasing function of z for $z < z_0$ and a decreasing function of z for $z > z_0$. We compute the *nonparametric maximum likelihood estimator*. The estimated function will be a step function, which is increasing and then decreasing as a function of z. Confidence bands are not computed. See the section on *Unimodal estimates*.
- If `smoother="valley"`, we assume that $\rho(z)$ is a function with a U shape, with a single minimum at a value z_0, so that $\rho(z)$ is a decreasing function of z for $z < z_0$ and an increasing function of z for $z > z_0$. We compute the *nonparametric maximum likelihood estimator*. The estimated function will be a step function, which is decreasing and then increasing as a function of z. Confidence bands are not computed. See the section on *Unimodal estimates*.
- If `smoother="piecewise"`, the estimate of $\rho(z)$ is piecewise constant. The range of covariate values is divided into several intervals (ranges or bands). The endpoints of these intervals are the breakpoints, which may be specified by the argument `breaks`; there is a sensible default. The estimate of $\rho(z)$ takes a constant value on each interval. The estimate of $\rho(z)$ in each interval of covariate values is simply the average intensity (number of points per unit length) in the relevant sub-region of the network. If `do.CI=TRUE` (the default), confidence bands are also computed, assuming a Poisson point process.

See Baddeley (2018) for a comparison of these estimation techniques for two-dimensional point patterns.

If the argument `weights` is present, then the contribution from each data point `X[i]` to the estimate of ρ is multiplied by `weights[i]`.

If the argument `subset` is present, then the calculations are performed using only the data inside this spatial region.

This technique assumes that `covariate` has continuous values. It is not applicable to covariates with categorical (factor) values or discrete values such as small integers.

The argument covariate should be a pixel image, or a function, or one of the strings "x" or "y" signifying the cartesian coordinates. It will be evaluated on a fine grid of locations, with spatial resolution controlled by the arguments eps,nd,random. The argument nd specifies the total number of test locations on the linear network, eps specifies the linear separation between test locations, and random specifies whether the test locations have a randomised starting position.

Value

A function value table (object of class "fv") containing the estimated values of ρ (and confidence limits) for a sequence of values of Z. Also belongs to the class "rhohat" which has special methods for print, plot and predict.

Smooth estimates

Smooth estimators of $\rho(z)$ were proposed by Baddeley and Turner (2005) and Baddeley et al (2012). Similar estimators were proposed by Guan (2008) and in the literature on relative distributions (Handcock and Morris, 1999).

The estimated function $\rho(z)$ will be a smooth function of z.

The smooth estimation procedure involves computing several density estimates and combining them. The algorithm used to compute density estimates is determined by smoother:

- If smoother="kernel", the smoothing procedure is based on fixed-bandwidth kernel density estimation, performed by density.default.
- If smoother="local", the smoothing procedure is based on local likelihood density estimation, performed by locfit::locfit.

The argument method determines how the density estimates will be combined to obtain an estimate of $\rho(z)$:

- If method="ratio", then $\rho(z)$ is estimated by the ratio of two density estimates, The numerator is a (rescaled) density estimate obtained by smoothing the values $Z(y_i)$ of the covariate Z observed at the data points y_i. The denominator is a density estimate of the reference distribution of Z. See Baddeley et al (2012), equation (8). This is similar but not identical to an estimator proposed by Guan (2008).
- If method="reweight", then $\rho(z)$ is estimated by applying density estimation to the values $Z(y_i)$ of the covariate Z observed at the data points y_i, with weights inversely proportional to the reference density of Z. See Baddeley et al (2012), equation (9).
- If method="transform", the smoothing method is variable-bandwidth kernel smoothing, implemented by applying the Probability Integral Transform to the covariate values, yielding values in the range 0 to 1, then applying edge-corrected density estimation on the interval $[0, 1]$, and back-transforming. See Baddeley et al (2012), equation (10).

If horvitz=TRUE, then the calculations described above are modified by using Horvitz-Thompson weighting. The contribution to the numerator from each data point is weighted by the reciprocal of the baseline value or fitted intensity value at that data point; and a corresponding adjustment is made to the denominator.

If do.CI=TRUE (the default), pointwise confidence intervals for the true value of $\rho(z)$ are also calculated for each z, and will be plotted as grey shading. The confidence intervals are derived using the central limit theorem, based on variance calculations which assume a Poisson point process. If positiveCI=FALSE, the lower limit of the confidence interval may sometimes be negative, because the confidence intervals are based on a normal approximation to the estimate of $\rho(z)$. If positiveCI=TRUE, the confidence limits are always positive, because the confidence interval is based on a normal approximation to the estimate of $\log(\rho(z))$. For consistency with earlier versions, the default is positiveCI=FALSE for smoother="kernel" and positiveCI=TRUE for smoother="local".

Monotone estimates

The nonparametric maximum likelihood estimator of a monotone function $\rho(z)$ was described by Sager (1982). This method assumes that $\rho(z)$ is either an increasing function of z, or a decreasing function of z. The estimated function will be a step function, increasing or decreasing as a function of z.

This estimator is chosen by specifying smoother="increasing" or smoother="decreasing". The argument method is ignored this case.

To compute the estimate of $\rho(z)$, the algorithm first computes several primitive step-function estimates, and then takes the maximum of these primitive functions.

If smoother="decreasing", each primitive step function takes the form $\rho(z) = \lambda$ when $z \leq t$, and $\rho(z) = 0$ when $z > t$, where and λ is a primitive estimate of intensity based on the data for $Z \leq t$. The jump location t will be the value of the covariate Z at one of the data points. The primitive estimate λ is the average intensity (number of points divided by area) for the region of space where the covariate value is less than or equal to t.

If horvitz=TRUE, then the calculations described above are modified by using Horvitz-Thompson weighting. The contribution to the numerator from each data point is weighted by the reciprocal of the baseline value or fitted intensity value at that data point; and a corresponding adjustment is made to the denominator.

Confidence intervals are not available for the monotone estimators.

Unimodal estimators

If smoother="valley" then we estimate a U-shaped function. A function $\rho(z)$ is U-shaped if it is decreasing when $z < z_0$ and increasing when $z > z_0$, where z_0 is called the critical value. The nonparametric maximum likelihood estimate of such a function can be computed by profiling over z_0. The algorithm considers all possible candidate values of the critical value z_0, and estimates the function $\rho(z)$ separately on the left and right of z_0 using the monotone estimators described above. These function estimates are combined into a single function, and the Poisson point process likelihood is computed. The optimal value of z_0 is the one which maximises the Poisson point process likelihood.

If smoother="mountain" then we estimate a function which has an inverted U shape. A function $\rho(z)$ is inverted-U-shaped if it is increasing when $z < z_0$ and decreasing when $z > z_0$. The nonparametric maximum likelihood estimate of such a function can be computed by profiling over z_0 using the same technique *mutatis mutandis*.

Confidence intervals are not available for the unimodal estimators.

Randomisation

By default, rhohat adds a small amount of random noise to the data. This is designed to suppress the effects of discretisation in pixel images.

This strategy means that rhohat does not produce exactly the same result when the computation is repeated. If you need the results to be exactly reproducible, set jitter=FALSE and random=FALSE.

The values of the covariate *at the data points* are randomly perturbed by adding a small amount of noise using the function jitter. To reduce this effect, set jitterfactor to a number smaller than 1. To suppress this effect entirely, set jitter=FALSE.

The values of the covariate *along the network* are sampled at a regularly-spaced grid on the network. The grid starts from a random position on each segment of the network. To suppress this behaviour, set random=FALSE.

Author(s)

Smoothing algorithm by Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Ya-Mei Chang, Yong Song, and Rolf Turner <rolfturner@posteo.net>.

Nonparametric maximum likelihood algorithm by Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

References

Baddeley, A., Chang, Y.-M., Song, Y. and Turner, R. (2012) Nonparametric estimation of the dependence of a point process on spatial covariates. *Statistics and Its Interface* **5** (2), 221–236.

Baddeley, A. and Turner, R. (2005) Modelling spatial point patterns in R. In: A. Baddeley, P. Gregori, J. Mateu, R. Stoica, and D. Stoyan, editors, *Case Studies in Spatial Point Pattern Modelling*, Lecture Notes in Statistics number 185. Pages 23–74. Springer-Verlag, New York, 2006. ISBN: 0-387-28311-0.

Baddeley, A. (2018) A statistical commentary on mineral prospectivity analysis. Chapter 2, pages 25–65 in *Handbook of Mathematical Geosciences: Fifty Years of IAMG*, edited by B.S. Daya Sagar, Q. Cheng and F.P. Agterberg. Springer, Berlin.

Guan, Y. (2008) On consistent nonparametric intensity estimation for inhomogeneous spatial point processes. *Journal of the American Statistical Association* **103**, 1238–1247.

Handcock, M.S. and Morris, M. (1999) *Relative Distribution Methods in the Social Sciences*. Springer, New York.

Sager, T.W. (1982) Nonparametric maximum likelihood estimation of spatial patterns. *Annals of Statistics* **10**, 1125–1136.

See Also

rho2hat, methods.rhohat, parres.

See lppm for a parametric method for the same problem.

Examples

```
Y <- runiflpp(30, simplenet)
rhoY <- rhohat(Y, "y")
```

```
## do spiders prefer to be in the middle of a segment?
teepee <- linfun(function(x,y,seg,tp){ tp }, domain(spiders))
rhotee <- rhohat(spiders, teepee)
rhoteeM <- rhohat(spiders, teepee, smoother="mountain")
if(interactive()) {
  plot(rhotee, main="Spider preference for mid-segment")
  plot(rhoteeM, add=TRUE, .y ~ .x, lwd=3)
}
```

`rjitter.lpp` *Random Perturbation of a Point Pattern on a Network*

Description

Applies independent random displacements to each point in a point pattern on a network.

Usage

```
## S3 method for class 'lpp'
rjitter(X, radius, ..., nsim = 1, drop = TRUE)
```

Arguments

`X`	A point pattern on a linear network (object of class `"lpp"`).
`radius`	Scale of perturbations. A positive numerical value. Each point will be displaced by a random distance, with maximum displacement equal to this value.
`...`	Ignored.
`nsim`	Number of simulated realisations to be generated.
`drop`	Logical. If `nsim=1` and `drop=TRUE` (the default), the result will be a point pattern, rather than a list containing a point pattern.

Details

The function `rjitter` is generic. This function is the method for the class `"lpp"` of point patterns on a linear network.

Each of the points in `X` will be displaced along the network by a random amount, independently of other points. The maximum displacement distance is specified by `radius`. Each point remains on the same line segment of the network as it originally was.

Value

A point pattern on a linear network (object of class `"lpp"`) or a list of such point patterns.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

rjitter for point patterns in two dimensions.

Examples

```
X <- runiflpp(3, simplenet)
plot(X, pch=16)
Y <- rjitter(X, 0.1)
plot(Y, add=TRUE, cols=3)
```

---

rlpp *Random Points on a Linear Network*

Description

Generates n independent random points on a linear network with a specified probability density.

Usage

```
rlpp(n, f, ..., nsim=1, drop=TRUE)
```

Arguments

n	Number of random points to generate. A nonnegative integer giving the number of points, or an integer vector giving the numbers of points of each type.
f	Probability density (not necessarily normalised). A pixel image on a linear network (object of class "linim") or a function on a linear network (object of class "linfun"). Alternatively, f can be a list of functions or pixel images, giving the densities of points of each type.
...	Additional arguments passed to f if it is a function or a list of functions.
nsim	Number of simulated realisations to generate.
drop	Logical value indicating what to do when nsim=1. If drop=TRUE (the default), the result is a point pattern. If drop=FALSE, the result is a list with one entry which is a point pattern.

Details

The linear network L, on which the points will be generated, is determined by the argument f.

If f is a function, it is converted to a pixel image on the linear network, using any additional function arguments ....

If n is a single integer and f is a function or pixel image, then independent random points are generated on L with probability density proportional to f.

If n is an integer vector and f is a list of functions or pixel images, where n and f have the same length, then independent random points of several types are generated on L, with n[i] points of type i having probability density proportional to f[[i]].

Value

If nsim = 1 and drop=TRUE, a point pattern on the linear network, i.e.\ an object of class "lpp". Otherwise, a list of such point patterns.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

See Also

runiflpp

Examples

```
g <- function(x, y, seg, tp) { exp(x + 3*y) }
f <- linfun(g, simplenet)

rlpp(20, f)

plot(rlpp(20, f, nsim=3))
```

---

roc.lpp *Receiver Operating Characteristic for Data on a Network*

Description

Computes the Receiver Operating Characteristic curve for a point pattern on a linear network or a fitted point process model on a linear network.

Usage

```
## S3 method for class 'lpp'
roc(X, covariate,
                  ...,
                  baseline = NULL, high = TRUE, weights = NULL,
                  method = "raw",
                  CI = "none", alpha=0.05,
                  subset=NULL)

## S3 method for class 'lppm'
roc(X, covariate=NULL,
                   ..., baseline=NULL, high=TRUE,
                   method = "raw",
                   CI = "none", alpha=0.05,
                   leaveoneout=FALSE, subset=NULL)
```

Arguments

X	Point pattern on a network (object of class "lpp") or fitted point process model on a network (object of class "lppm").
covariate	Spatial covariate. Either a function(x,y), a pixel image (object of class "im" or "linim"), or one of the strings "x" or "y" indicating the Cartesian coordinates. Traditionally omitted when X is a fitted model.
...	Arguments passed to as.mask controlling the pixel resolution for calculations.
baseline	Optional. A spatial object giving a baseline intensity. Usually a function(x,y) or a pixel image (object of class "im" or "linim") giving the baseline intensity at any location on the network. Alternatively a point pattern on the network (object of class "lpp") giving the locations of the reference population.
high	Logical value indicating whether the threshold operation should favour high or low values of the covariate.
weights	Optional. Numeric vector of weights attached to the data points.
method	The method or methods that should be used to estimate the ROC curve. A character vector: current choices are "raw", "monotonic", "smooth" and "all". See Details.
CI	Character string (partially matched) specifying whether confidence intervals should be computed, and for which method. See Details.
alpha	Numeric value between 0 and 1. The confidence intervals will have confidence level 1-alpha. The default gives 95% confidence intervals.
subset	Optional. A spatial window (object of class "owin") specifying a subset of the data, from which the ROC should be calculated.
leaveoneout	Logical value specifying (for roc.lppm) whether the fitted intensity of the model at each of the original data points should be computed by the leave-one-out procedure (i.e. by removing the data point in question from the point pattern, re-fitting the model to the reduced point pattern, and computing the intensity of this modified model at the point in question) as described in Baddeley et al (2025). It is also possible to specify leaveoneout=c(TRUE,FALSE) so that both versions are calculated.

Details

The command roc computes the Receiver Operating Characteristic curve. The area under the ROC is computed by auc.

The function roc is generic, with methods for point patterns, fitted point process models and other kinds of data.

This help file describes the methods for classes "lpp" and "lppm".

For a point pattern X and a covariate Z, the ROC is a plot showing the ability of the covariate to separate the spatial domain into areas of high and low density of points. For each possible threshold z, the algorithm calculates the fraction $a(z)$ of area in the study region where the covariate takes a value greater than z, and the fraction $b(z)$ of data points for which the covariate value is greater than z. The ROC is a plot of $b(z)$ against $a(z)$ for all thresholds z.

For a fitted point process model, the ROC shows the ability of the fitted model intensity to separate the spatial domain into areas of high and low density of points. The ROC is **not** a diagnostic for the goodness-of-fit of the model (Lobo et al, 2007).

Value

Function value table (object of class `"fv"`) which can be plotted to show the ROC curve. Also belongs to class `"roc"`.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

References

Baddeley, A., Rubak, E., Rakshit, S. and Nair, G. (2025) ROC curves for spatial point patterns and presence-absence data. doi:10.48550/arXiv.2506.03414..

Lobo, J.M., Jiménez-Valverde, A. and Real, R. (2007) AUC: a misleading measure of the performance of predictive distribution models. *Global Ecology and Biogeography* **17**(2) 145–151.

Nam, B.-H. and D'Agostino, R. (2002) Discrimination index, the area under the ROC curve. Pages 267–279 in Huber-Carol, C., Balakrishnan, N., Nikulin, M.S. and Mesbah, M., *Goodness-of-fit tests and model validity*, Birkhäuser, Basel.

See Also

auc

Examples

```
plot(roc(spiders, "x"))
fit <- lppm(spiders ~ x)
plot(roc(fit))
```

---

rpoislpp *Poisson Point Process on a Linear Network*

Description

Generates a realisation of the Poisson point process with specified intensity on the given linear network.

Usage

```
rpoislpp(lambda, L, ..., nsim=1, drop=TRUE, ex=NULL)
```

Arguments

lambda	Intensity of the Poisson process. A single number, a function(x,y), a pixel image (object of class "im"), or a vector of numbers, a list of functions, or a list of images.
L	A linear network (object of class "linnet", see linnet). Can be omitted in some cases: see Details.
...	Arguments passed to rpoisppOnLines.
nsim	Number of simulated realisations to generate.
drop	Logical value indicating what to do when nsim=1. If drop=TRUE (the default), the result is a point pattern. If drop=FALSE, the result is a list with one entry which is a point pattern.
ex	Optional. A point pattern on a network (object of class "lpp") which serves as an example to determine the default values of lambda and L. See Details.

Details

A random number of random points is generated on the network L, according to a Poisson point process with intensity lambda points per unit length. The random points are generated by rpoisppOnLines. See the help file for rpoisppOnLines for information.

Argument L can be omitted, and defaults to as.linnet(lambda), when lambda is a function on a linear network (class "linfun") or a pixel image on a linear network ("linim").

If ex is given, then it serves as an example for determining lambda and L. The default value of lambda will be the average intensity (number per unit length) of points in ex (or the average intensity of the points of each type if ex is multitype). The default value of L will be the network on which ex is defined.

Value

If nsim = 1 and drop=TRUE, a point pattern on the linear network, i.e.\ an object of class "lpp". Otherwise, a list of such point patterns.

Author(s)

Ang Qi Wei <aqw07398@hotmail.com> and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

See Also

rpoisppOnLines, runiflpp, rlpp, lpp, linnet.

Examples

```
X <- rpoislpp(5, simplenet)
plot(X)
# multitype
Y <- rpoislpp(c(a=5, b=5), simplenet)
# using argument 'ex' to make a pattern like 'X'
Z <- rpoislpp(ex=X)
```

rSwitzerlpp *Switzer-type Point Process on Linear Network*

Description

Generate a realisation of the Switzer-type point process on a linear network.

Usage

```
rSwitzerlpp(L, lambdacut, rintens = rexp, ...,
         cuts=c("points", "lines"))
```

Arguments

L	Linear network (object of class "linnet").
lambdacut	Intensity of Poisson process of breakpoints.
rintens	Optional. Random variable generator used to generate the random intensity in each component.
...	Additional arguments to rintens.
cuts	String (partially matched) specifying the type of random cuts to be generated.

Details

This function generates simulated realisations of the Switzer-type point process on a network, as described in Baddeley et al (2017).

The linear network is first divided into pieces by a random mechanism:

- if cuts="points", a Poisson process of breakpoints with intensity lambdacut is generated on the network, and these breakpoints separate the network into connected pieces.
- if cuts="lines", a Poisson line process in the plane with intensity lambdacut is generated; these lines divide space into tiles; the network is divided into subsets associated with the tiles. Each subset may not be a connected sub-network.

In each piece of the network, a random intensity is generated using the random variable generator rintens (the default is a negative exponential random variable with rate 1). Given the intensity value, a Poisson process is generated with the specified intensity.

The intensity of the final process is determined by the mean of the values generated by rintens. If rintens=rexp (the default), then the parameter rate specifies the inverse of the intensity.

Value

Point pattern on a linear network (object of class "lpp") with an attribute "breaks" containing the breakpoints (if cuts="points") or the random lines (if cuts="lines").

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

References

Baddeley, A., Nair, G., Rakshit, S. and McSwiggan, G. (2017) 'Stationary' point processes are uncommon on linear networks. *STAT* **6**, 68–78.

See Also

rcelllpp

Examples

```
plot(rSwitzerlpp(domain(spiders), 0.01, rate=100))

plot(rSwitzerlpp(domain(spiders), 0.0005, rate=100, cuts="l"))
```

---

rThomaslpp *Simulate Thomas Process on Linear Network*

Description

Generate a random point pattern, a realisation of the Thomas cluster process, on a linear network.

Usage

```
rThomaslpp(kappa, scale, mu, L, ..., nsim=1, drop=TRUE)
```

Arguments

kappa	Intensity of the Poisson process of cluster centres. A single positive number, a function(x,y), or a pixel image (object of class "im" or "linim").
scale	Standard deviation of random displacement (along the network) of a point from its cluster centre.
mu	Mean number of points per cluster (a single positive number) or reference intensity for the cluster points (a function or a pixel image).
L	Linear network (object of class "linnet") on which the point pattern should be generated.
...	Arguments passed to rpoisppOnLines.
nsim	Number of simulated realisations to generate.
drop	Logical value indicating what to do when nsim=1. If drop=TRUE (the default), the result is a point pattern. If drop=FALSE, the result is a list with one entry which is a point pattern.

Details

This function generates realisations of the Thomas cluster process on a linear network, described by Baddeley et al (2017).

Argument L can be omitted, and defaults to as.linnet(kappa), when kappa is a function on a linear network (class "linfun") or a pixel image on a linear network ("linim").

Value

A point pattern on a network (object of class "lpp") or a list of point patterns on the network.

Author(s)

Greg McSwiggan and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

References

Baddeley, A., Nair, G., Rakshit, S. and McSwiggan, G. (2017) 'Stationary' point processes are uncommon on linear networks. *STAT* **6** (1) 68–78.

Baddeley, A., Nair, G., Rakshit, S., McSwiggan, G. and Davies, T.M. (2021) Analysing point patterns on networks — a review. *Spatial Statistics* **42**, 100435, DOI 10.1016/j.spasta.2020.100435.

See Also

rpoislpp

Examples

```
plot(rThomaslpp(4, 0.07, 5, simplenet))
```

---

runiflpp *Uniform Random Points on a Linear Network*

Description

Generates n random points, independently and uniformly distributed, on a linear network.

Usage

```
runiflpp(n, L, nsim=1, drop=TRUE, ex=NULL)
```

Arguments

n	Number of random points to generate. A nonnegative integer, or a vector of integers specifying the number of points of each type.
L	A linear network (object of class "linnet", see linnet).
nsim	Number of simulated realisations to generate.
drop	Logical value indicating what to do when nsim=1. If drop=TRUE (the default), the result is a point pattern. If drop=FALSE, the result is a list with one entry which is a point pattern.
ex	Optional. A point pattern on a network (object of class "lpp") which serves as an example to determine the default values of n and L. See Details.

Details

The specified number n of random points is generated with uniform distribution on the network L. The random points are generated using runifpointOnLines.

If n is an integer vector, then a multitype point pattern is generated, with n[i] random points of type i.

If ex is given, then it serves as an example for determining n and L. The default value of n will be the number of points in ex (or the number of points of each type in ex if it is multitype). The default value of L will be the network on which ex is defined.

Value

If nsim = 1 and drop=TRUE, a point pattern on a linear network (object of class "lpp"). Otherwise, a list of such point patterns.

Author(s)

Ang Qi Wei <aqw07398@hotmail.com> and Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

See Also

rlpp for non-uniform random points; rpoislpp for Poisson point process;

lpp, linnet

Examples

```
 X <- runiflpp(10, simplenet)
 plot(X)
# marked
 Z <- runiflpp(c(a=10, b=3), simplenet)
# using 'ex'
 U <- runiflpp(ex=Z)
```

---

sdr.lpp *Sufficient Dimension Reduction for a Point Pattern on a Linear Network*

Description

Given a point pattern on a linear network, and a set of predictors, find a minimal set of new predictors, each constructed as a linear combination of the original predictors.

Usage

```
## S3 method for class 'lpp'
sdr(X, covariates,
            method = c("DR", "NNIR", "SAVE", "SIR", "TSE"),
            Dim1 = 1, Dim2 = 1, predict=FALSE, ...)
```

Arguments

X	A point pattern on a linear network (object of class "lpp").
covariates	A list of pixel images (objects of class "im" or "linim") to serve as predictor variables.
method	Character string indicating which method to use. See Details.
Dim1	Dimension of the first order Central Intensity Subspace (applicable when method is "DR", "NNIR", "SAVE" or "TSE").
Dim2	Dimension of the second order Central Intensity Subspace (applicable when method="TSE").
predict	Logical value indicating whether to compute the new predictors as well.
...	Extra arguments are ignored.

Details

This is the method for sdr for the class "lpp" of point patterns on a linear network.

Given a point pattern X and predictor variables $Z_1, \ldots, Z_p$, Sufficient Dimension Reduction methods (Guan and Wang, 2010) attempt to find a minimal set of new predictor variables, each constructed by taking a linear combination of the original predictors, which explain the dependence of X on $Z_1, \ldots, Z_p$. The methods do not assume any particular form of dependence of the point pattern on the predictors. The predictors are assumed to be Gaussian random fields.

Available methods are:

method="DR"	directional regression
method="NNIR"	nearest neighbour inverse regression
method="SAVE" &	sliced average variance estimation
method="SIR" &	sliced inverse regression
method="TSE" &	two-step estimation

The result includes a matrix B whose columns are estimates of the basis vectors of the space of new predictors. That is, the jth column of B expresses the jth new predictor as a linear combination of the original predictors.

If predict=TRUE, the new predictors are also evaluated. They can also be evaluated using sdrPredict.

Value

A list with components B, M or B, M1, M2 where B is a matrix whose columns are estimates of the basis vectors for the space, and M or M1,M2 are matrices containing estimates of the kernel.

If predict=TRUE, the result also includes a component Y which is a list of pixel images giving the values of the new predictors.

Author(s)

Based on a Matlab original, for two-dimensional point patterns, by Yongtao Guan. Adapted to R, and to linear networks, by Suman Rakshit.

References

Guan, Y. and Wang, H. (2010) Sufficient dimension reduction for spatial point processes directed by Gaussian random fields. *Journal of the Royal Statistical Society, Series B*, **72**, 367–387.

See Also

`sdrPredict` to compute the new predictors from the coefficient matrix.

`dimhat` to estimate the subspace dimension.

`subspaceDistance`

Examples

```
#   sdr(bei, bei.extra)

   xim <- as.linim(function(x,y) { x }, simplenet)
   yim <- as.linim(function(x,y) { y }, simplenet)
   X <- runiflpp(30, simplenet)
   sdr(X, list(x=xim, y=yim))
```

---

shortestpath *Shortest Path Between Two Points on a Linear Network*

Description

Find the shortest path between two given points on a linear network.

Usage

```
shortestpath(X, i=1, j=2)
```

Arguments

`X`	Point pattern on a linear network (object of class `"lpp"`).
`i`	Integer index of the start point
`j`	Integer index of the end point

Details

The shortest path in the network between the two specified points `X[i]` and `X[j]` is determined.

The result is a line segment pattern (object of class `"psp"`) consisting of (in order) a line segment joining `X[i]` to a vertex of the network, then a series of segments joining adjacent vertices of the network, then a line segment joining a vertex to `X[j]`.

The result has an attribute `"steps"` which is an integer vector giving the sequence of vertices of the network through which the shortest path passes. This vector will have length zero if `X[i]` and `X[j]` lie on the same segment of the network. Otherwise it will contain a sequence of integers which index the vertices as given in `vertices(domain(X))`.

Value

Line segment pattern (object of class "psp") with an attribute "steps" which is an integer vector.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>.

See Also

The *length* of the shortest path is computed by pairdist.lpp.

Examples

```
X <- if(interactive()) chicago[c(20, 39)] else runiflpp(2, simplenet)
P <- shortestpath(X)
if(interactive()) {
  plot(X, pch=16, main="shortest path")
  ## draw the path
  plot(P, add=TRUE, col=2, lwd=2)
  ## draw the vertices on the path
  V <- vertices(L)
  steps <- attr(P, "steps")
  plot(V[steps], add=TRUE, col=3)
}
```

---

simulate.lppm *Simulate a Fitted Point Process Model on a Linear Network*

Description

Generates simulated realisations from a fitted Poisson point process model on a linear network.

Usage

```
  ## S3 method for class 'lppm'
simulate(object, nsim=1, ...,
                         new.coef=NULL,
                         progress=(nsim > 1),
                         drop=FALSE)
```

Arguments

object	Fitted point process model on a linear network. An object of class "lppm".
nsim	Number of simulated realisations.
progress	Logical flag indicating whether to print progress reports for the sequence of simulations.
new.coef	New values for the canonical parameters of the model. A numeric vector of the same length as coef(object).

...	Arguments passed to predict.lppm to determine the spatial resolution of the image of the fitted intensity used in the simulation.
drop	Logical. If nsim=1 and drop=TRUE, the result will be a point pattern, rather than a list containing a point pattern.

Details

This function is a method for the generic function simulate for the class "lppm" of fitted point process models on a linear network.

Only Poisson process models are supported so far.

Simulations are performed by rpoislpp.

Value

A list of length nsim containing simulated point patterns (objects of class "lpp") on the same linear network as the original data used to fit the model. The result also belongs to the class "solist", so that it can be plotted, and the class "timed", so that the total computation time is recorded.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

, Rolf Turner <rolfturner@posteo.net>

and Ege Rubak <rubak@math.aau.dk>

See Also

lppm, rpoislpp, simulate

Examples

```
fit <- lppm(unmark(chicago) ~ y)
simulate(fit)[[1]]
```

Smooth.lpp *Spatial Smoothing of Observations on a Network*

Description

Performs spatial smoothing of numeric values observed at a set of locations on a network. Uses kernel smoothing.

Usage

```
## S3 method for class 'lpp'
Smooth(X, sigma,
                    ...,
                    at=c("pixels", "points"),
                    weights=rep(1, npoints(X)),
                    leaveoneout=TRUE)
```

Arguments

X	A marked point pattern on a linear network (object of class "lpp").
sigma	Smoothing bandwidth. A single positive number. See density.lpp.
...	Further arguments passed to density.lpp to control the kernel smoothing and the pixel resolution of the result.
at	String specifying whether to compute the smoothed values at a grid of pixel locations (at="pixels") or only at the points of X (at="points").
weights	Optional weights attached to the observations. A numeric or logical valued vector, pixel image, function or expression, or one of the strings "x" or "y" representing the cartesian coordinates. The expression may involve the variables x,y,marks representing the coordinates and marks of the point pattern.
leaveoneout	Logical value indicating whether to compute a leave-one-out estimator. Applicable only when at="points".

Details

The function Smooth.lpp performs spatial smoothing of numeric values observed at a set of irregular locations on a linear network.

Smooth.lpp is a method for the generic function Smooth for the class "lpp" of point patterns. Thus you can type simply Smooth(X).

Smoothing is performed by kernel weighting, using the Gaussian kernel by default. If the observed values are $v_1, \ldots, v_n$ at locations $x_1, \ldots, x_n$ respectively, then the smoothed value at a location u is

$$g(u) = \frac{\sum_i k(u, x_i) v_i}{\sum_i k(u, x_i)}$$

where k is the kernel. This is known as the Nadaraya-Watson smoother (Nadaraya, 1964, 1989; Watson, 1964). The type of kernel is determined by further arguments ... which are passed to density.lpp

The argument X must be a marked point pattern on a linear network (object of class "lpp"). The points of the pattern are taken to be the observation locations x_i, and the marks of the pattern are taken to be the numeric values v_i observed at these locations.

The marks are allowed to be a data frame. Then the smoothing procedure is applied to each column of marks.

The numerator and denominator are computed by density.lpp. The arguments ... control the smoothing kernel parameters.

The optional argument weights allows numerical weights to be applied to the data. If a weight w_i is associated with location x_i, then the smoothed function is (ignoring edge corrections)

$$g(u) = \frac{\sum_i k(u, x_i) v_i w_i}{\sum_i k(u, x_i) w_i}$$

Value

If X *has a single column of marks:*

- If at="pixels" (the default), the result is a pixel image on the network (object of class "linim"). Pixel values are values of the interpolated function.
- If at="points", the result is a numeric vector of length equal to the number of points in X. Entries are values of the interpolated function at the points of X.

If X *has a data frame of marks:*

- If at="pixels" (the default), the result is a named list of pixel images on the network (objects of class "linim"). There is one image for each column of marks. This list also belongs to the class "solist", for which there is a plot method.
- If at="points", the result is a data frame with one row for each point of X, and one column for each column of marks. Entries are values of the interpolated function at the points of X.

The return value has attribute "sigma" which reports the smoothing bandwidth that was used.

Very small bandwidth

If the chosen bandwidth sigma is very small, kernel smoothing is mathematically equivalent to nearest-neighbour interpolation.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

References

Nadaraya, E.A. (1964) On estimating regression. *Theory of Probability and its Applications* **9**, 141–142.

Nadaraya, E.A. (1989) *Nonparametric estimation of probability densities and regression curves*. Kluwer, Dordrecht.

Watson, G.S. (1964) Smooth regression analysis. *Sankhya A* **26**, 359–372.

See Also

Smooth, density.lpp.

Examples

```
X <- spiders
if(!interactive()) X <- X[owin(c(0,1100), c(0, 500))]
marks(X) <- coords(X)$x
plot(Smooth(X, 50))
Smooth(X, 50, at="points")
```

subset.lpp *Subset of Point Pattern Satisfying A Condition*

Description

Given a point pattern on a linear network, return the subset of points which satisfy a specified condition.

Usage

```
## S3 method for class 'lpp'
subset(x, subset, select, drop=FALSE, ...)
```

Arguments

x	A point pattern on a linear network (object of class "lpp").
subset	Logical expression indicating which points are to be kept. The expression may involve the names of spatial coordinates (x, y), network coordinates (seg, tp), the marks, and (if there is more than one column of marks) the names of individual columns of marks. Missing values are taken as false. See Details.
select	Expression indicating which columns of marks should be kept. The *names* of columns of marks can be used in this expression, and will be treated as if they were column indices. See Details.
drop	Logical value indicating whether to remove unused levels of the marks, if the marks are a factor.
...	Ignored.

Details

This is a method for the generic function subset. It extracts the subset of points of x that satisfy the logical expression subset, and retains only the columns of marks that are specified by the expression select. The result is always a point pattern, with the same window as x.

The argument subset determines the subset of points that will be extracted. It should be a logical expression. It may involve the variable names x and y representing the Cartesian coordinates; the names of other spatial coordinates or local coordinates; the name marks representing the marks; and (if there is more than one column of marks) the names of individual columns of marks. The default is to keep all points.

The argument select determines which columns of marks will be retained (if there are several columns of marks). It should be an expression involving the names of columns of marks (which will be interpreted as integers representing the positions of these columns). For example if there are columns of marks named A to Z, then select=D:F is a valid expression and means that columns D, E and F will be retained. Similarly select=-(A:C) is valid and means that columns A to C will be deleted. The default is to retain all columns.

Setting subset=FALSE will produce an empty point pattern (i.e. containing zero points) in the same window as x. Setting select=FALSE or select= -marks will remove all the marks from x.

The argument drop determines whether to remove unused levels of a factor, if the resulting point pattern is multitype (i.e. the marks are a factor) or if the marks are a data frame in which some of the columns are factors.

The result is always a point pattern, of the same class as x. Spatial coordinates (and local coordinates) are always retained. To extract only some columns of marks or coordinates as a data frame, use subset(as.data.frame(x), ...)

Value

A point pattern of the same class as x, in the same spatial window as x. The result is a subset of x, possibly with some columns of marks removed.

Other kinds of subset arguments

Alternatively the argument subset can be any kind of subset index acceptable to [.lpp. This argument selects which points of x will be retained.

Warning: if the argument subset is a window, this is interpreted as specifying the subset of points that fall inside that window, but the resulting point pattern has the same window as the original pattern x.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

subset.ppp, [.lpp.

Examples

```
v <- subset(chicago, x + y > 1100 & marks == "assault")

vv <- subset(chicago, x + y > 1100 & marks == "assault", drop=TRUE)
```

---

superimpose.lpp *Superimpose Several Point Patterns on Linear Network*

Description

Superimpose any number of point patterns on the same linear network.

Usage

```
  ## S3 method for class 'lpp'
superimpose(..., L=NULL)
```

Arguments

...	Any number of arguments, each of which represents a point pattern on the same linear network. Each argument can be either an object of class "lpp", giving both the spatial coordinates of the points and the linear network, or a list(x,y) or list(x,y,seg,tp) giving just the spatial coordinates of the points.
L	Optional. The linear network. An object of class "linnet". This argument is required if none of the other arguments is of class "lpp".

Details

This function is used to superimpose several point patterns on the same linear network. It is a method for the generic function superimpose.

Each of the arguments ... can be either a point pattern on a linear network (object of class "lpp" giving both the spatial coordinates of the points and the linear network), or a list(x,y) or list(x,y,seg,tp) giving just the spatial coordinates of the points. These arguments must represent point patterns on the *same* linear network.

The argument L is an alternative way to specify the linear network, and is required if none of the arguments ... is an object of class "lpp".

The arguments ... may be *marked* patterns. The marks of each component pattern must have the same format. Numeric and character marks may be "mixed". If there is such mixing then the numeric marks are coerced to character in the combining process. If the mark structures are all data frames, then these data frames must have the same number of columns and identical column names.

If the arguments ... are given in the form name=value, then the names will be used as an extra column of marks attached to the elements of the corresponding patterns.

Value

An object of class "lpp" representing the combined point pattern on the linear network.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

Rolf Turner <rolfturner@posteo.net>

Ege Rubak <rubak@math.aau.dk>

and Greg McSwiggan.

See Also

superimpose

Examples

```
X <- rpoislpp(5, simplenet)
Y <- rpoislpp(10, simplenet)
superimpose(X,Y) # not marked
superimpose(A=X, B=Y) # multitype with types A and B
```

terminalvertices *Terminal Vertices of a Linear Network*

Description

Finds the terminal vertices of a linear network.

Usage

```
terminalvertices(L)
```

Arguments

L	A linear network (object of class "linnet").

Details

Given the linear network L, this function examines the vertices (segment endpoints) of the network and determines which of them are 'terminal' vertices (i.e. the endpoint of only one segment). These terminal vertices are returned as a point pattern on the network.

Value

A point pattern on the same linear network (object of class "lpp").

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk> and Mehdi Moradi <m2.moradi@yahoo.com>.

See Also

vertices.linnet.

Examples

```
B <- terminalvertices(simplenet)
plot(simplenet, main="")
plot(B, add=TRUE, pch=16, cex=2)
```

`text.lpp` *Add Text Labels to Point Pattern on a Network*

Description

Plots a text label at the location of each point, for a point pattern on a linear network.

Usage

```
## S3 method for class 'lpp'
text(x, ...)
```

Arguments

`x`	A point pattern on a linear network (class `"lpp"`).
`...`	Additional arguments passed to `text.default`.

Details

This function is a method for the generic `text`. A text label is added to the existing plot, at the location of each point in the point pattern `x`, or near the location of the midpoint of each segment in the segment pattern `x`.

Additional arguments `...` are passed to `text.default` and may be used to control the placement of the labels relative to the point locations, and the size and colour of the labels.

By default, the labels are the serial numbers 1 to `n`, where `n` is the number of points or segments in `x`. This can be changed by specifying the argument `labels`, which should be a vector of length `n`.

Value

Null.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

`text.default`, `text.ppp`

Examples

```
X <- runiflpp(5, simplenet)
plot(X)
text(X, pos=2, col="blue")
```

thinNetwork *Remove Vertices or Segments from a Linear Network*

Description

Delete some vertices and/or segments from a linear network or related object.

Usage

```
thinNetwork(X, retainvertices=NULL, retainedges=NULL)
```

Arguments

X	A linear network (object of class "linnet"), a point pattern on a linear network (object of class "lpp") or a pixel image on a linear network (object of class "linim").
retainvertices	Optional. Subset index specifying which vertices should be retained (not deleted).
retainedges	Optional. Subset index specifying which edges (segments) should be retained (not deleted).

Details

This function deletes some of the vertices and edges (segments) in the linear network.

The arguments retainvertices and retainedges can be any kind of subset index: a vector of positive integers specifying which vertices/edges should be retained; a vector of negative integers specifying which vertices/edges should be deleted; or a logical vector specifying whether each vertex/edge should be retained (TRUE) or deleted (FALSE).

Vertices are indexed in the same sequence as in vertices(as.linnet(X)). Segments are indexed in the same sequence as in as.psp(as.linnet(X)).

The argument retainedges has higher precedence than retainvertices in the sense that:

- If retainedges is given, then any vertex which is an endpoint of a retained edge will also be retained.
- If retainvertices is given and retainedges is **missing**, then any segment joining two retained vertices will also be retained.
- Thus, when both retainvertices and retainedges are given, it is possible that more vertices will be retained than those specified by retainvertices.

After the network has been altered, other consequential changes will occur, including renumbering of the segments and vertices. If X is a point pattern on a linear network, then data points will be deleted if they lie on a deleted edge. If X is a pixel image on a linear network, then the image will be restricted to the new sub-network.

Value

An object of the same kind as X.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au> and Suman Rakshit.

See Also

linnet to make a network;

connected.linnet to extract connected components.

repairNetwork.

Examples

```
L <- simplenet
plot(L, main="thinNetwork(L, retainedges=c(-3, -5))")
text(midpoints.psp(as.psp(L)), labels=1:nsegments(L), pos=3)
Lsub <- thinNetwork(L, retainedges=c(-3, -5))
plot(Lsub, add=TRUE, col="blue", lwd=2)
```

---

threads *Identify Uninterrupted Threads in a Linear Network*

Description

Given a linear network, find the threads. A thread is a set of connected edges which do not pass through any forks in the network.

Usage

```
threads(X, what = c("tessellation", "labels"))
```

Arguments

X	A linear network (object of class "linnet").
what	String (partially matched) specifying the kind of result.

Details

A 'thread' in a network is a subset of the edges of the network which does not pass through any forks in the network.

Given a linear network X, this function identifies the threads in X and assigns a label to each edge (segment) of the network indicating which thread it belongs to.

Formally a thread is a set of edges joining successive vertices $v_1, \ldots, v_n$ of the network such that

- there is an edge of the network joining v_i and v_{i+1} for each i
- each of the intermediate vertices vertices $v_2, \ldots, v_{n-1}$ has degree 2 (i.e. there are exactly 2 edges of the network which end at the vertex)
- the terminal vertices v_1 and v_n do not have degree 2, unless they are the same vertex.

Every edge (segment) of the network belomgs to a unique thread. This algorithm assigns a label to each edge indicating which thread it belongs to. If `what="labels"` (the default), the result is a factor of length equal to `nsegments(X)` giving the classification of segments. If `what="tessellation"`, the result is a tessellation of `X` (object of class `"lintess"`) in which the tiles of the tessellation are the threads.

Value

A factor, or a tessellation on the network (object of class `"lintess"`).

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>

See Also

`connected.linnet`

Examples

```
A <- edges(letterR)
B <- edges(disc(npoly=16, centre=centroid.owin(letterR)))
L <- as.linnet(superimpose(A,B))
plot(threads(L),
     col=rainbow, scramble.cols=TRUE,
     lwd=2, show.window=FALSE)
```

---

tile.lengths *Compute Lengths of Tiles in a Tessellation on a Network*

Description

Computes the length of each tile in a tessellation on a linear network.

Usage

```
tile.lengths(x)
```

Arguments

`x`	A tessellation on a linear network (object of class `"lintess"`).

Details

A tessellation on a linear network `L` is a partition of the network into non-overlapping pieces (tiles). Each tile consists of one or more line segments which are subsets of the line segments making up the network. A tile can consist of several disjoint pieces.

This command computes the length of each of the tiles that make up the tessellation `x`. The result is a numeric vector.

Value

A numeric vector.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

lintess

Examples

```
X <- runiflpp(5, simplenet)
A <- lineardirichlet(X)
plot(A)
tile.lengths(A)
```

---

tilenames.lintess *Names of Tiles in a Tessellation on a Network*

Description

Extract or Change the Names of the Tiles in a Tessellation on a Network.

Usage

```
## S3 method for class 'lintess'
tilenames(x)

## S3 replacement method for class 'lintess'
tilenames(x) <- value
```

Arguments

x	A tessellation on a linear network (object of class "lintess").
value	Character vector giving new names for the tiles.

Details

These functions extract or change the names of the tiles that make up the tessellation x.

If the tessellation is a regular grid, the tile names cannot be changed.

Value

tilenames returns a character vector.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

lintess, tiles

Examples

```
B <- lineardirichlet(runiflpp(5, simplenet))
tilenames(B)
tilenames(B) <- letters[1:5]
```

---

treebranchlabels *Label Vertices of a Tree by Branch Membership*

Description

Given a linear network which is a tree (acyclic graph), this function assigns a label to each vertex, indicating its position in the tree.

Usage

```
treebranchlabels(L, root = 1)
```

Arguments

L	Linear network (object of class "linnet"). The network must have no loops.
root	Root of the tree. An integer index identifying which point in vertices(L) is the root of the tree.

Details

The network L should be a tree, that is, it must have no loops.

This function computes a character string label for each vertex of the network L. The vertex identified by root (that is, vertices(L)[root]) is taken as the root of the tree and is given the empty label "".

- If there are several line segments which meet at the root vertex, each of these segments is the start of a new branch of the tree; the other endpoints of these segments are assigned the labels "a", "b", "c" and so on.
- If only one segment issues from the root vertex, the other endpoint of this segment is assigned the empty label "".

A similar rule is then applied to each of the newly-labelled vertices. If the vertex labelled "a" is joined to two other unlabelled vertices, these will be labelled "aa" and "ab". The rule is applied recursively until all vertices have been labelled.

If L is not a tree, the algorithm will terminate, but the results will be nonsense.

Value

A vector of character strings, with one entry for each point in `vertices(L)`.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>

See Also

`deletebranch`, `extractbranch`, `treeprune` for manipulating a network using the branch labels.

`linnet` for creating a network.

Examples

```
# make a simple tree
m <- simplenet$m
m[8,10] <- m[10,8] <- FALSE
L <- linnet(vertices(simplenet), m)
plot(L, main="")
# compute branch labels
tb <- treebranchlabels(L, 1)
tbc <- paste0("[", tb, "]")
text(vertices(L), labels=tbc, cex=2)
```

---

treeprune *Prune Tree to Given Level*

Description

Prune a tree by removing all the branches above a given level.

Usage

```
treeprune(X, root = 1, level = 0)
```

Arguments

`X`	Object of class `"linnet"` or `"lpp"`.
`root`	Index of the root vertex amongst the vertices of `as.linnet(X)`.
`level`	Integer specifying the level above which the tree should be pruned.

Details

The object `X` must be either a linear network, or a derived object such as a point pattern on a linear network. The linear network must be an acyclic graph (i.e. must not contain any loops) so that it can be interpreted as a tree.

This function removes all vertices for which `treebranchlabels` gives a string more than `level` characters long.

Value

Object of the same kind as X.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>

See Also

treebranchlabels for calculating the branch labels.

deletebranch for removing entire branches. extractbranch for extracting entire branches.

linnet for creating networks.

Examples

```
# make a simple tree
m <- simplenet$m
m[8,10] <- m[10,8] <- FALSE
L <- linnet(vertices(simplenet), m)
plot(L, main="")
# compute branch labels
tb <- treebranchlabels(L, 1)
tbc <- paste0("[", tb, "]")
text(vertices(L), labels=tbc, cex=2)
# prune tree
tp <- treeprune(L, root=1, 1)
plot(tp, add=TRUE, col="blue", lwd=3)
```

---

unstack.lpp *Separate Multiple Columns of Marks*

Description

Given a spatial pattern on a network, with several columns of marks, take one column at a time, and return a list of spatial patterns each having only one column of marks.

Usage

```
## S3 method for class 'lpp'
unstack(x, ...)

## S3 method for class 'lintess'
unstack(x, ...)
```

Arguments

x	A spatial point pattern (object of class "lpp") or a tessellation on a linear network (object of class "lintess").
...	Ignored.

Details

The functions defined here are methods for the generic unstack. The functions expect a spatial object x which has several columns of marks; they separate the columns, and return a list of spatial objects, each having only one column of marks.

If x has several columns of marks (i.e. marks(x) is a matrix, data frame or hyperframe with several columns), then y <- unstack(x) is a list of spatial objects, each of the same kind as x. The jth entry y[[j]] is equivalent to x except that it only includes the jth column of marks(x).

If x has no marks, or has only a single column of marks, the result is a list consisting of one entry, which is x.

Value

A list, of class "solist", whose entries are objects of the same type as x.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

unstack

unstack.ppp, unstack.msr.

See also methods for the generic split such as split.ppx which applies to "lpp" objects.

Examples

```
X <- runiflpp(5, simplenet)
marks(X) <- data.frame(id=1:5, code=factor(letters[1:5]))
unstack(X)
```

Window.lpp *Extract Window of Spatial Object on a Network*

Description

Given a spatial object on a network, these functions extract the window in which the network is defined.

Usage

```
 ## S3 method for class 'lpp'
Window(X, ...)

 ## S3 method for class 'lppm'
Window(X, ...)
```

Arguments

X	A spatial object.
...	Ignored.

Details

These are methods for the generic function Window which extract the spatial window in which the object X is defined.

For the methods defined here, X should be a spatial object on a linear network (object of class "lpp" or "lppm").

Value

An object of class "owin" (see owin.object) specifying an observation window.

Author(s)

Adrian Baddeley <Adrian.Baddeley@curtin.edu.au>, Rolf Turner <rolfturner@posteo.net> and Ege Rubak <rubak@math.aau.dk>.

See Also

Window.

Examples

```
Window(spiders)
```

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