

Package ‘selectspm’

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Type Package

Title Select point patterns models based on minimum contrast and AIC

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Depends spatstat, ecespa

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Description Package to fit and select point patterns models based on minimum contrast and AIC

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select.model2	<i>Fit and select point pattern models based in minimum contrast and AIC</i>
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Description

Fits Poisson, Poisson cluster, several inhomogeneous Poisson and several inhomogeneous Poisson cluster processes to a spatial point pattern and select the best fitting based on AIC.

Usage

```
select.model2(pp, sigmas, r, nlarge = 10000, q = 1/4, p = 2, correction = "iso")
ipc.estK2(mippp, lambda = NULL, correction = "iso", r = NULL, sigma2 = NULL,
          rho = NULL, q = 1/4, p = 2, nlarge = NULL, ...)
aic.function(r, dtheta, npar)
  ## S3 method for class 'selectedmod'
plot(x, ...)
  ## S3 method for class 'selectedmod'
print(x, ...)
```

Arguments

pp	Unmarked point pattern with the ppp format of spatstat
sigmas	Vector with the sigma values (standard deviations of the Gaussian kernel) for estimating different intensity surfaces with density.ppp.
r	Vector of values for the argument r at which the (in)homogeneous K function should be evaluated. First element should be 0.
nlarge	A number of points. In spatstat, if the number of points exceeds nlarge, then only the border correction will be computed (by default) for K(r). If you have a large number of points (n) and you want your border correction to be applied, set nlarge > n.
q	q parameter of the dtheta (i.e., minimum contrast) function.
p	p parameter of the dtheta (i.e., minimum contrast) function.
correction	Any selection of the options "border", "bord.modif", "isotropic", "Ripley", "translate", "translation", "none" or "best". It specifies the edge correction(s) to be applied.
mippp	Unmarked point pattern with the ppp format of spatstat
lambda	Optional. Values of the estimated intensity function. Either a vector giving the intensity values at the points of the pattern mippp, a pixel image (object of class "im") giving the intensity values at all locations, a fitted point process model (object of class "ppm" or "kppm") or a function(x,y) which can be evaluated to give the intensity value at any location.
sigma2	Starting value in the optimization for the squared standard deviation of the Gaussian dispersion around parent points in the in(homogeneous) Poisson cluster process.

rho	Starting value in the optimization for the intensity of parent points in the in(homogeneous) Poisson cluster process.
...	Additional arguments passed to the optim function (or to the plot and print methods).
dtheta	Minimum contrast discrepancy, i.e., sum of squared differences between the normalized empirical and theoretical K functions.
npar	Number of parameters fitted in the model.
x	An object of class "selectedmod", i.e., the result of using function select.model2().

Details

select.model2 is a wrap to fit and select different point processes using standard tools in of **spatstat** and of **ecespa**. `ipc.estK2` fits (in)homogeneous models as the function `ipc.estK` of **ecespa** but, in addition, it allows setting the argument `nlarge` and passing options to `optim`. AIC calculation (actually AICc) is made by `aic.function`. More details in Jara et al. (in revision).

Value

select.model2 returns an object of class "selectedmod", i.e., a list with components:

dtheta	vector with the minimized discrepancy values for each fitted model.
best.dtheta	the minimum of the minimized discrepancy values.
best.model	The best of the fitted models.
models	vector with the names of the fitted models
HPPs	A list with the intensity objects employed to fit each inhomogeneous model
sigmas	vector with the sigma values (standard deviations of the Gaussian kernel) employed to estimate the different intensity surfaces.
aics	vector with the AIC values of each model.
Kas	data.frame with the empirical K functions employed to fit each model.

`ipc.estK` gives an object of class 'ecespa.minconfit', basically a list with the following components:

sigma2	Parameter σ^2 .
rho	Parameter ρ .
d.theta	Minimized value of the contrast criterion $D(\theta)$.
Kobs	Values of the observed K-function.
Kfit	Values of the fitted K-function.
r	Sequence of distances at which Kobs and Kfit have been estimated.
data	Original point pattern.
lambda	Original intensity object.
dataname	Name of the original point pattern.
lambdaname	Name of the original intensity object.

q *q* exponent of the contrast criterion.
 p *p* exponent of the contrast criterion.

aic.function returns a one-row data.frame, with the following items:

n number of observations employed to compute AIC; i.e., number of r values where K(r) was estimated.
 K number of parameters of the model.
 RSS "Residual Sum of Squares". It is the value of the discrepancy function Dtheta.
 LL Loglikelihood.
 AIC AIC value.
 AICc Small sample AIC value.

Author(s)

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References

Jara, A., De la Cruz, M., Espinosa, C.I., Mendez, M. & Escudero, A. (in revision). Does spatial heterogeneity blur the signature of dispersal syndromes on spatial patterns of woody species? A test in a tropical dry forest.

Examples

```
## Not run:
# Get the data
data(lansing)

# Split the multivariate pp in their individual components
lansing.sp<-split(lansing)

# Define the sequence of r's at which estimate K(r)
r<- seq(0,0.25,le=101)

# Define different standard deviations for the Gaussian kernel
# to estimate different intensity surfaces
sigmas<- seq(0.1,1,by=0.05)

# Note that lansing is defined in a (0,1) x (0,1) window and this affects
# the election of r and sigma values

# Fit 40 models (1 Poisson, 1 Poisson cluster, 19 inhomogeneous Poisson
# and 19 inhomogeneous Poisson cluster) to maple and select the better ones
maple.model <- select.model2(lansing.sp$maple, sigmas=sigmas, r=r)
# show the AICc value and the fitted parameters for the best model in each class
maple.model

# Draw the empirical and theoretical models to visually asses the fitting.
# P = Poisson; HPP= heterogeneous (i.e. inhomogeneous) Poisson;
```

```
# PC = Poisson cluster; HPC=heterogeneous (i.e. inhomogeneous) Poisson cluster
plot(maple.model)

# fFit and select models to all species
lansing.models<-lapply(lansing.sp, function(x) select.model2(x, sigmas=sigmas, r=r))
lapply(lansing.models, function(x)x)

## End(Not run)
```

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