Introduction to `spatstat`

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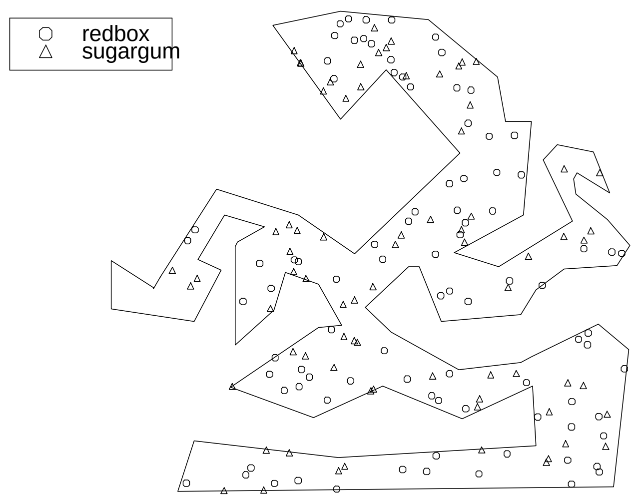
`spatstat` version 1.1-2

Abstract

`spatstat` is a library in S-PLUS/R for the statistical analysis of point pattern data. This document is a brief introduction to the package for users.

1 Introduction

`Spatstat` is a contributed library in S-PLUS and R for the statistical analysis of spatial data. Version 1.1 of the library deals mainly with patterns of points in the plane. The points may carry 'marks', and the spatial region in which the points were recorded may have arbitrary shape. Here is an example:



The package supports

- creation, manipulation and plotting of point patterns
- exploratory data analysis
- simulation of point process models
- parametric model-fitting by maximum pseudolikelihood

The point process models fitted by maximum pseudolikelihood may be quite general Gibbs/Markov models; they may include spatial trend, dependence on covariates, and interpoint interactions of any order (i.e. not restricted to pairwise interactions). Models are specified by a `formula` in the S language, and are fitted using a single function `mpl` analogous to `glm` and `gam`.

This document is an introduction to the main features of `spatstat` and its use. Please see the "`spatstat` Quick Reference" page for an annotated list of all functions in the library. See the online help or printed manual for detailed information about each function.

Demonstration

You may like to try the following quick demonstration of the package. A more extensive demonstration can be seen by typing `demo(spatstat)`.

`library(spatstat)`	Attach spatstat library
`data(swedishpines)`	Find "Swedish Pines" dataset
`X <- swedishpines`	Rename it
`plot(X)`	Plot it
`K <- Kest(X)`	Estimate its K function
`conspire(K, c(ripley,theo)~r)`	Plot the estimated K function
`plot(allstats(X))`	Plot the F, G, J and K functions
`fit <- mpl(X, ~1, Strauss(r=7))`	Fit a Strauss process model
`fit`	Describe the fitted model
`Xsim <- rmh("strauss",`	
`c(0.03,0.2,7),X$window, n.start=X$n)`	Simulate from fitted model
`plot(Xsim)`	Plot simulated pattern
`data(demopat)`	Artificial data in irregular window, with 2 types of points
`plot(demopat, box=FALSE)`	Plot the pattern
`plot(alltypes(demopat, "K"))`	Plot array of cross-type K functions
`mpl(demopat,`	
`~marks + polynom(x,2), Poisson())`	Fit inhomogeneous multitype Poisson

2 Creating point patterns

2.1 Overview

Point patterns

A point pattern is represented in `spatstat` by an object of class `"ppp"`. This makes it easy to plot a point pattern, manipulate it and subject it to analysis.

A dataset in this format contains the x, y coordinates of the points, optional 'mark' values attached to the points, and a description of the spatial region or 'window' in which the pattern was observed. See `help(ppp.object)` for further details.

To obtain a `"ppp"` object you can

- use one of the datasets supplied with the package;
- create one from data in R, using `ppp()`;
- create one from data in a text file, using `scanpp()`;
- convert data from other R libraries, using `as.ppp()`;
- generate a random pattern using one of the simulation routines.

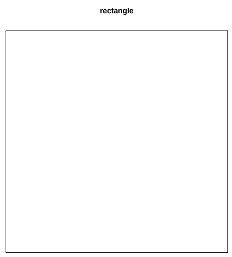
These possibilities are elaborated below.

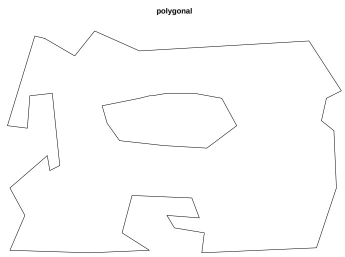
Spatial windows

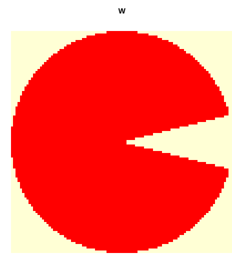
Note that, when you create a new point pattern object, you need to specify the spatial region or window in which the pattern was observed. There is intentionally no automatic "guessing" of the window dimensions from the points alone. [1]

The window may have arbitrary shape; it may be a rectangle, a polygon, a collection of polygons (including holes), or a binary image.

[1] However, the function `ripras` will compute an estimate of the window given only the coordinates of the points.







If the observation window needs to be stored as a dataset in its own right, it is represented in `spatstat` by an object of class `"owin"`. See `help(owin.object)` for further details. Objects of this class can be plotted and manipulated in a few simple ways. They can be created using the function `owin()`.

The simplest way to create a point pattern with a non-rectangular window is to use the functions `ppp()` and/or `owin()`.

Marks

Each point in a spatial point pattern may carry additional information called a 'mark'. For example, points which are classified into two or more different types (on/off, case/control, species, colour, etc) may be regarded as marked points, with a mark which identifies which type they are. Data recording the locations and heights of trees in a forest can be regarded as a marked point pattern where the mark attached to a tree's location is the tree height.

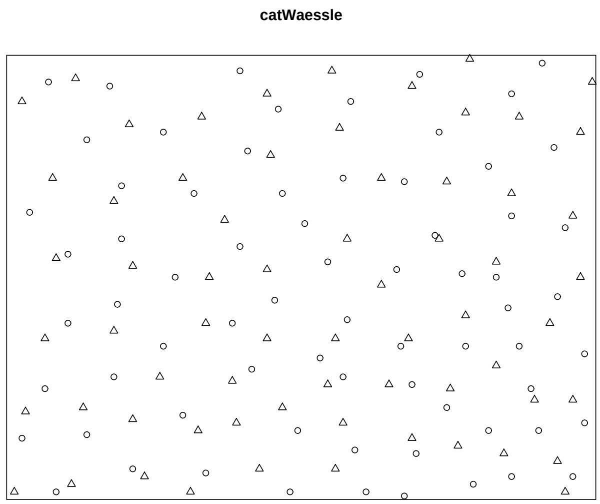
The current version of `spatstat` supports marked point patterns of two kinds:

continuous marks : the mark attached to each point is a single real number (e.g. tree height);

multitype pattern : points are classified into several types; the mark attached to each point is a level of a factor (e.g. tree species).

The mark values must be given in a vector `marks` of the same length as the coordinate vectors `x` and `y`. This is interpreted so that `marks[i]` is the mark attached to the point `(x[i],y[i])`.

Note: To distinguish between the cases of continuous marks and multitype points, `spatstat` requires that for a multitype point pattern, `marks` must be a `factor`.



2.2 Standard datasets

Some standard point pattern datasets are supplied with the package. They include:

`amacrine`	Austin Hughes' rabbit amacrine cells	multitype
`bramblecanes`	Bramble Canes data	multitype
`cells`	Crick-Ripley biological cells data	
`ganglia`	Wässle et al. cat retinal ganglia data	multitype
`hamster`	Aherne's hamster tumour data	multitype
`lansing`	Lansing Woods data	multitype
`longleaf`	Longleaf Pines data	continuous marks
`nztrees`	Mark-Esler-Ripley trees data	
`redwood`	Strauss-Ripley redwood saplings data	
`redwoodfull`	Strauss redwood saplings data (full set)	
`swedishpines`	Strand-Ripley Swedish pines data	
`demopat`	artificial data	irregular window, multitype

See the Demonstration in the Introduction for an example of how to use these datasets.

2.3 Creating point patterns using `ppp()`

The function `ppp()` will create a point pattern (an object of class `"ppp"`) from data in R.

Point pattern in rectangular window

Suppose the x, y coordinates of the points of the pattern are contained in vectors `x` and `y` of equal length. If the window of observation is a rectangle, then

```
ppp(x, y, xrange, yrange)
```

will create the point pattern. Here `xrange, yrange` must be vectors of length 2 giving the x and y dimensions, respectively, of the rectangle. For example `ppp(x, y, c(0,1), c(0,1))` would give you a point pattern in the unit square; this is the default so you could also just type `ppp(x, y)`.

To create a marked point pattern, use the additional argument `marks`:

```
ppp(x, y, xrange, yrange, marks=m)
```

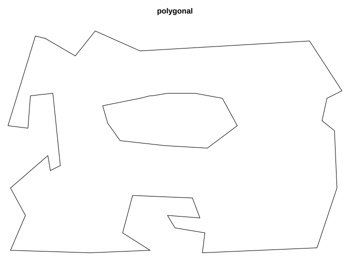
where `m` is a vector of the same length as `x` and `y`. Remember that if you intend to create a multitype pattern (where the points are classified into a finite number of possible types) then `m` must be a `factor` (use `factor` or `as.factor` to make it one).

Point pattern in polygonal window

Spatstat supports polygonal windows of arbitrary shape and topology. That is, the boundary of the window may consist of one or more closed polygonal curves, which do not intersect themselves or each other. The window may have 'holes'. Type

```
ppp(x, y, poly=p)
```

to create a point pattern with a polygonal window. Again, `x` and `y` are the vectors of coordinates of the points. The argument `poly=p` indicates that the window is polygonal and its boundary is given by the dataset `p`.



If the window boundary is a single polygon, then `p` should be a list with components `x` and `y` giving the coordinates of the vertices of the window boundary, **traversed anticlockwise**. For example,

```
ppp(x, y, poly=list(x=c(0,1,0), y=c(0,0,1)))
```

will create a point pattern inside the triangle with corners $(0,0)$, $(1,0)$ and $(0,1)$.

Note that polygons should **not** be closed, i.e. the last vertex should **not** equal the first vertex. The same convention is used in the standard plotting function `polygon()`, so you can check that `p` is correct by using `polygon(p)` to display it.

If the window boundary consists of several separate polygons, then `p` should be a list, each of whose components `p[[i]]` is a list with components `x` and `y` describing one of the polygons. The vertices of each polygon should be traversed **anticlockwise for external boundaries** and **clockwise for internal boundaries (holes)**. For example, in

```
ppp(x, y, poly=list(
                    list(x=c(0,10,0), y=c(0,0,10)),
                    list(x=c(5,5,6,6), y=c(5,6,6,5)))
```

the window is a large triangle with a small square hole. Notice that the first boundary polygon is traversed anticlockwise and the second clockwise because it is a hole.

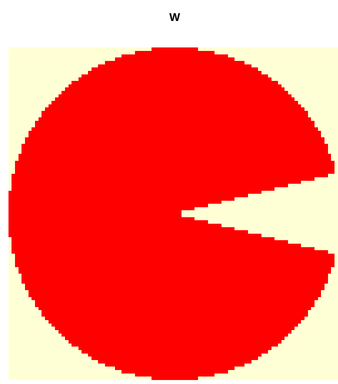
A marked point pattern is created by adding the argument `marks` exactly as above.

Point pattern in binary mask

The window for the point pattern may be described by a discrete pixel approximation. Type

```
ppp(x, y, mask=m, xrange, yrange)
```

to create the pattern. Here `m` should be a matrix with logical entries; it will be interpreted as a binary pixel image whose entries are `TRUE` where the corresponding pixel belongs to the window.



The rectangle with dimensions `xrange, yrange` is divided into equal rectangular pixels. The correspondence between matrix indices `m[i,j]` and cartesian coordinates is slightly idiosyncratic: the **rows** of `m` correspond to the y coordinate, and the columns to the x coordinate. The entry `m[i,j]` is `TRUE` if the point `(xx[j],yy[i])` (sic) belongs to the window, where `xx, yy` are vectors of pixel coordinates equally spaced over `xrange` and `yrange` respectively.

Image masks can be read from data files or created by analytic equations. For example to create a point pattern inside the unit disc:

```
w <- owin(c(-1,1), c(-1,1), mask=matrix(TRUE, 100, 100))
X <- raster.x(w)
Y <- raster.y(w)
M <- (X^2 + Y^2 <= 1)
pp <- ppp(x, y, c(-1,1), c(-1,1), mask=M)
```

The first line creates a window (an object of class `"owin"`) that is a binary image mask in which all of the pixel values are `TRUE`. The next two lines create matrices `X, Y` of the same dimensions as the pixel image, which contain respectively the x and y coordinates of each pixel. The fourth line defines a logical matrix `M` whose entries are `TRUE` where the inequality $x^2 + y^2 \leq 1$

holds, in other words, where the centre of the pixel lies inside the unit disc. The last line creates a point pattern with this window.

A marked point pattern is created by adding the argument `marks` exactly as above.

2.4 Scanning point pattern data from text files

The simple function `scanpp()` will read point pattern coordinate data from a text file (in table format) and create a point pattern object from it. See `help(scanpp)` for details.

2.5 Converting other data types

The convenient function `as.ppp()` converts data from other formats into point pattern objects in `spatstat`. It will accept point pattern objects from the Venables-Ripley `spatial` library (class `"spp"`), data frames with appropriate dimensions or column labels, and raw data. See `help(as.ppp)` for details.

2.6 Generating random point patterns

The following functions in `spatstat` generate random patterns of points from various stochastic models. They return a point pattern (as an object of class `"ppp"`).

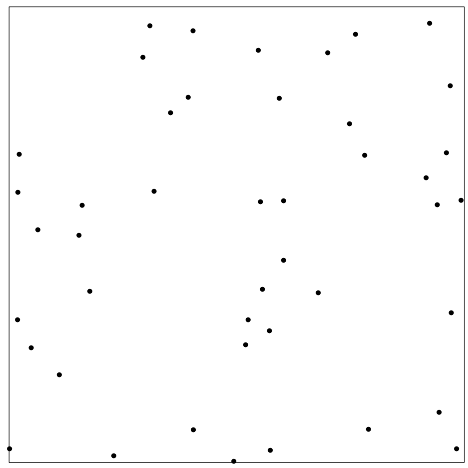
`runifpoint`	generate n independent uniform random points
`rpoispp`	simulate the (in)homogeneous Poisson point process
`rMaternI`	simulate the Matérn Model I inhibition process
`rMaternII`	simulate the Matérn Model II inhibition process
`rSSI`	simulate Simple Sequential Inhibition
`rNeymanScott`	simulate a general Neyman-Scott process
`rMatClust`	simulate the Matérn Cluster process
`rThomas`	simulate the Thomas process
`rmh`	run Metropolis-Hastings algorithm

For example

```
plot(rMaternI(200,0.05))
```

will plot one realisation of the Matérn Model I inhibition process with parameters $\beta = 200$ and $r = 0.05$. See the help entries for these functions for further details.

rMaternI(100, 0.05)



The function `rmh` is a basic implementation of the Metropolis-Hastings algorithm with birth, death and shift proposals. It will currently generate simulated realisations of the Strauss process, Strauss process with a hard core, the Soft Core process, Geyer's saturation process, two pairwise interaction processes proposed by Peter Diggle, and multitype versions of the Strauss and Strauss/hard core processes. Version 1.1-1 is a basic implementation which we will extend and modify in future.

3 Manipulating point patterns and windows

3.1 Plotting

To plot the point pattern object `X`, type

```
plot(X)
```

which invokes `plot.ppp()`. See `help(plot.ppp)` for details. Plotting is isometric, i.e. the physical scales of the x and y axes are the same.

To plot just the window of observation of `X`, just type `plot(X$window)`. This calls `plot.owin()`.

3.2 Subsets of point patterns

The `spatstat` library supports the extraction of subsets of a point pattern, using the array indexing operator `"["`.

This performs either "*thinning*" (retaining/deleting some points of a point pattern) or "*trimming*" (reducing the window of observation to a smaller subregion and retaining only those points which lie in the subregion).

If `X` is a point pattern object then

```
X[subset, ]
```

will cause the point pattern to be "thinned". The argument `subset` should be a logical vector of length equal to the number of points in `X`. The points `(X$x[i], X$y[i])` for which `subset[i]=FALSE` will be deleted. The result is another point pattern object, with the same window as `X`, but containing a subset of the points of `X`.

The pattern will be "trimmed" if we call

```
X[ , window]
```

where `window` is an object of class `"owin"` specifying the window of observation to which the point pattern `X` will be restricted. Only those points of `X` lying inside the new `window` will be retained.

See `help(subset.ppp)` for full details.

3.3 Other operations on point patterns

Use the function `unmark` to remove marks from a marked point pattern. For example `plot(unmark(X))` will plot just the locations of the points in a marked point pattern `X`.

Use the function `cut` to transform the marks of a point pattern from numerical values into factor levels.

The function `superimpose` will combine several point patterns into a single point pattern. It accepts any number of arguments, which must all be `"ppp"` objects:

```
U <- superimpose(X, Y, Z)
```

The functions `rotate, shift` and `affine` will subject the point pattern to a planar rotation, translation and affine transformation respectively.

3.4 Manipulating spatial windows

As explained above, a point pattern object contains a description of the spatial region or window in which the pattern was observed. This is an object of class `"owin"`. It is often convenient to create, manipulate and plot these windows in their own right. The following functions are available; see their help files for details.

Creating new windows

`owin`	create a window
`as.owin`	convert other data into a window
`bounding.box`	Find smallest rectangle enclosing the window
`erode.owin`	Erode window by a distance r
`rotate.owin`	Rotate the window
`shift.owin`	Translate the window in the plane
`affine.owin`	Apply an affine transformation
`complement.owin`	Invert (inside $\leftrightarrow$ outside)
`ripras`	Estimate the window, given only the points

Digital approximations:

It is possible (and sometimes necessary) to approximate a window using a discrete grid of pixels.

`as.mask`	Make a discrete pixel approximation of a given window
`nearest.raster.point`	map continuous coordinates to raster locations
`raster.x`	raster x coordinates
`raster.y`	raster y coordinates

Geometrical computations with windows:

`inside.owin`	determine whether a point is inside a window
`area.owin`	compute window's area
`diameter`	compute window's diameter
`eroded.areas`	compute areas of eroded windows
`bdist.points`	compute distances from data points to window boundary
`bdist.pixels`	compute distances from all pixels to window boundary
`centroid.owin`	compute centroid (centre of mass) of window

4 Exploratory Data Analysis

4.1 Summary statistics

The library will compute estimates of the summary functions

$F(r)$, the empty space function

$G(r)$, the nearest neighbour distance distribution function

$K(r)$, the reduced second moment function ("Ripley's K")

$J(r)$, the function $J = (1 - G)/(1 - F)$

$g(r)$, the pair correlation function $g(r) = [\frac{d}{dr}K(r)]/(2\pi r)$

for a point pattern, and their analogues for marked point patterns.

These estimates can be used for exploratory data analysis and in formal inference about a spatial point pattern. They are well described in the literature, e.g. Ripley (1981), Diggle (1983), Cressie (1991), Stoyan et al (1995). The J-function was introduced by van Lieshout and Baddeley (1996).

The point pattern has to be assumed to be "stationary" (statistically homogeneous under translations) in order that the functions F, G, J, K be well-defined and the corresponding estimators approximately unbiased. (There is an extension of the K function to inhomogeneous patterns; see below).

The empty space function F of a stationary point process X is the cumulative distribution function of the distance from a fixed point in space to the nearest point of X. The nearest neighbour function G is the c.d.f. of the distance from a point *of the pattern* X to the nearest other point of X. The J function is the ratio $J(r) = (1 - G(r))/(1 - F(r))$. The K function is defined so that $\lambda K(r)$ equals the expected number of additional points of X within a distance r of a point of X, where λ is the intensity (expected number of points per unit area).

In exploratory analyses, the estimates of F, G, J and K are useful statistics. F summarises the sizes of gaps in the pattern; G summarises the clustering of close pairs of points; J is a comparison between these two effects; and K is a second order measure of spatial association.

For inferential purposes, the estimates of F, G, J, K are usually compared to their true values for a completely random (Poisson) point process, which are

$$\begin{aligned} F(r) &= 1 - \exp(-\lambda \pi r^2) \\ G(r) &= 1 - \exp(-\lambda \pi r^2) \\ J(r) &= 1 \\ K(r) &= \pi r^2 \end{aligned}$$

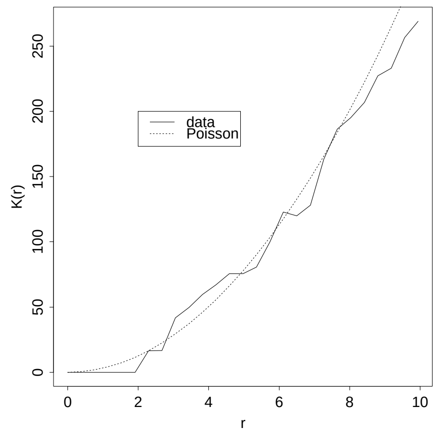
where again λ is the intensity. Deviations between the empirical and theoretical curves may suggest spatial clustering or spatial regularity.

4.2 Implementation in `spatstat`

The corresponding `spatstat` library functions are :

`Fest`	empty space function F
`Gest`	nearest neighbour distribution function G
`Kest`	Ripley's K-function
`Jest`	J-function
`allstats`	all four functions F, G, J, K
`pcf`	pair correlation function
`Kinhom`	K function for inhomogeneous patterns

The routines `Fest, Gest, Jest, Kest, pcf, Kinhom` each return a data frame. A column labelled `r` contains the values of the argument r for which the summary function ($F(r)$, etc) has been evaluated. Other columns give the estimates of the summary function itself ($F(r)$, etc) by various methods. Another column `theo` contains the theoretical (Poisson) value of the same function.



These columns can be plotted against each other for the purposes of exploratory data analysis. For example

```
G <- Gest(X)
plot(G$r, G$km, type="l")
```

Will produce a plot of $\widehat{G}(r)$ against r, where $\widehat{G}$ is the Kaplan-Meier estimate of the nearest neighbour function G. More elegantly

```
plot(km ~ r, data=G, type="l")
```

gives the same plot. To plot several curves together, use our function `conspire` (for "plot together"):

```
conspire(G, cbind(km, rs, theo) ~ r)
```

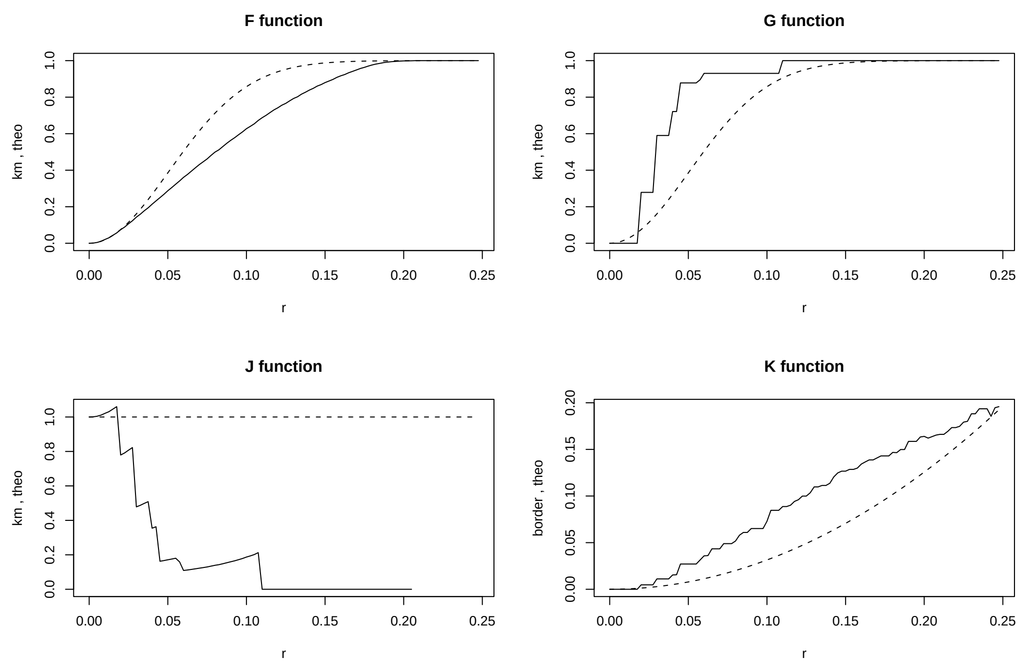
will plot the Kaplan-Meier estimate `G$km`, the border corrected (reduced sample) estimate `G$rs`, and the theoretical Poisson value, against r.

For a quick first analysis of a point pattern it is often convenient to hit

```
plot(allstats(X))
```

which plots estimates of the F, G, J and K functions in a single display. See section 4.4 for more information.

Four summary functions for redwood.



4.3 Summary statistics for a multitype point pattern:

Analogues of the G, J and K functions have been defined in the literature for "multitype" point patterns, that is, patterns in which each point is classified as belonging to one of a finite number of possible types (e.g. on/off, species, colour). The best known of these is the cross K function $K_{ij}(r)$ derived by counting, for each point of type i, the number of type j points lying closer than r units away.

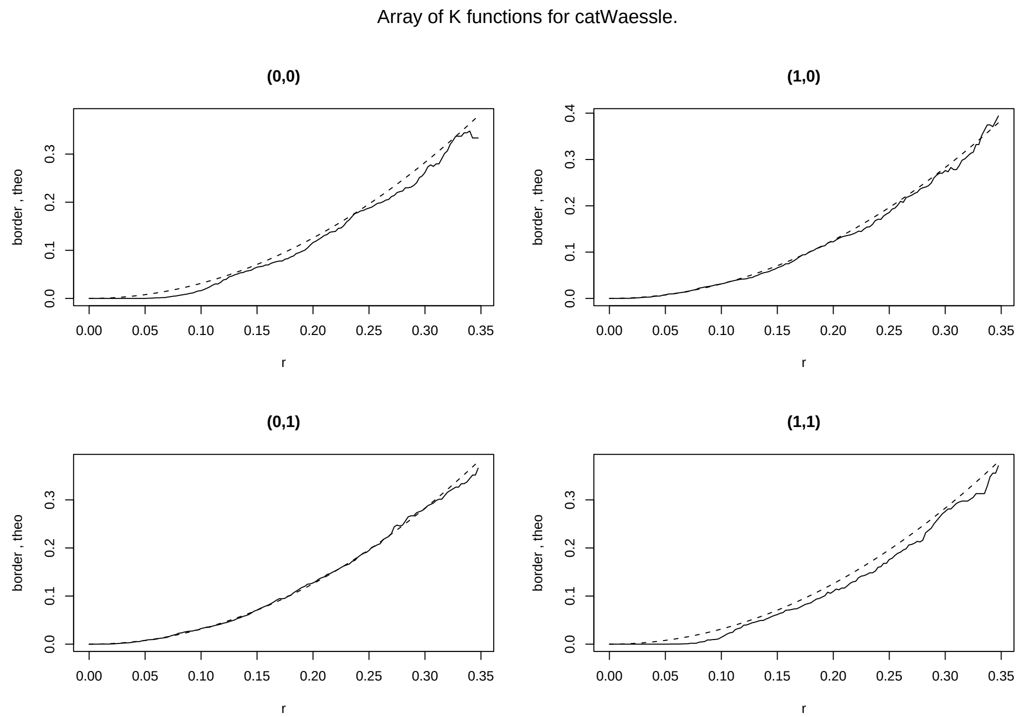
`Gcross,Gdot,Gmulti`	multitype nearest neighbour distributions $G_{ij}, G_{i\bullet}$
`Kcross,Kdot, Kmulti`	multitype K-functions $K_{ij}, K_{i\bullet}$
`Jcross,Jdot,Jmulti`	multitype J-functions $J_{ij}, J_{i\bullet}$
`alltypes`	array of multitype functions

These functions (with the exception of `alltypes`) operate in a very similar way to `Gest, Jest, Kest` with additional arguments specifying the type(s) of points to be studied.

To compute and plot the cross K function $K_{ij}(r)$ for all possible pairs of types i and j,

```
plot(alltypes(X,"K"))
```

See the next section for further information.



4.4 Function arrays

A function array is a collection of functions $f_{i,j}(r)$ indexed by integers i and j. An example is the set of cross K functions $K_{ij}(r)$ for all possible pairs of types i and j in a multitype point pattern. It is best to think of this as a genuine matrix or array.

A function array is represented in `spatstat` by an object of type `"fasp"`. It can be stored, plotted, indexed and subsetted in a natural way. If `Z` is a function array, then

```
plot(Z)
plot(Z[,3:5])
```

will plot the entire array, and then plot the subarray consisting only of columns 3 to 5. See `help(fasp.object)`, `help(plot.fasp)` and `help("[.fasp")` for details.

The value returned by `alltypes` is a function array. `alltypes` computes a summary statistic for each possible type, or each possible pairs of types, in a multitype point pattern. For example if `X` is a multitype point pattern with 3 possible types,

```
Z <- alltypes(X, "K")
```

yields a 3×3 function array such that (say) `Z[1,2]` represents the cross-type K function $K_{1,2}(r)$ between types 1 and 2. The command `plot(Z)` will plot the entire set of cross K functions as a two-dimensional array of plot panels. Arguments to `plot.fasp` can be used to change the plotting style, the range of the axes, and to select which estimator of K_{ij} is plotted.

The value returned by `allstats` is a 2×2 function array containing the F, G, J and K functions of an (unmarked) point pattern.

4.5 Summary functions for a marked point pattern

Some point patterns are marked, but not multitype. That is, the points may carry marks that do not belong to a finite list of possible types. The marks might be continuous numerical values, complex numbers, etc.

An example in `spatstat` is the dataset `longleaf` where the marks represent tree diameters. You can easily recognise whether a point pattern is multitype or not by the behaviour of the plot function: a multitype pattern is plotted using different plotting symbols for each type, while a marked point pattern with numerical marks is plotted using circles of radius proportional to the marks.

There are a few ways to study such patterns in `spatstat`:

- the function `markcorr` computes the mark correlation function of an arbitrary marked point pattern. See the help file for `markcorr`.
- you can convert a marked point pattern to a multitype point pattern using the function `cut.ppp`, for example, classifying the marks into High, Medium and Low, then apply the abovementioned functions for multitype point patterns. This is usually a good exploratory step.

- the functions `Kmulti, Gmulti, Jmulti` operate on arbitrary marked point patterns. They require arguments `I, J` identifying two subsets of the point pattern. These two subsets will be treated as two discrete types.
- ignore the marks (use the function `unmark` to remove them) and analyse only the locations of the points.

5 Model fitting

`spatstat` enables parametric models of spatial point processes to be fitted to point pattern data. The scope of possible models is very wide. Models may include spatial trend, dependence on covariates, and interpoint interactions of any order (i.e. we are not restricted to pairwise interactions). Models are specified by formulae in the `S` language and fitted by a function `mpl()` analogous to `glm()` and `gam()`.

Parameters are estimated by the method of maximum pseudolikelihood, using a computational device developed by Berman & Turner (1992) and Baddeley & Turner (2000). Although maximum pseudolikelihood may be inefficient, it has the virtue that we can implement it in software with great generality.

For example if `X` is a point pattern,

```
mpl(X, ~1, Strauss(r=0.1), ....)
```

fits the stationary Strauss process with interaction radius $r = 0.1$, and

```
mpl(X, ~x, Strauss(r=0.07), ....)
```

fits the non-stationary Strauss process with a loglinear spatial trend of the form $b(x, y) = \exp(a + bx)$.

The value returned by `mpl()` is a "fitted point process model" of class `"ppm"`. It can be plotted and predicted, in a manner analogous to the plotting and prediction of fitted generalised linear models.

5.1 Models

Here is a very brief summary of parametric models for point processes. See Baddeley & Turner (2000), Cox & Isham (1980), and the excellent surveys by Ripley (1988, 1989).

The point pattern dataset $\mathbf{x}$ is assumed to be a realisation of a random point process X in W. Typically the null model (or the null hypothesis) will be the homogeneous Poisson point process. Other models will be specified by their likelihood with respect to the Poisson process. Thus we assume X has a probability density $f(\mathbf{x}; \theta)$ with respect to the distribution of the Poisson process with intensity 1 on W. The distribution is governed by a p-dimensional parameter θ.

We frequently use the *Papangelou conditional intensity* defined, for a location $u \in W$ and a point pattern $\mathbf{x}$, as

$$\lambda_\theta(u, \mathbf{x}) = \frac{f(\mathbf{x} \cup \{u\};\ \theta)}{f(\mathbf{x} \setminus u;\ \theta)}$$

Effectively our technique fits a model to the conditional intensity.

Here are four important examples.

the homogeneous Poisson process with intensity $\lambda > 0$ has conditional intensity

$$\lambda(u, \mathbf{x}) = \lambda$$

the inhomogeneous Poisson process on W with rate or intensity function $\lambda : W \to \mathsf{R}$, has conditional intensity

$$\lambda(u, \mathbf{x}) = \lambda(u).$$

In statistical models, the intensity $\lambda_\theta(u)$ will depend on θ to reflect 'spatial trend' (a change in intensity across the region of observation) or dependence on a covariate.

the Strauss process on W with parameters $\beta > 0$ and $0 \leq \gamma \leq 1$ and interaction radius $r > 0$, has conditional intensity

$$\lambda(u, \mathbf{x}) = \beta \cdot \gamma^{t(u,\mathbf{x})}$$

where $t(u, \mathbf{x})$ is the number of points of $\mathbf{x}$ that lie within a distance r of the location u. If $\gamma < 1$, the term $\gamma^{t(u,\mathbf{x})}$ makes it unlikely that the pattern will contain many points that are close together.

the pairwise interaction process on W with trend or activity function $b_\theta : W \to \mathsf{R}_+$ and interaction function $h_\theta : W \times W \to \mathsf{R}_+$ has conditional intensity

$$\lambda(u, \mathbf{x}) = b_\theta(u) \prod_i h_\theta(u, x_i)$$

The term $b_\theta(u)$ influences the intensity of points, and introduces a spatial trend if $b_\theta(\cdot)$ is not constant. The terms $h_\theta(u, x_i)$ introduce dependence ('interaction') between different points of the process X.

Our technique only estimates parameters θ for which the model is in "canonical exponential family" form,

$$\begin{aligned} f(\mathbf{x}; \theta) &= \alpha(\theta) \exp(\theta^\mathsf{T} V(\mathbf{x})) \\ \lambda_\theta(u, \mathbf{x}) &= \exp(\theta^\mathsf{T} S(u, \mathbf{x})) \end{aligned}$$

where $V(\mathbf{x})$ and $S(u, \mathbf{x})$ are statistics, and $\alpha(\theta)$ is the normalising constant.

5.2 Implementation in `spatstat`

The model-fitting function is called `mpl()` and is strongly analogous to `glm()` or `gam()`. It is called in the form

```
mpl(X, formula, interaction, ...)
```

where `X` is the point pattern dataset, `formula` is an S language formula describing the systematic part of the model, and `interact` is an object of class `"interact"` describing the stochastic dependence between points in the pattern.

What this means is that we write the conditional intensity $\lambda_\theta(u, \mathbf{x})$ as a loglinear expression with two components:

$$\lambda(u, \mathbf{x}) = \exp(\theta_1 B(u) + \theta_2 C(u, \mathbf{x}))$$

where $\theta = (\theta_1, \theta_2)$ are parameters to be estimated.

The term $B(u)$ depends only on the spatial location u, so it represents "spatial trend" or spatial covariate effects. It is treated as a "systematic" component of the model, analogous to the systematic part of a generalised linear model, and is described in `spatstat` by an S language formula.

The term $C(u, \mathbf{x})$ represents "stochastic interactions" or dependence between the points of the random point process. It is regarded as a "distributional" component of the model analogous to the distribution family in a generalised linear model. It is described in `spatstat` by an object of class `"interact"` that we create using specialised `spatstat` functions.

For example

```
mpl(X, ~1, Strauss(r=0.1), ....)
```

fits the stationary Strauss process with interaction radius $r = 0.1$. The spatial trend formula `~1` is a constant, meaning the process is stationary. The argument `Strauss(r=0.1)` is an object representing the interpoint interaction structure of the Strauss process with interaction radius $r = 0.1$. Similarly

```
mpl(X, ~x, Strauss(r=0.1), ....)
```

fits the non-stationary Strauss process with a loglinear spatial trend of the form $b(x, y) = \exp(a + bx)$ where a and b are parameters to be fitted, and x, y are the cartesian coordinates.

Spatial trend

The `formula` argument of `mpl()` describes any spatial trend and covariate effects. The default is `~1`, which corresponds to a process without spatial trend or covariate effects. The formula `~x` corresponds to a spatial trend of the form $\lambda(x, y) = \exp(a + bx)$, while `~x + y` corresponds to $\lambda(x, y) = \exp(a + bx + cy)$ where x, y are the Cartesian coordinates. These could be replaced by any `S` language formula (with empty left hand side) in terms of the reserved names `x, y` and `marks`, or in terms of some spatial covariates which you must then supply.

You can easily construct spatial covariates from the Cartesian coordinates. For example

```
mpl(X, ~ ifelse(x > 2, 0, 1), Poisson())
```

fits an inhomogeneous Poisson process with different, constant intensities on each side of the line $x = 2$.

`spatstat` provides a function `polynom` which generates polynomials in 1 or 2 variables. For example

```
~ polynom(x, y, 2)
```

represents a polynomial of order 2 in the Cartesian coordinates x and y. This would give a "log-quadratic" spatial trend. The distinction between `polynom` and `poly` is explained below.

It is slightly more tricky to include *observed* spatial covariates; see section 5.6.

Interaction terms

The higher order ("interaction") structure can be specified using one of the following functions. They yield an object (of class `"interact"`) describing the interpoint interaction structure of the model.

- `Poisson()` .... Poisson process
- `Strauss()` .... Strauss process
- `StraussHard()` ... Strauss process with a hard core
- `Softcore()` .... Pairwise interaction, soft core potential
- `PairPiece()` ..... Pairwise interaction, piecewise constant potential
- `DiggleGratton()` Diggle-Gratton potential
- `Geyer()` .... Geyer's saturation process
- `OrdThresh()` ..... Ord process with threshold potential

Note that `mpl()` estimates only the "exponential family" type parameters of a point process model. These are parameters θ such that the loglikelihood is linear in θ. Other so-called "irregular" parameters (such as the interaction radius r of the Strauss process) cannot be estimated by this technique, and their values must be specified a priori, as arguments to the interaction function).

For more advanced use, the following functions will accept "user-defined potentials" in the form of an arbitrary `S` language function. They effectively allow arbitrary point process models of these three classes.

- `Pairwise()` .... Pairwise interaction, user-supplied potential
- `Ord()` .... Ord model, user-supplied potential
- `Saturated()`... Saturated pairwise model, user-supplied potential

The brave user may also generate completely new point process models using the foregoing as templates.

5.3 Fitted models

The value returned by mpl() is a "fitted point process model" of class "ppm". It can be stored, inspected, plotted and predicted.

```
fit <- mpl(X, ~1, Strauss(r=0.1), ...)
fit
plot(fit)
pf <- predict(fit)
```

Printing the fitted object fit will produce text output describing the fitted model. Plotting the object will display the spatial trend and the conditional intensity, as perspective plots, contour plots and image plots. The predict method computes either the spatial trend or the conditional intensity at new locations.

A trap for young players

Note that problems may arise if you use predict on a point process model whose systematic component is expressed in terms of one of the functions poly(), bs(), lo(), or ns(). For example

```
fit <- mpl(X, ~ poly(x,2), Poisson())
p <- predict(fit)
```

The same problem occurs with predict for generalised linear models and generalised additive models. Each of the abovementioned functions returns a data frame, containing variables that are transformations of the variables given as arguments of the function. However the transformations themselves depend on the values of the arguments. For example poly performs Gram-Schmidt orthonormalisation. Hence the fitted coefficients contained in the fit object are not appropriate when we predict at new locations — **not even for the default call to predict(fit) above**.

For this reason we have supplied the function polynom which does not perform any data-dependent transformation, and yields a data frame whose columns are just the powers of its arguments. Replacing poly by polynom in the code above *does* work correctly.

5.4 Fitting models to multitype point patterns

The function `mpl()` will also fit models to multitype point patterns. A multitype point pattern is a point pattern in which the points are each classified into one of a finite number of possible types (e.g. species, colours, on/off states). In `spatstat` a multitype point pattern is represented by a `"ppp"` object `X` containing a vector `X$marks`, <u>which must be a `factor`</u>.

Interaction component

Naturally an appropriate specification of the interaction for such a model must be available. Apart from the Poisson process, so far interaction functions have been written for the following:

`MultiStrauss()`	multitype Strauss process
`MultiStraussHard()`	multitype Strauss/hard core process

For the multitype Strauss process, a matrix of "interaction radii" must be specified. If there are m distinct levels (possible values) of the marks, we require a matrix `r` in which `r[i,j]` is the interaction radius r_{ij} between types i and j. For the multitype Strauss/hard core model, a matrix of "hardcore radii" must be supplied as well. These matrices will be of dimension $m \times m$ and must be symmetric. See the help files for these functions.

Trend component

The first-order component ("trend") of a multitype point process model may depend on the marks. For example, a stationary multitype Poisson point process could have different (constant) intensities for each possible mark. A general nonstationary process could have a different spatial trend surface for each possible mark.

In order to represent the dependence of the trend on the marks, the trend formula passed to `mpl()` may involve the reserved name `marks`.

The trend formula `~ 1` states that the trend is constant and does not depend on the marks. The formula `~marks` indicates that there is a separate, constant intensity for each possible mark. The correct way to fit the multitype Poisson process is

```
mpl(X, ~ marks, Poisson())
```

Getting more elaborate, the trend formula might involve both the marks and the spatial locations or spatial covariates. For example the trend formula `~marks + polynom(x,y,2)` signifies that the first order trend is a log-quadratic function of the cartesian coordinates, multiplied by a constant factor depending on the mark.

The formulae

```
~ marks * polynom(x,2)
~ marks + marks:polynom(x,2)
```

both specify that, for each mark, the first order trend is a different log-quadratic function of the cartesian coordinates. The second form looks "wrong" since it includes a "`marks` by `polynom`" interaction without having `polynom` in the model, but since `polynom` is a covariate rather than a factor this is is allowed, and makes perfectly good sense. As a result the two foregoing models are in fact equivalent. However, they will give output that is slightly different in appearance. For instance, suppose that there are 3 distinct marks. The first form of the model gives a "baseline" polynomial, say P_0, and two polynomials say P_1 and P_2. Assume that either Helmert or sum contrasts were used, so that the "sum constraints" apply. The trends corresponding to each of the marks would be given by $\exp(C_1 + P_0 + P_1)$, $\exp(C_2 + P_0 + P_2)$, and $\exp(C_3 + P_0 - P_1 - P_2)$ respectively, where C_1, C_2, and C_3 are the appropriate constant terms corresponding to each of the three marks.

The second model simply gives 3 polynomials, say p_1, p_2, and p_3, corresponding to each of the 3 marks. The trends would then be given by $\exp(c_1 + p_1)$, $\exp(c_2 + p_2)$, and $\exp(c_3 + p_3)$.

5.5 Quadrature schemes

The function `mpl` is an implementation of the technique of Baddeley & Turner (2000) which is based on a quadrature device originated by Berman & Turner (1992). Complete control over the quadrature technique is possible.

Indeed the function `mpl()` prefers to be provided with a "quadrature scheme" as its first argument, although it will make do with a point pattern and calculate a default quadrature scheme.

A quadrature scheme is an object of class `"quad"` giving the locations of quadrature points and the weights attached to them. See `help(quad.object)` for more details. The usual way to create a quadrature scheme is to use `quadscheme()`. For example:

```
Q <- quadscheme(simdat,gridcentres(simdat,50,50),
                                  nx=40,ny=40)
fit <- mpl(Q, ~polynom(x,y,3),Softcore(0.5),
                              correction="periodic")
```

Following are the most useful functions for manipulating quadrature schemes.

`quadscheme`	generate a Berman-Turner quadrature scheme for use by `mpl`
`default.dummy`	default pattern of dummy points
`gridcentres`	dummy points in a rectangular grid
`stratrand`	stratified random dummy pattern
`spokes`	radial pattern of dummy points
`corners`	dummy points at corners of the window
`gridweights`	quadrature weights by the grid-counting rule
`dirichlet.weights`	quadrature weights are Dirichlet tile areas

5.6 Observed spatial covariates

If you wish to model the dependence of a point pattern on a spatial covariate, there are several requirements.

- the covariate must be a quantity $Z(u)$ observable at each location u in the window (e.g. altitude, soil pH, or distance to another spatial pattern). There may be several such covariates, and they may be continuous valued or factors.
- the values $Z(x_i)$ of Z at each point of the data point pattern must be available.
- the values $Z(u)$ at *some other points* u in the window must be available.

To use `mpl()` you will need to construct a quadrature scheme based on the spatial locations where the covariate Z has been observed. Then the values of the covariate at these locations are passed to `mpl()` through the argument `data`.

For example, suppose that `X` is the observed point pattern and we are trying to model the effect of soil acidity (pH). Suppose we have measured the values of soil pH at the points x_i of the point pattern, and stored them in a vector `XpH`. Suppose we have measured soil pH at some other locations u in the window, and stored the results in a data frame `U` with columns `x, y, pH`. Then do as follows:

```
Q <- quadscheme(data=X, dummy=list(x=U$x, y=U$y))
df <- data.frame(pH=c(XpH, U$pH))
```

Then the rows of the data frame `df` correspond to the quadrature points in the quadrature scheme `Q`. To fit just the effect of pH, type

```
mpl(Q, ~ pH, Poisson(), data=df)
```

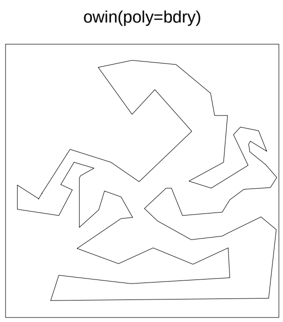
where the term `pH` in the formula `~ pH` agrees with the column label `pH` in the argument `data = df`. This will fit an inhomogeneous Poisson process with intensity that is a loglinear function of soil pH. You can also try (say)

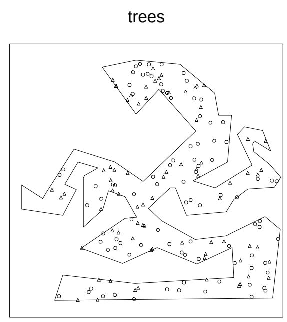
```
mpl(Q, ~ pH, Strauss(r=1), data=df)
mpl(Q, ~ factor(pH > 7), Poisson(), data=df)
mpl(Q, ~ polynom(x, 2) * factor(pH > 7), data=df)
```

6 Worked example

Suppose we have a data file `trees.tab` containing a table of x,y coordinates and species names for all trees in a paddock. The paddock has an irregular polygonal boundary whose vertex coordinates are stored in the file `paddock`. The following code will read in these data, plot the polygonal boundary, create the point pattern object and plot the point pattern.

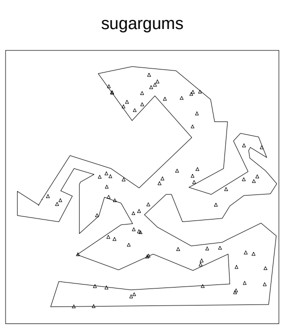
```
tab <- read.table("trees.tab", header=T)
bdry <- scan("paddock", what=list(x=0,y=0))
plot(owin(poly=bdry))
trees <- ppp(tab$x, tab$y, poly=bdry, marks=factor(tab$species))
plot(trees)
```





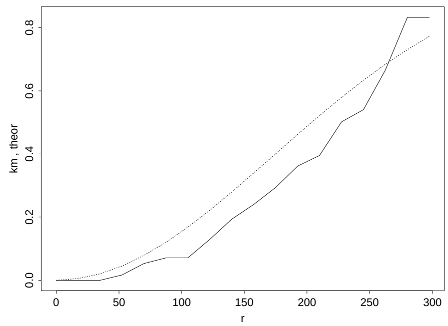
Next we inspect the pattern of sugar gums only, using the subset operation `"["` for point patterns:

```
sugargums <- trees[ trees$marks == "sugargum"]
plot(sugargums)
```



Next we compute and plot the cross-type G function between sugar gums and red box:

```
G <- Gcross(trees, "sugargum", "redbox")
conspire(G, cbind(km,theor) ~ r, type="l")
```



Next we fit a nonstationary Poisson process, with a separate log-cubic spatial trend for each species of tree:

```
fitsep <- mpl(trees, ~ marks * polynom(x,y,3), Poisson())
```

We also fit the sub-model in which the species trends are all proportional:

```
fitprop <- mpl(trees, ~ marks + polynom(x,y,3), Poisson())
```

and fit the stationary model in which each species has constant intensity:

```
fit0 <- mpl(trees, ~ marks, Poisson())
```

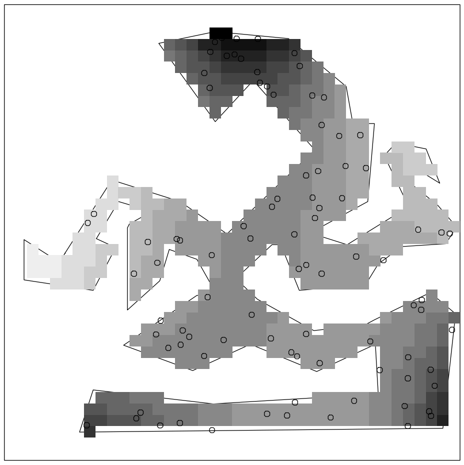
We plot the fitted trend surfaces for each tree:

```
plot(fitsep)
```

Finally we fit a nonstationary multitype Strauss / hard core process with a hard core operating between trees of the same species:

```
mymodel <- MultiStraussHard( levels(trees$marks),
               iradii=matrix(c(150,100,100,200), 2,2),
               hradii=matrix(c(50,NA,NA,50), 2,2))
fit <- mpl(trees, ~ marks * polynom(x,y,3), mymodel, rbord=20)
plot(fit, cif=F)
```

mark = redbox



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