Advanced R course on spatial point patterns

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SSAI 2017

Plan of Workshop

1. Introduction
2. Inhomogeneous Intensity
3. Intensity dependent on a covariate
4. Fitting Poisson models
5. Marked point patterns
6. Correlation
7. Envelopes and Monte Carlo tests
8. Spacing and nearest neighbours
9. Cluster and Cox models
10. Gibbs models
11. Multitype summary functions and models

The slides are a summary

These slides are a summary of
the most important concepts
in the workshop.

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Use them for review/reminder

Types of spatial data

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Three basic types of spatial data:

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- geostatistical

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- regional

Types of spatial data

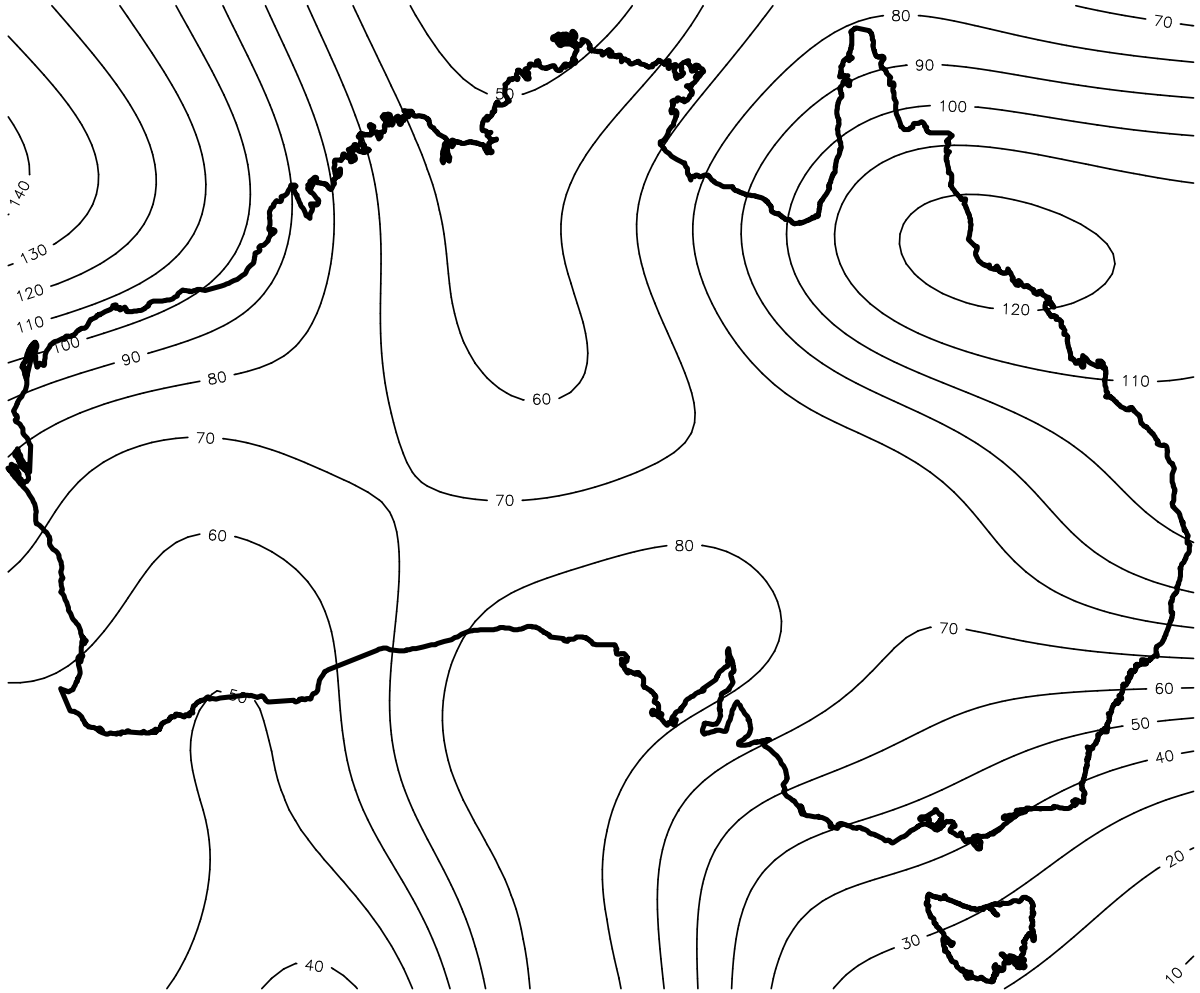
Three basic types of spatial data:

- geostatistical
- regional
- point pattern

Geostatistical data

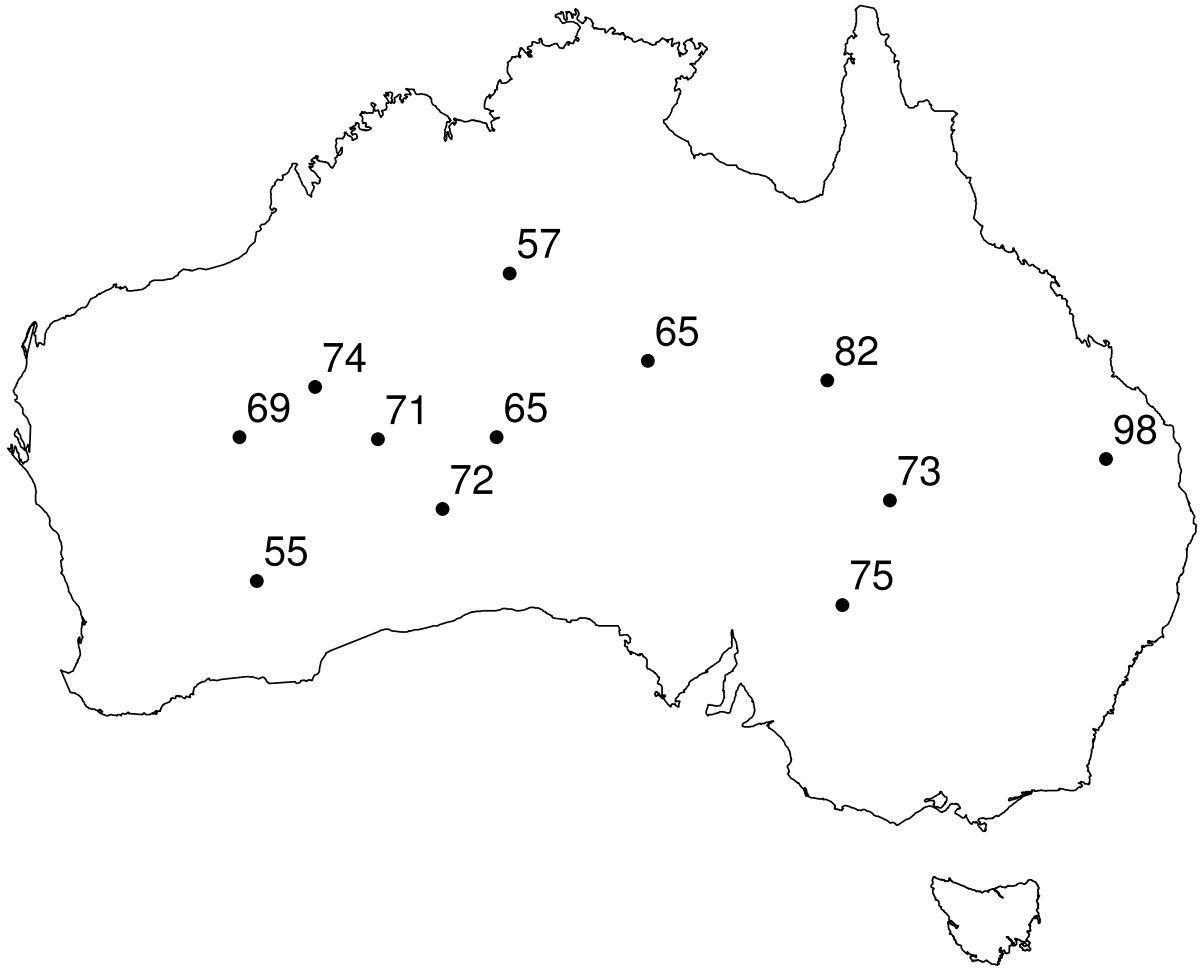
GEOSTATISTICAL DATA:

The quantity of interest has a value at any location, . . .



Geostatistical data

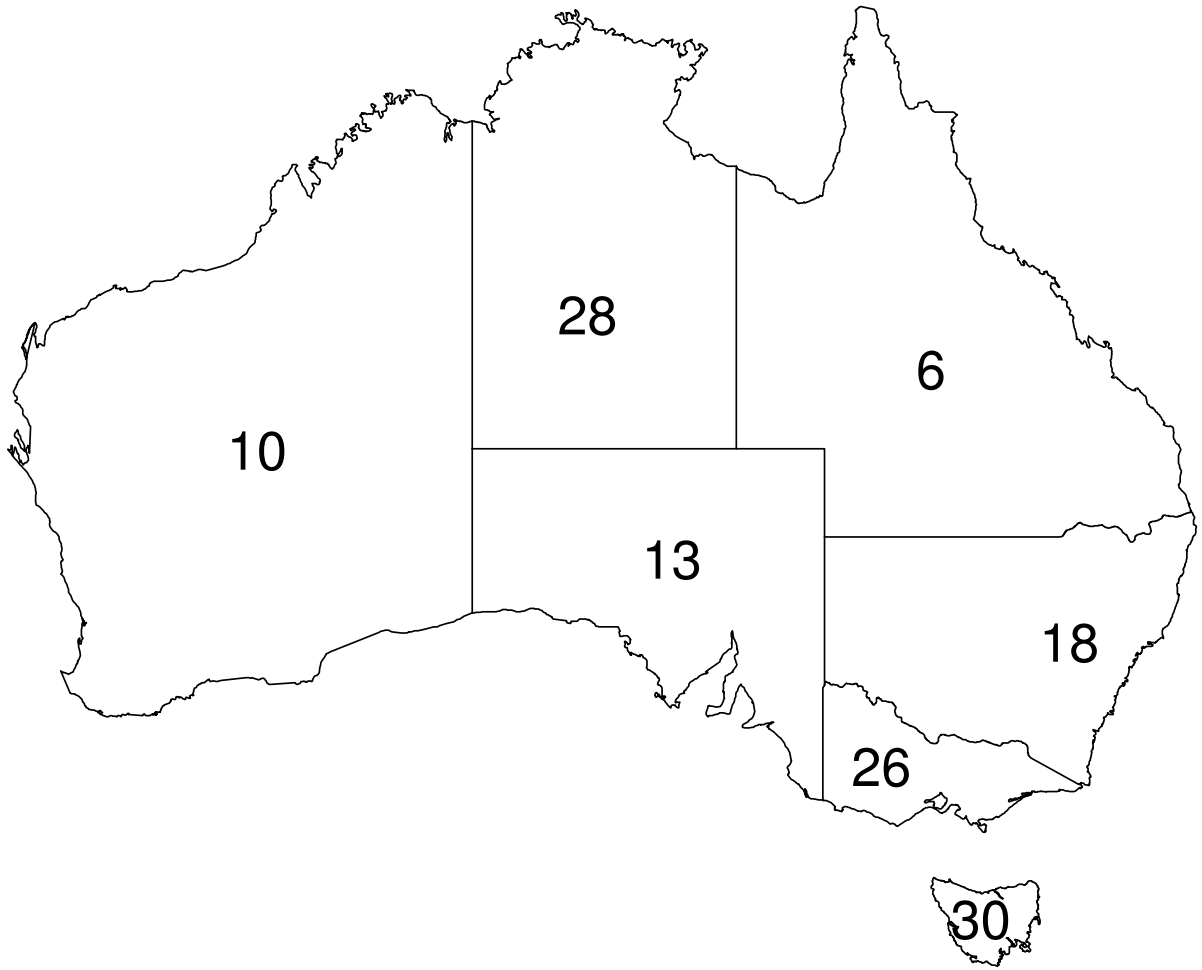
. . . but we only measure the quantity at certain sites. These values are our data.



Regional data

REGIONAL DATA:

The quantity of interest is only defined for regions. It is measured/reported for certain *fixed* regions.



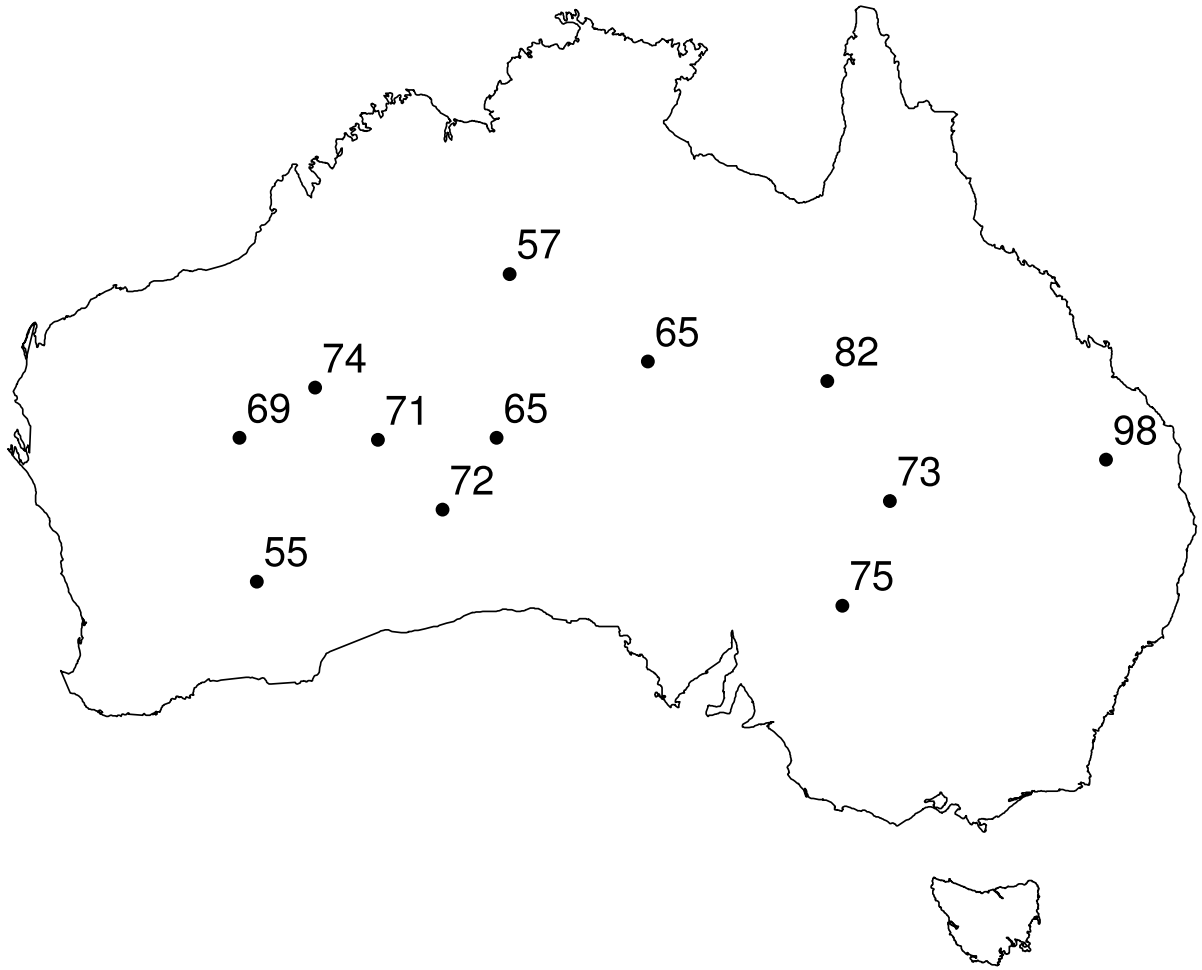
Point pattern data

POINT PATTERN DATA:

The main interest is in the *locations* of all occurrences of some event (e.g. tree deaths, meteorite impacts, robberies). Exact locations are recorded.

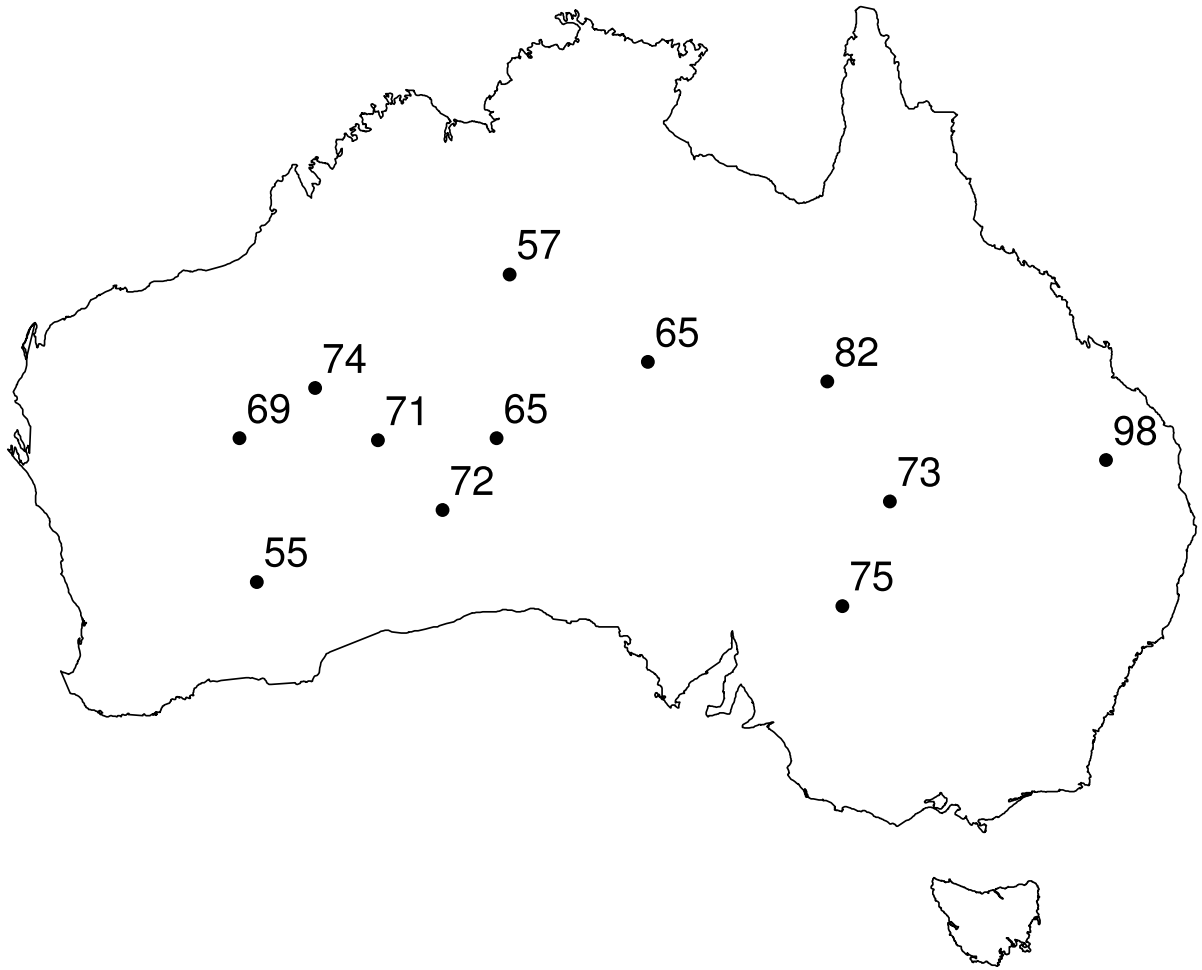
Points with marks

Points may also carry data (e.g. tree heights, meteorite composition)



Point pattern or geostatistical data?

POINT PATTERN OR GEOSTATISTICAL DATA?



Explanatory vs. response variables

Response variable: the quantity that we want to “predict” or “explain”

Explanatory variable: quantity that can be used to “predict” or “explain” the response.

Point pattern or geostatistical data?

Geostatistics treats the spatial locations as explanatory variables and the values attached to them as response variables.
Spatial point pattern statistics treats the spatial locations, and the values attached to them, as the response.

Point pattern or geostatistical data?

"Temperature is increasing as we move from South to North" — **geostatistics**
"Trees become less abundant as we move from South to North" — **point pattern statistics**

Software Overview

Software overview

For information on spatial statistics software in *R*:

Software overview

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- go to `cran.r-project.org`

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GIS = Geographical Information System

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ArcInfo

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ArcInfo proprietary `esri.com`

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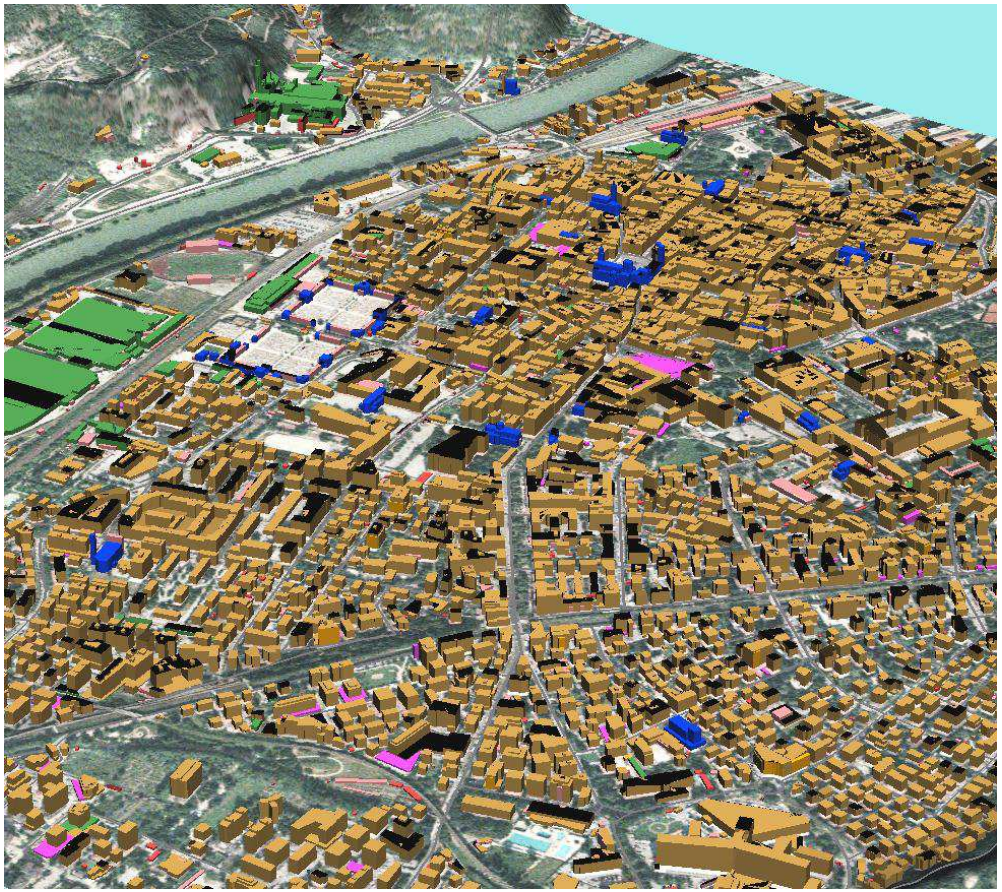
ArcInfo	proprietary	`esri.com`
GRASS	open source	`grass.osgeo.org`



Recommendations

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For visualisation of spatial data, especially for presentation graphics, use a GIS.

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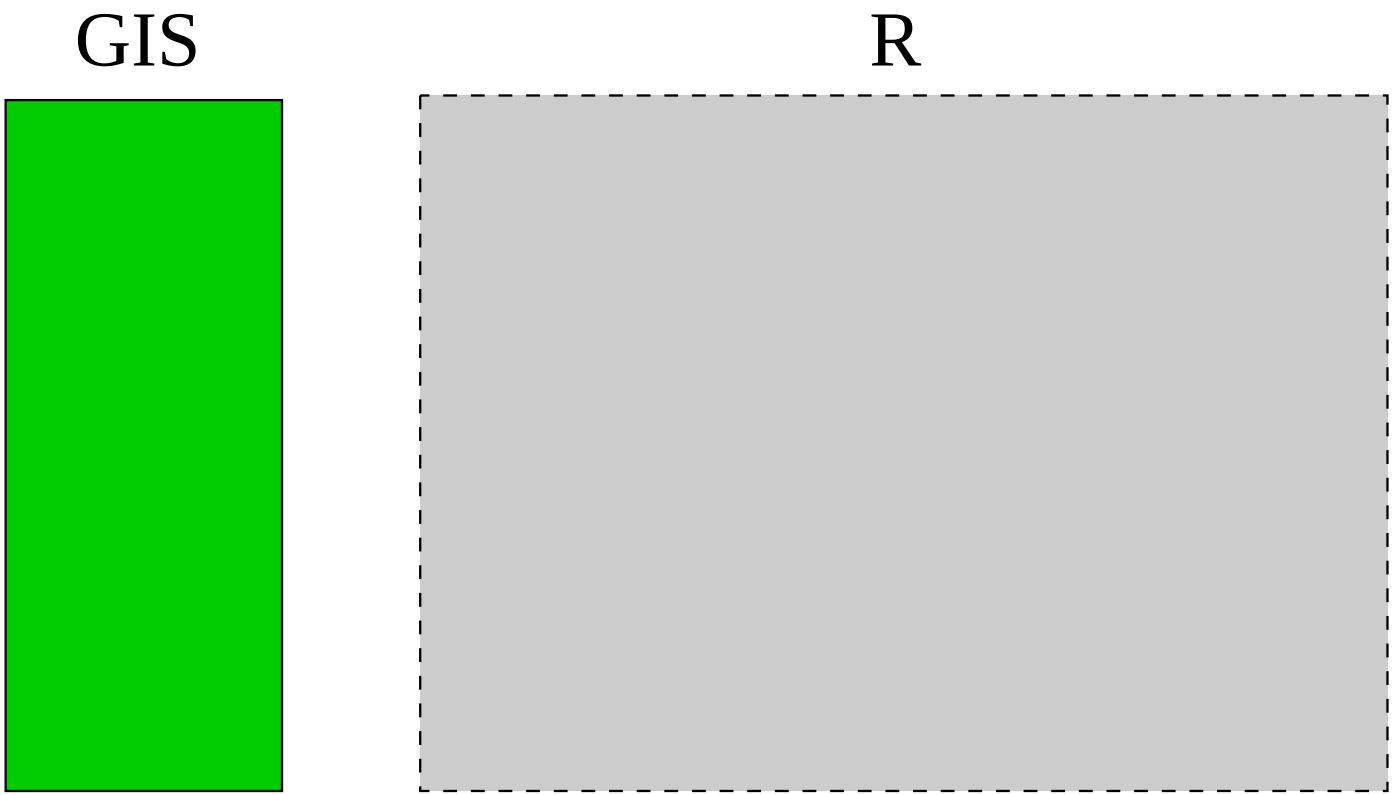
For statistical analysis of spatial data, use R.

Establish two-way communication between GIS and R, either through a direct software interface, or by reading/writing files in mutually acceptable format.

Putting the pieces together



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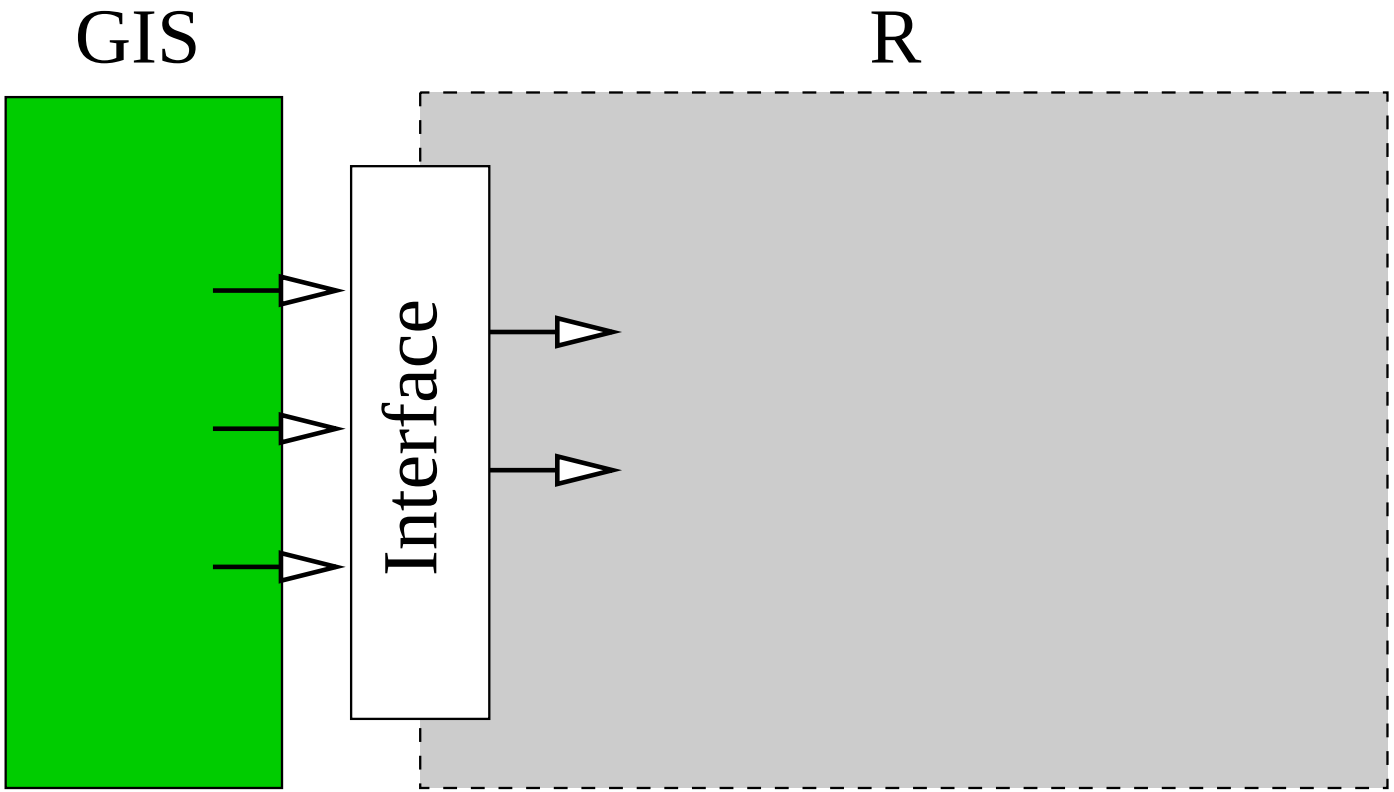
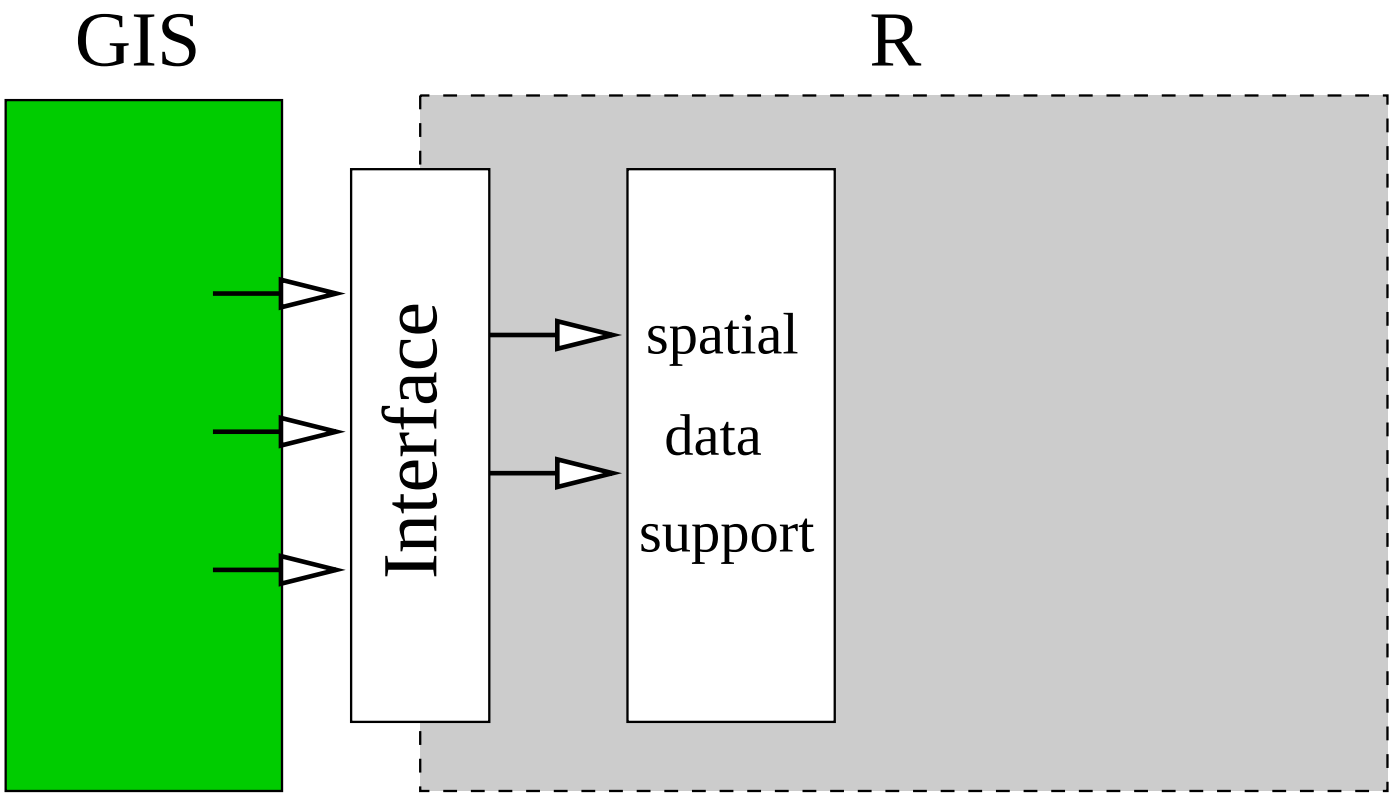


Interface between R and GIS (online or offline)

Putting the pieces together



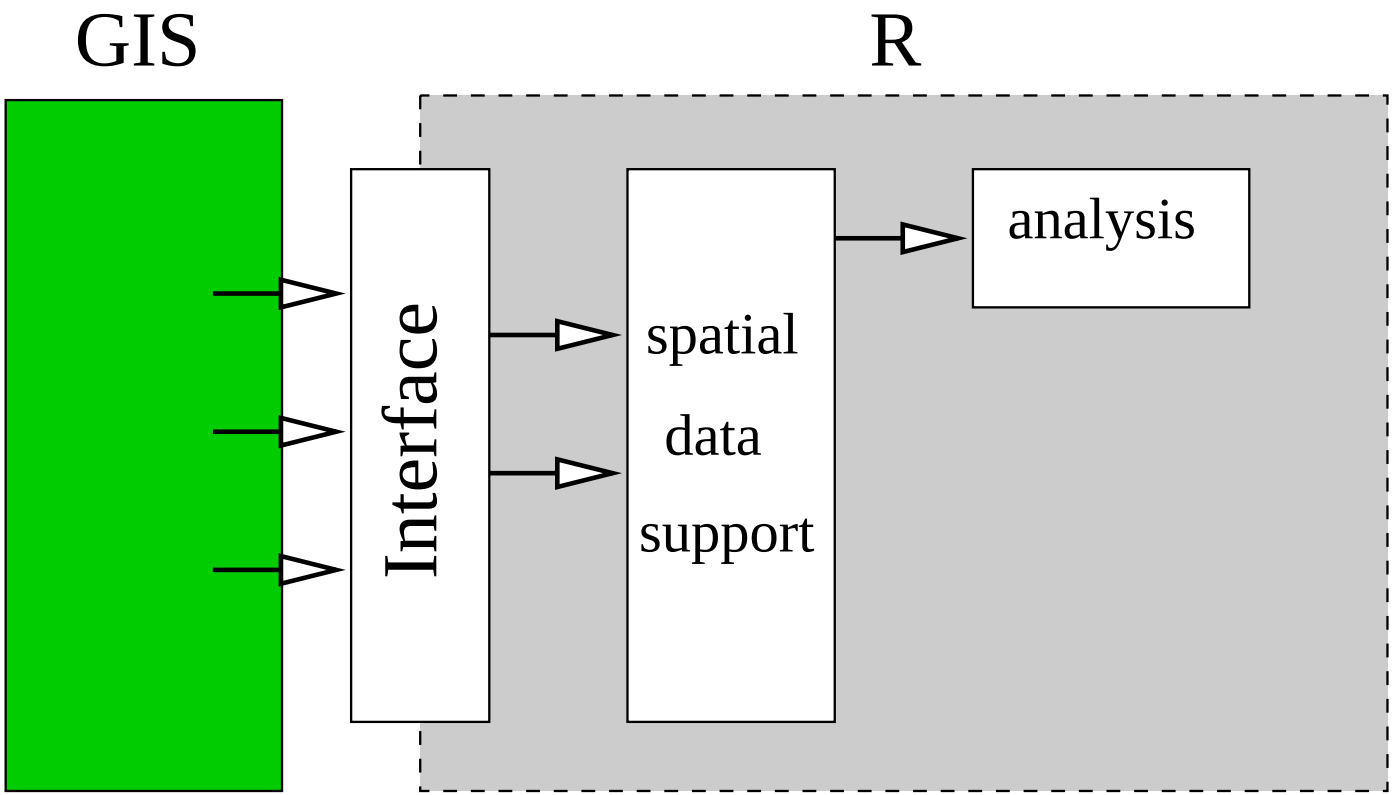
Support for spatial data: data structures, classes, methods

R packages supporting spatial data

R *packages supporting spatial data classes:*

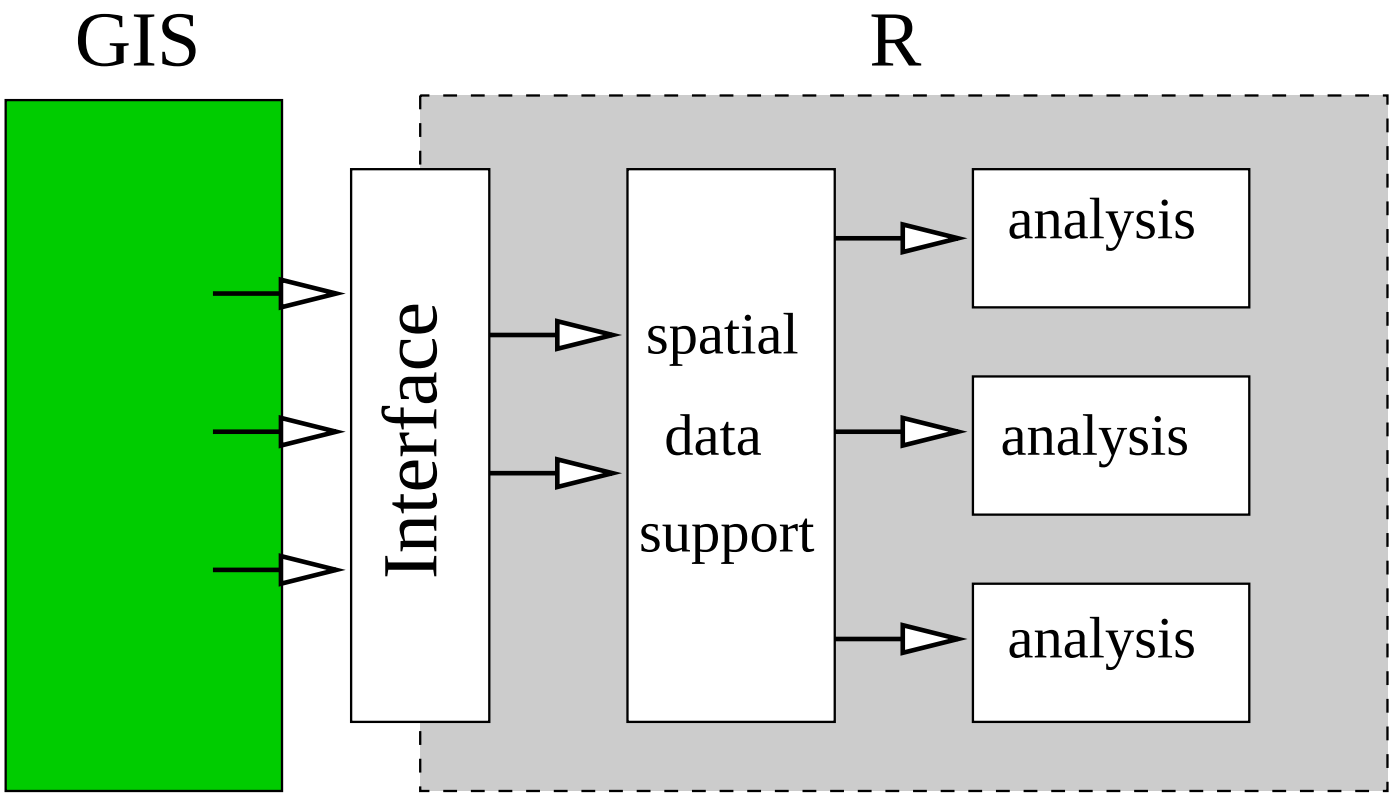
`sp`	generic
`maps`	polygon maps
`spatstat`	point patterns

Putting the pieces together



Capabilities for statistical analysis

Putting the pieces together



Multiple packages for different analyses

Statistical functionality

R *packages for geostatistical data*

`gstat`	classical geostatistics
`geoR`	model-based geostatistics
`RandomFields`	stochastic processes
`akima`	interpolation

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R *packages for regional data*

`spdep`	spatial dependence
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R *packages for point patterns*

`spatstat`	parametric modelling, diagnostics
`splancs`	nonparametric, space-time

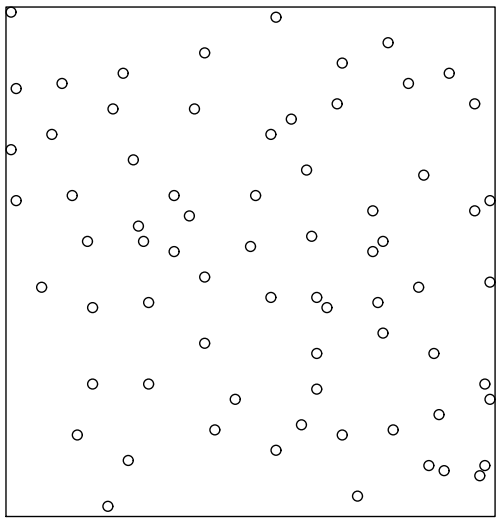
Spatial point patterns

Software

The R package `spatstat` supports statistical analysis for spatial point patterns.

Point patterns

A **point pattern** dataset gives the locations of objects/events occurring in a study region.



The points could represent trees, animal nests, earthquake epicentres, petty crimes, domiciles of new cases of influenza, galaxies, etc.

Marks

The points may have extra information called **marks** attached to them. The mark represents an "attribute" of the point.

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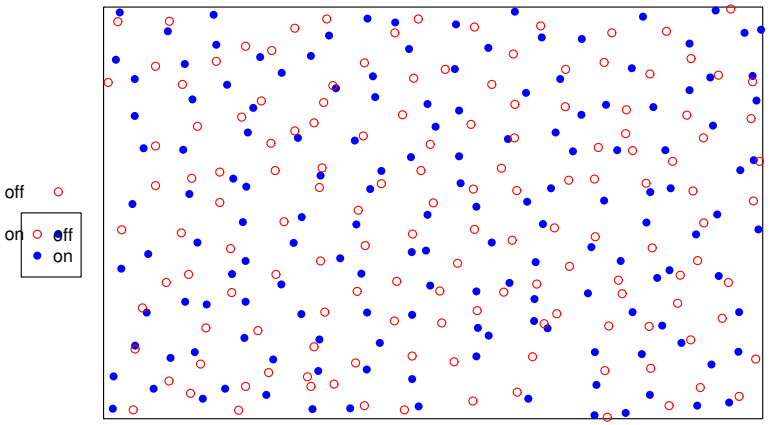
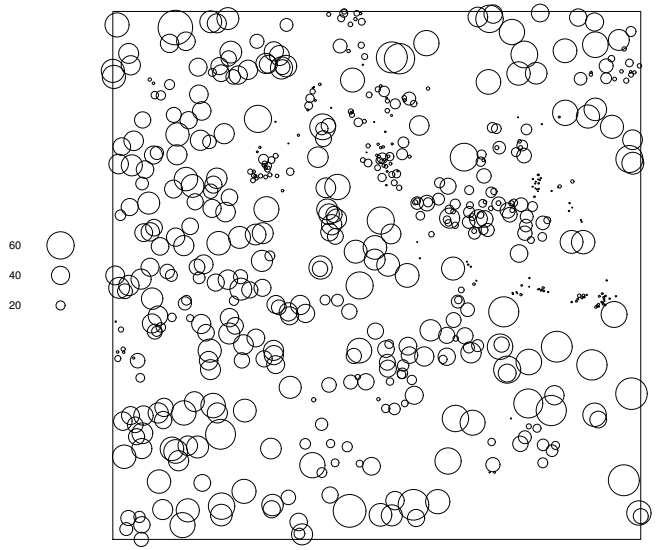
The mark variable could be *categorical*, e.g. species or disease status:



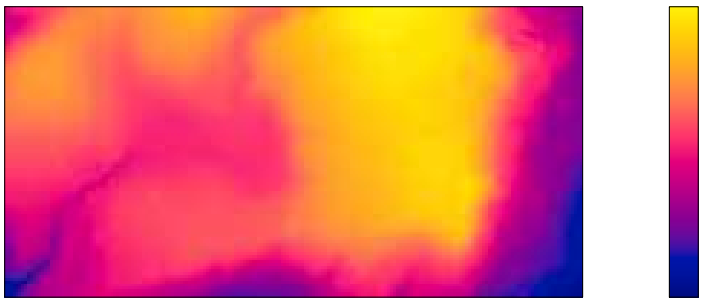
Continuous marks

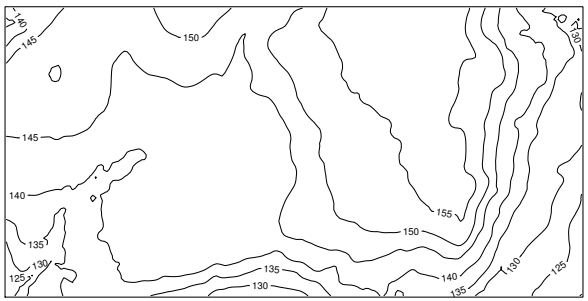
The mark variable could be *continuous*, e.g. tree diameter:



Covariates

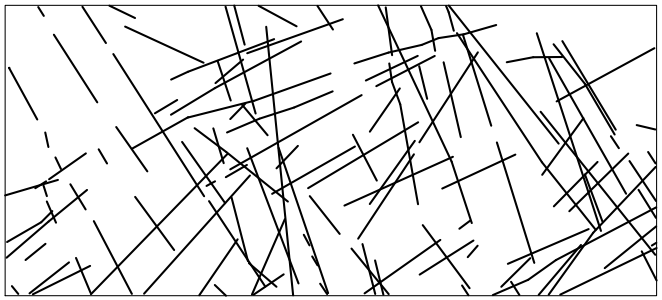
Our dataset may also include **covariates** — any data that we treat as explanatory, rather than as part of the 'response'.
Covariate data may be a *spatial function* $Z(u)$ defined at all spatial locations u, e.g. altitude, soil pH, displayed as a pixel image or a contour plot:





Covariates

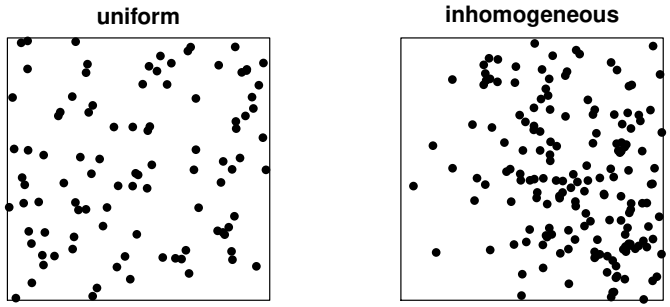
Covariate data may be another *spatial pattern* such as another point pattern, or a line segment pattern, e.g. a map of geological faults:



Intensity

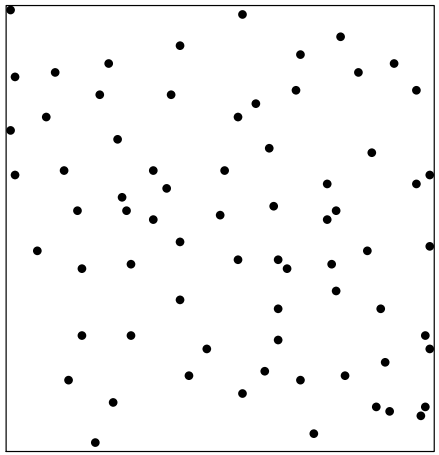
Intensity

‘Intensity’ is the average density of points (expected number of points per unit area). Intensity may be constant (‘uniform’) or may vary from location to location (‘non-uniform’ or ‘inhomogeneous’).



Swedish Pines data

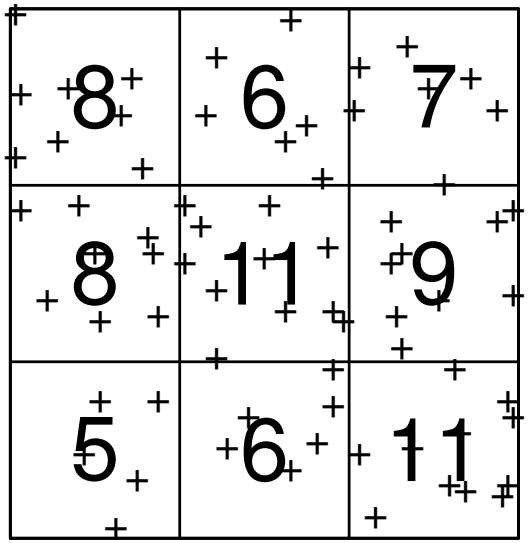
```
> data(swedishpines)
> P <- swedishpines
> plot(P)
```



Quadrat counts

Divide study region into rectangles ('quadrats') of equal size, and count points in each rectangle.

```
Q <- quadratcount(P, nx=3, ny=3)
Q
plot(Q, add=TRUE)
```



χ^2 test of uniformity

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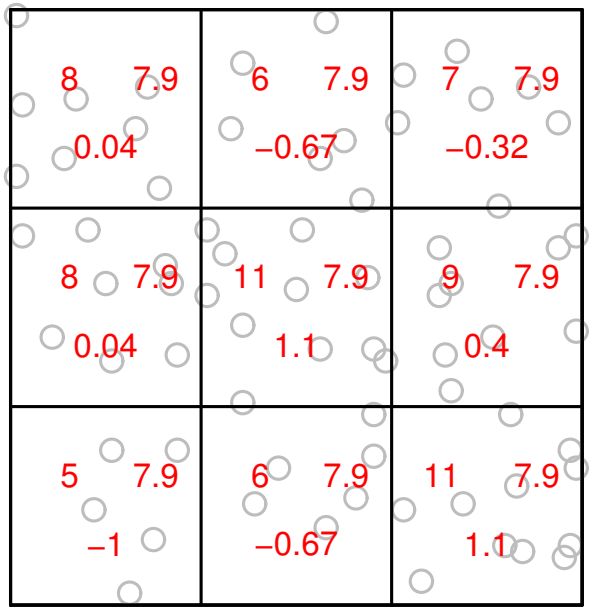
```
> quadrat.test(P, nx=3, ny=3)

        Chi-squared test of CSR using quadrat counts

data:  P
X-squared = 4.6761, df = 8, p-value = 0.7916
```

χ^2 test of uniformity

```
> QT <- quadrat.test(P, nx=3, ny=3)
> plot(P)
> plot(QT, add=TRUE)
```



Kernel smoothing

Kernel smoothed intensity

$$\widetilde{\lambda}(u) = \sum_{i=1}^{n} \kappa(u - x_i)$$

where $\kappa(u)$ is the kernel function and $x_1, \ldots, x_n$ are the data points.

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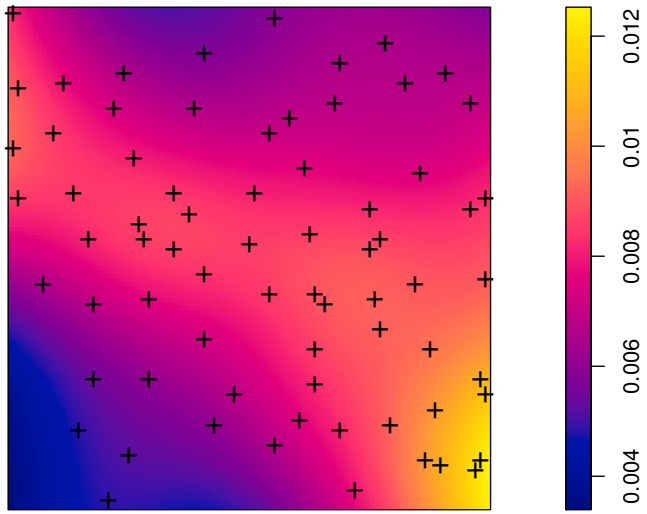
1. replace each data point by a square of chocolate
2. melt chocolate with hair dryer
3. resulting landscape is a *kernel smoothed estimate of intensity function*

Kernel smoothing

```
den <- density(P, sigma=15)
plot(den)
plot(P, add=TRUE)
```



Modelling intensity

A more searching analysis involves fitting *models* that describe how the point pattern intensity $\lambda(u)$ depends on spatial location u or on spatial covariates $Z(u)$.

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Intensity is modelled using a “log link”.

Modelling intensity

COMMAND	INTENSITY
`ppm(P ~1)`	$\log \lambda(u) = \beta_0$

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`ppm(P ~x)`	$\log \lambda((x,y)) = \beta_0 + \beta_1 x$
`ppm(P ~x + y)`	$\log \lambda((x,y)) = \beta_0 + \beta_1 x + \beta_2 y$

$\beta_0, \beta_1, \ldots$ denote parameters to be estimated.

Swedish Pines data

```
> ppm(P ~1)
Stationary Poisson process
Uniform intensity:      0.007
```

Swedish Pines data

```
> ppm(P ~x+y)
Nonstationary Poisson process
Trend formula: ~x + y
Fitted coefficients for trend formula:
  (Intercept)         x         y
    -5.1237    0.00461   -0.00025
```

Modelling intensity

COMMAND	INTENSITY
`ppm(P ~polynom(x,y,3))`	$\exp$(3rd order polynomial in x and y)

Modelling intensity

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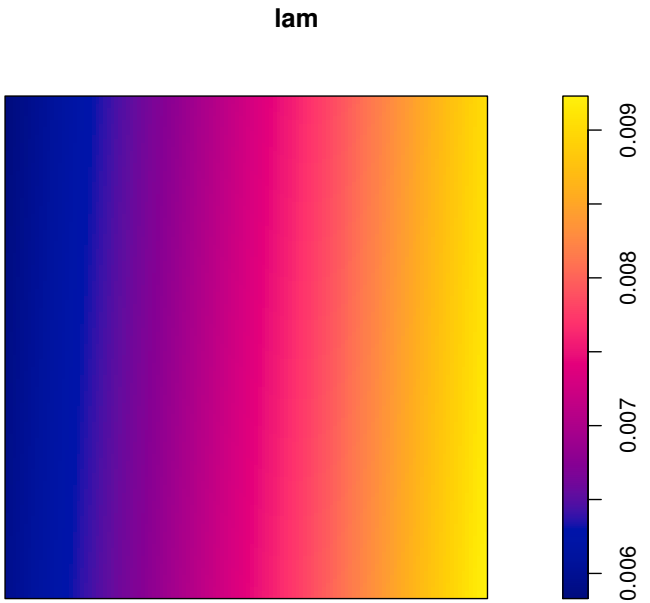
`ppm(P ~polynom(x,y,3))`	$\exp$(3rd order polynomial in x and y)
`ppm(P ~I(y > 18))`	different constants above and below the line $y = 18$

Fitted intensity

```
fit <- ppm(P ~x+y)
lam <- predict(fit)
plot(lam)
```

The `predict` method computes fitted values of intensity function $\lambda(u)$ at a grid of locations.



Likelihood ratio test

```
fit0 <- ppm(P ~1)
fit1  <- ppm(P ~polynom(x,y,2))
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Analysis of Deviance Table

Model 1: ~1                                                    Poisson
Model 2: ~x + y + I(x^2) + I(x * y) + I(y^2)                    Poisson
  Npar Df Deviance Pr(>Chi)
1    1
2    6  5   7.4821   0.1872
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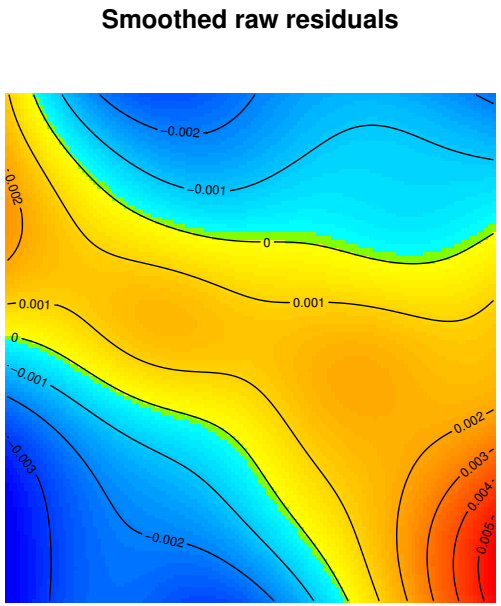
```

The p-value 0.19 exceeds 0.05 so the log-quadratic spatial trend is *not significant*.

Residuals

```
diagnose.ppm(fit0, which="smooth")
```



Spatial covariates

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- distance from location u to another feature

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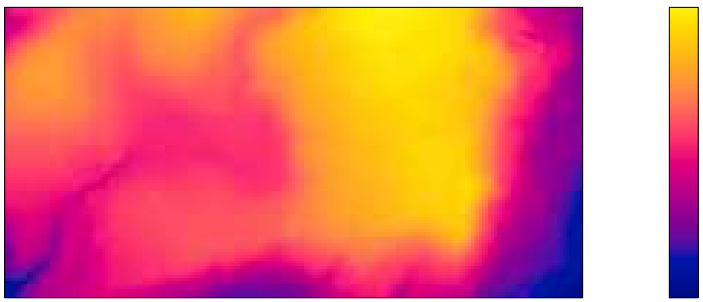
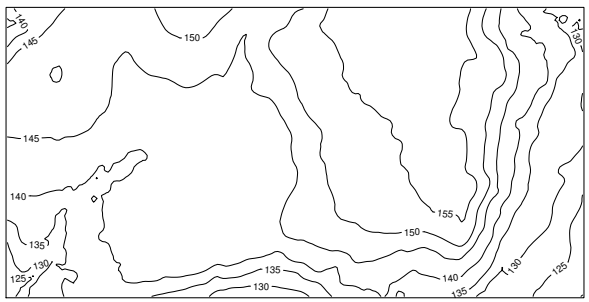
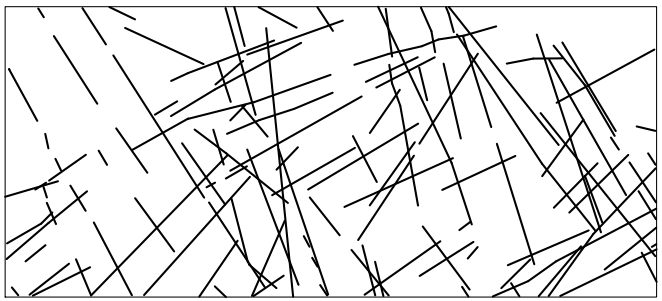




Covariates

Covariate data may be another *spatial pattern* such as another point pattern, or a line segment pattern:



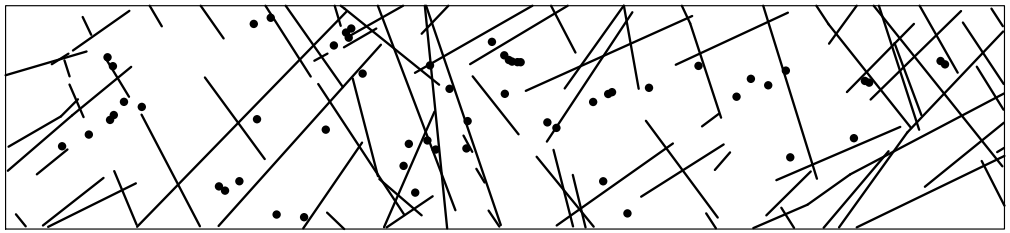
Covariate effects

For a point pattern dataset with covariate data, we typically

- investigate whether the intensity depends on the covariates
- allow for covariate effects on intensity before studying dependence between points

Example: Queensland copper data

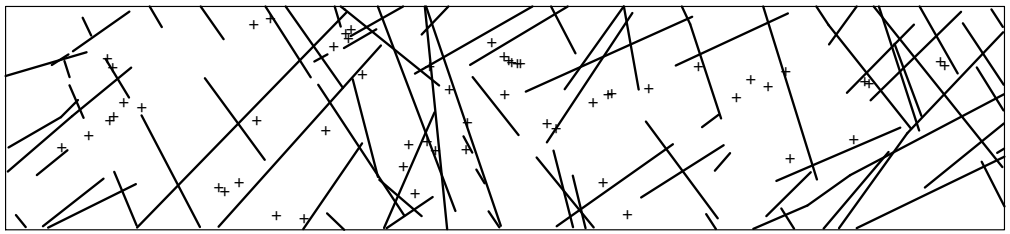
A intensive mineralogical survey yields a map of copper deposits (essentially pointlike at this scale) and geological faults (straight lines). The faults can easily be observed from satellites, but the copper deposits are hard to find.



Main question: whether the faults are 'predictive' for copper deposits (e.g. copper less/more likely to be found near faults).

Copper data

```
data(copper)
P <- copper$SouthPoints
Y <- copper$SouthLines
plot(P)
plot(Y, add=TRUE)
```



Copper data

For analysis, we need a value $Z(u)$ defined at each location u.

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Example: $Z(u) =$ distance from u to nearest line.

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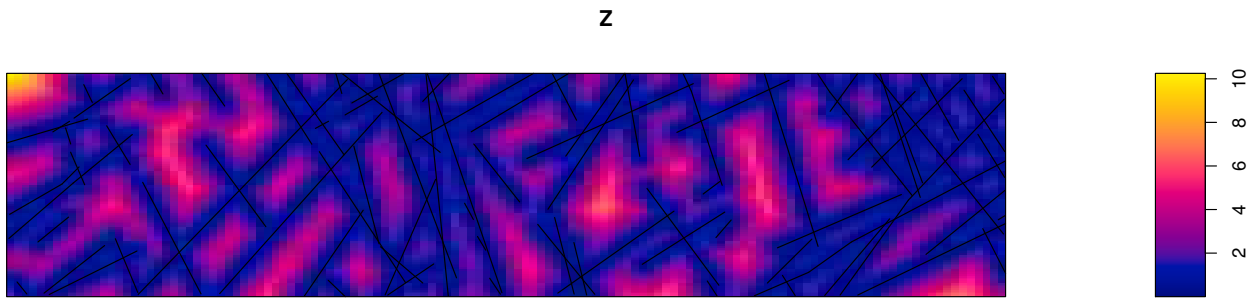
Example: $Z(u) =$ distance from u to nearest line.

```
Z <- distmap(Y)
plot(Z)
```



Lurking variable plot

We want to determine whether intensity depends on a spatial covariate Z.

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Plot $C(z)$ against z, where $C(z)$ = fraction of data points x_i for which $Z(x_i) \leq z$.

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Also plot $C_0(z)$ against z, where $C_0(z) =$ fraction of area of study region where $Z(u) \leq z$.

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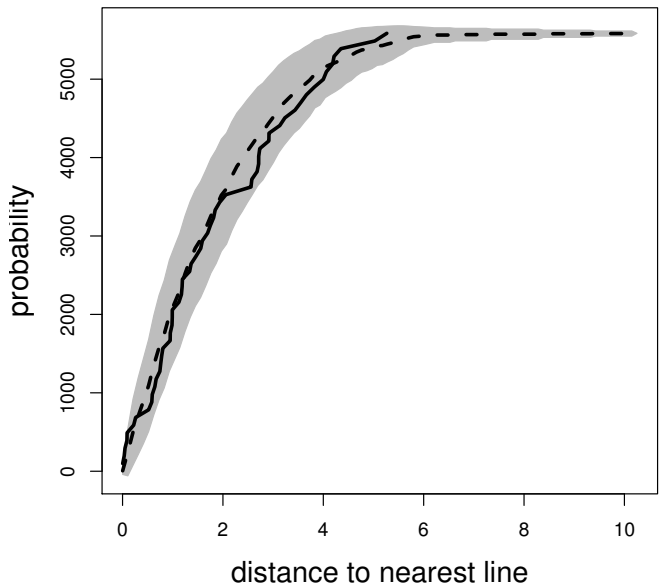
```
lurking(ppm(P), Z)
```

Lurking variable plot

We want to determine whether intensity depends on a spatial covariate Z.
Plot $C(z)$ against z, where $C(z)$ = fraction of data points x_i for which $Z(x_i) \leq z$.
Also plot $C_0(z)$ against z, where $C_0(z) =$ fraction of area of study region where $Z(u) \leq z$.

```
lurking(ppm(P), Z)
```



Kolmogorov-Smirnov test

Formal test of agreement between $C(z)$ and $C_0(z)$.

Kolmogorov-Smirnov test

Formal test of agreement between $C(z)$ and $C_0(z)$.

```
> kstest(P, Z)

        Spatial Kolmogorov-Smirnov test of CSR

data:  covariate 'Z' evaluated at points of 'P'
         and transformed to uniform distribution under CSR
D = 0.1163, p-value = 0.3939
alternative hypothesis: two-sided
```

Copper data

```
Z <- distmap(Y)
ppm(P ~ Z)
```

Fits the model

$$\log \lambda(u) = \beta_0 + \beta_1 Z(u)$$

where $Z(u)$ is the distance from u to the nearest line segment.

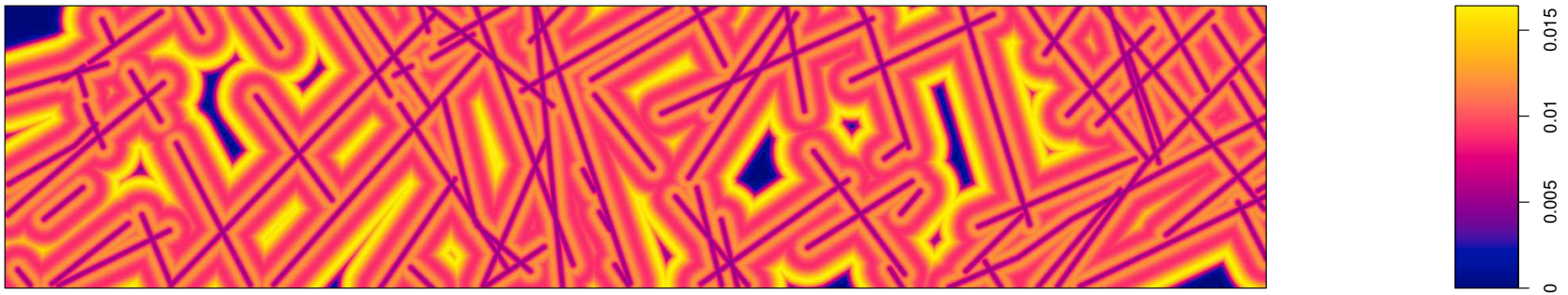
Copper data

```
Z <- distmap(Y)
ppm(P ~ polynom(Z,5))
```

fits a model in which $\log \lambda(u)$ is a 5th order polynomial function of $Z(u)$.

Copper data

```
fit <- ppm(P ~polynom(Z,5))
plot(predict(fit))
```

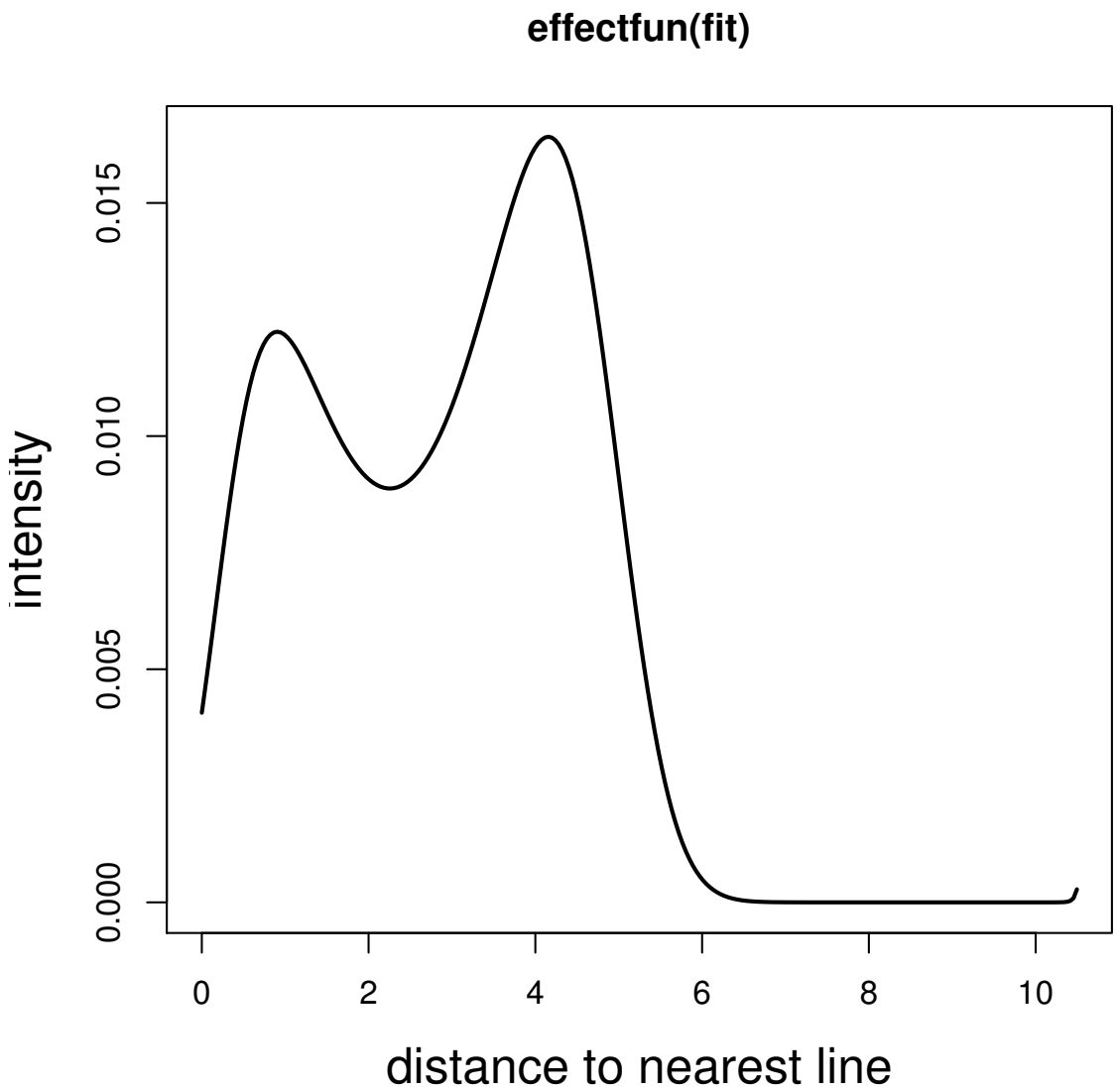


Copper data

```
plot(effectfun(fit))
```

plots fitted curve of λ against Z.

Copper data


effectfun(fit)
intensity
0.000
0.005
0.010
0.015
0
2
4
6
8
10
distance to nearest line

Likelihood ratio test

```
fit0 <- ppm(P ~1)
fit1  <- ppm(P ~polynom(Z,5))
anova(fit0, fit1, test="Chi")
```

Likelihood ratio test

```
  fit0 <- ppm(P ~1)
  fit1  <- ppm(P ~polynom(Z,5))
  anova(fit0, fit1, test="Chi")
Analysis of Deviance Table

Model 1: ~1                                                 Poisson
Model 2: ~Z + I(Z^2) + I(Z^3) + I(Z^4) + I(Z^5)  Poisson
  Npar Df Deviance Pr(>Chi)
1    1
2    6  5   3.6476   0.6012
```

Likelihood ratio test

```
  fit0 <- ppm(P ~1)
  fit1  <- ppm(P ~polynom(Z,5))
  anova(fit0, fit1, test="Chi")
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Model 1: ~1                                                Poisson
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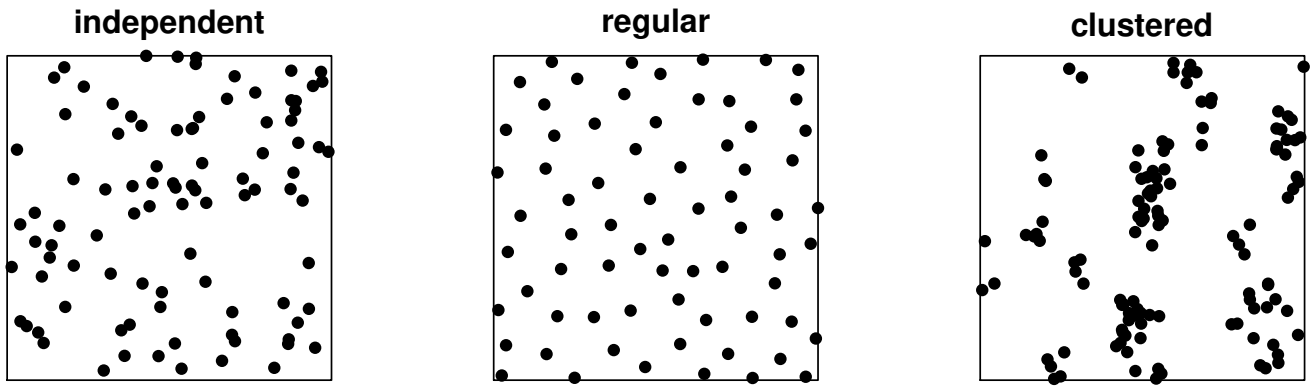
  Npar Df Deviance Pr(>Chi)
1    1
2    6  5   3.6476   0.6012
```

The p-value 0.81 exceeds 0.05 so the 5th order polynomial is *not significant*.

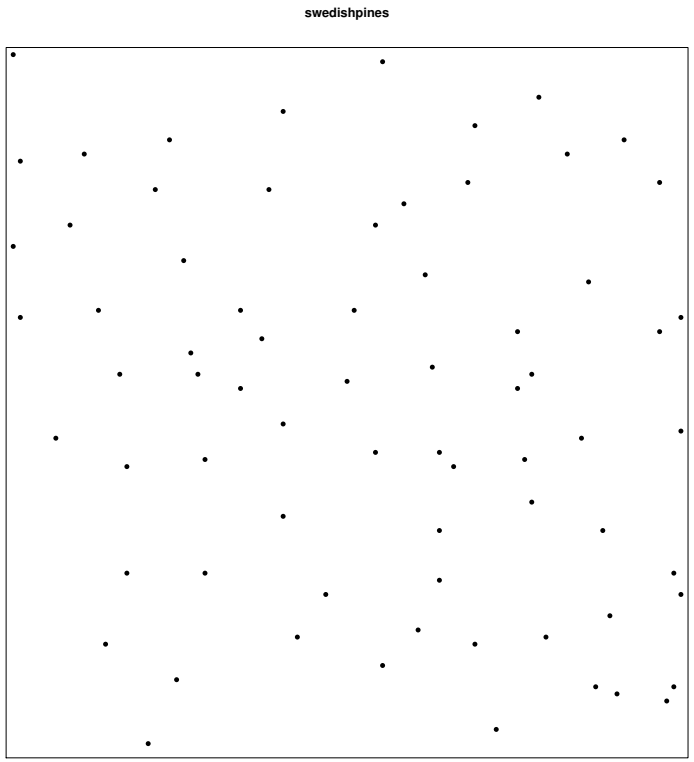
Interaction

'**Interpoint interaction**' is stochastic dependence between the points in a point pattern. Usually we expect dependence to be strongest between points that are close to one another.



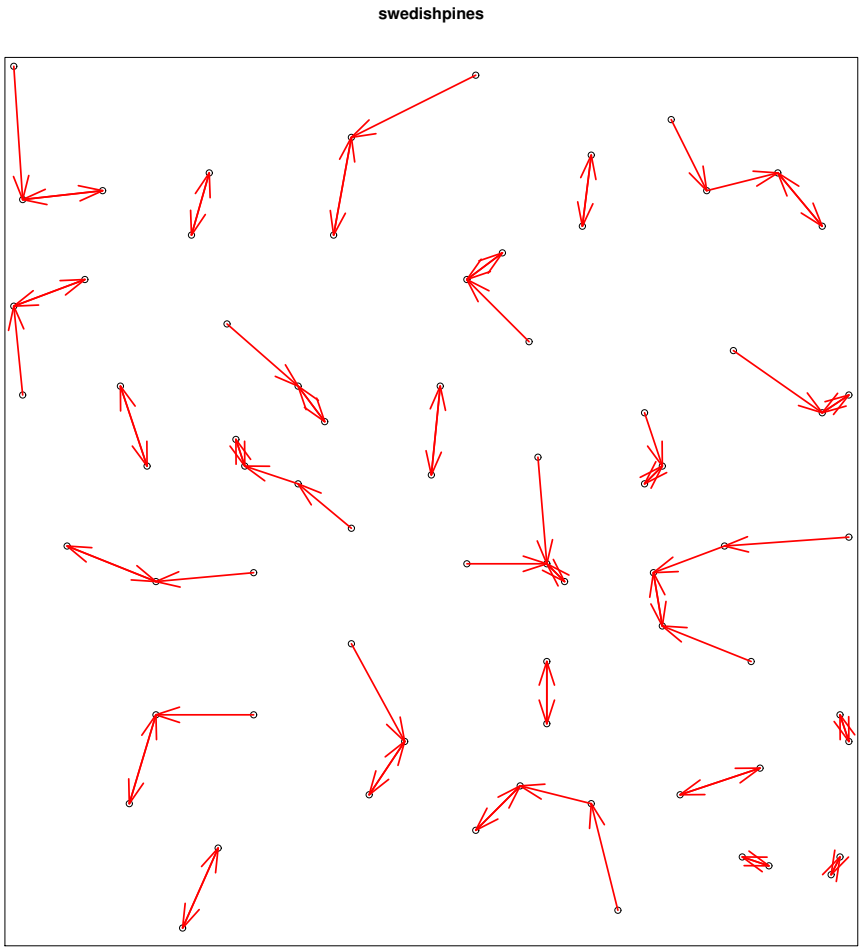
Example

Example: spacing between points in Swedish Pines data



Example

nearest neighbour distance = distance from a given point to the nearest other point



Example

Summary approach:

Example

Summary approach:

1. calculate average nearest-neighbour distance

Example

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2. divide by the value expected for a completely random pattern.

Clark & Evans (1954)

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Clark & Evans (1954)

```
> mean(nndist(swedishpines))
[1] 7.90754
> clarkevans(swedishpines)
   naive Donnelly      cdf
1.360082 1.291069 1.322862
```

Example

Summary approach:

1. calculate average nearest-neighbour distance
2. divide by the value expected for a completely random pattern.

Clark & Evans (1954)

```
> mean(nndist(swedishpines))
[1] 7.90754
> clarkevans(swedishpines)
   naive Donnelly      cdf
1.360082 1.291069 1.322862
```

Value greater than 1 suggests a regular pattern.

Example

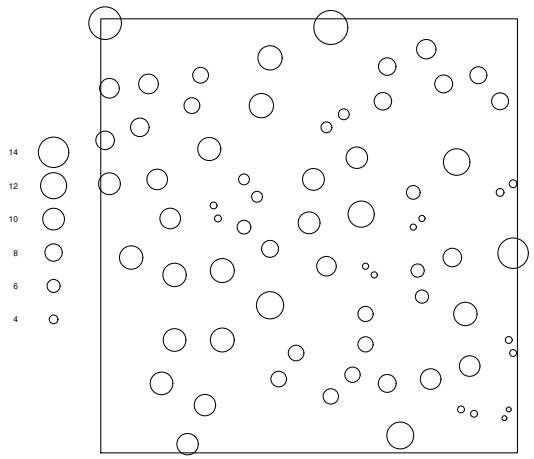
Exploratory approach:

Example

Exploratory approach:

- plot NND for each point

```
P <- swedishpines
marks(P) <- nndist(P)
plot(P, markscale=0.5)
```



Example

Exploratory approach:

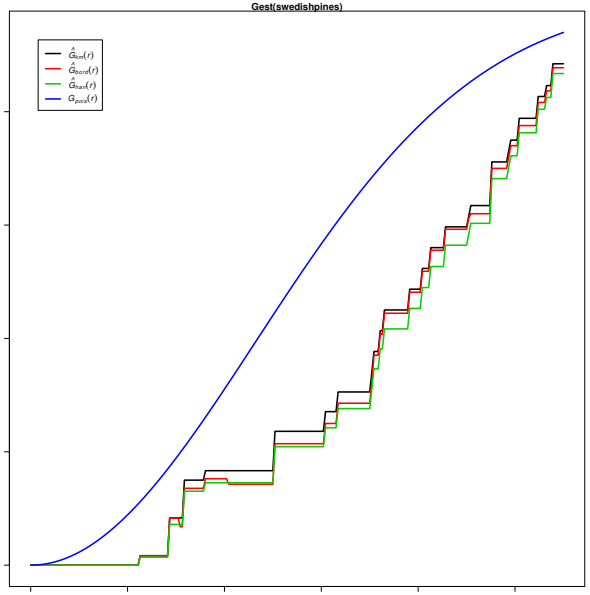
- plot NND for each point

Example

Exploratory approach:

- plot NND for each point
- look at empirical distribution of NND's

```
plot(Gest(swedishpines))
```



Example

Modelling approach:

Example

Modelling approach:

- Fit a stochastic model to the point pattern, with likelihood based on the NND's.

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- Fit a stochastic model to the point pattern, with likelihood based on the NND's.

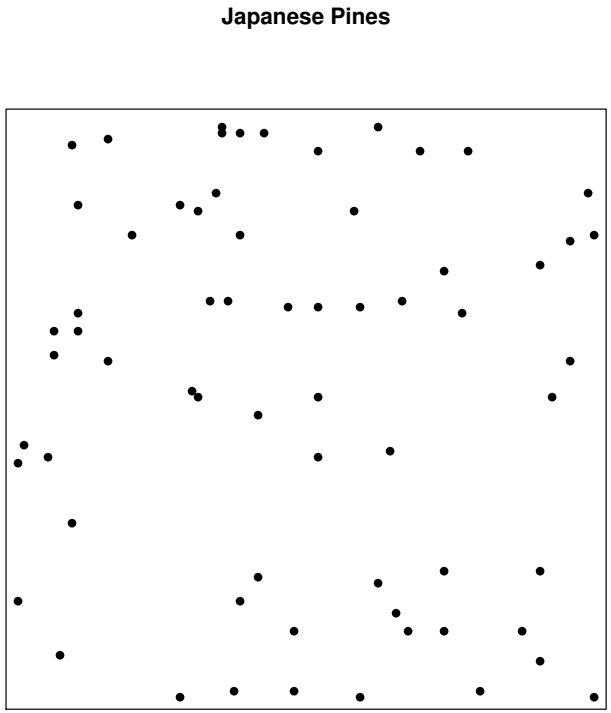
```
> ppm(P ~1, Geyer(4,1))

Stationary Geyer saturation process
First order term:
      beta
0.00971209
Fitted interaction parameter gamma: 0.6335
```

Example: Japanese pines

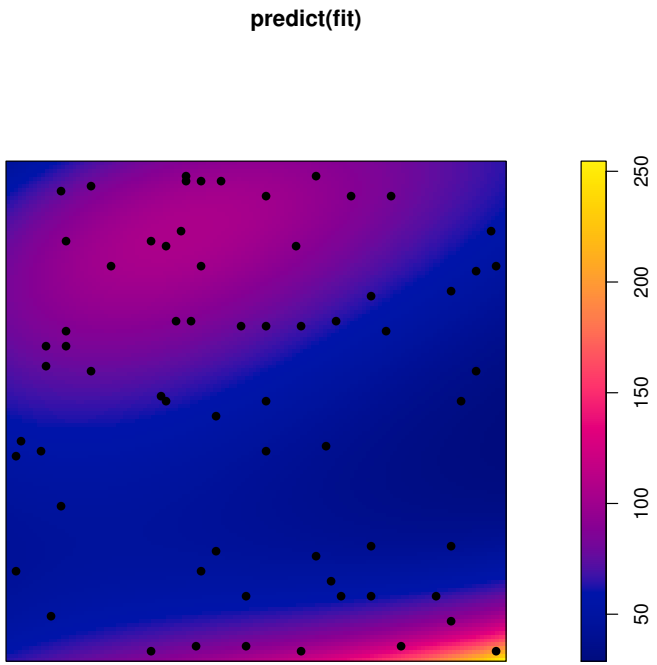
Locations of 65 saplings of Japanese pine in a 5.7×5.7 metre square sampling region in a natural stand.

```
data(japanesepines)
J <- japanesepines
plot(J)
```



Japanese Pines

```
fit <- ppm(J ~polynom(x,y,3))
plot(predict(fit))
plot(J, add=TRUE)
```

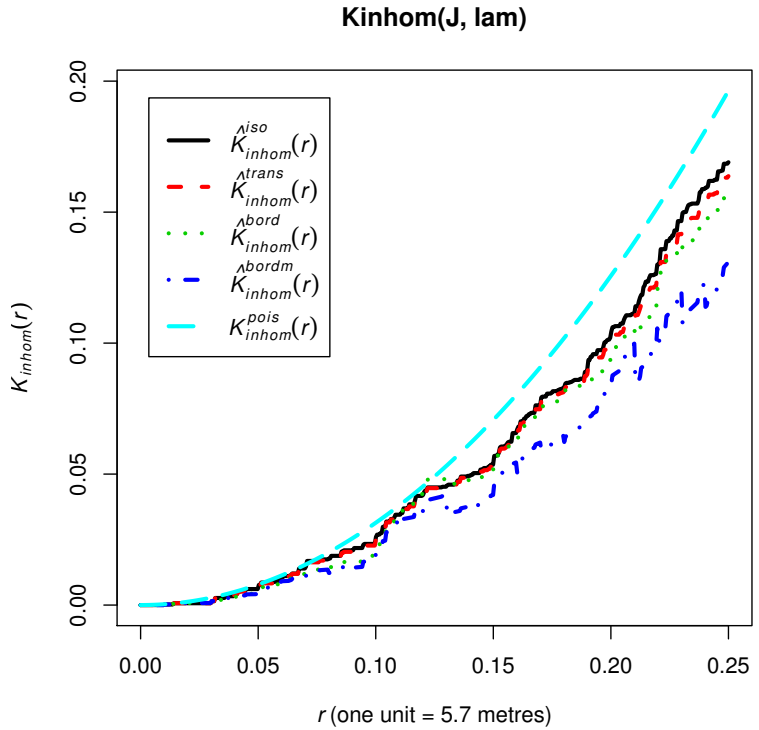


Adjusting for inhomogeneity

If the intensity function $\lambda(u)$ is known, or estimated from data, then some statistics can be adjusted by counting each data point x_i with a weight $w_i = 1/\lambda(x_i)$.

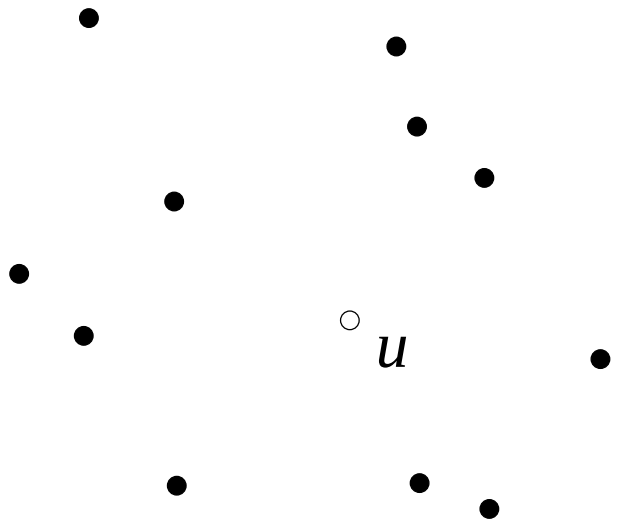
Inhomogeneous K-function

```
lam <- predict(fit)
plot(Kinhom(J, lam))
```



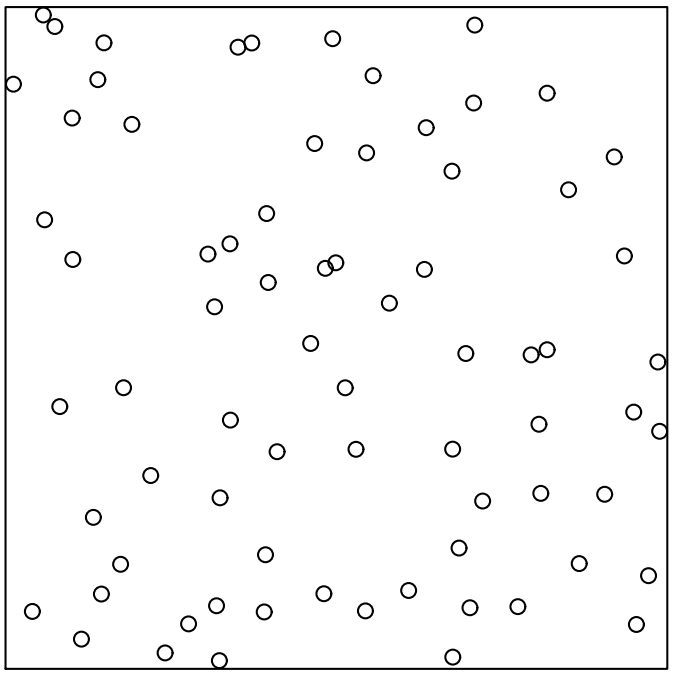
Conditional intensity

A point process model can also be defined through its *conditional intensity* $\lambda(u \mid \mathbf{x})$.
This is essentially the conditional probability of finding a point of the process at the location u, given complete information about the rest of the process $\mathbf{x}$.

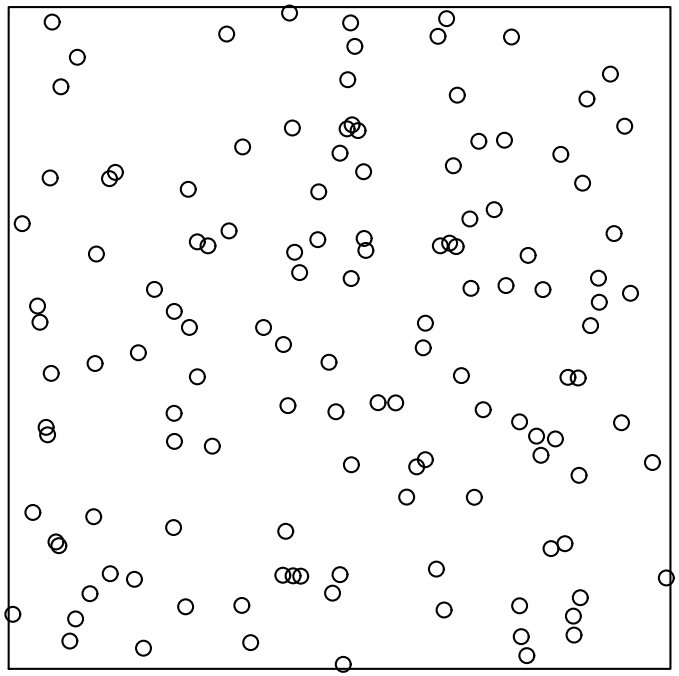


Strauss process

Strauss($\gamma = 0.2$)



Strauss($\gamma = 0.7$)



Fitting Gibbs models

The command `ppm` will also fit Gibbs models, using the technique of 'maximum pseudolikelihood'.

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```
data(swedishpines)
ppm(swedishpines ~1, Strauss(r=7))
```

Fitting Gibbs models

The command `ppm` will also fit Gibbs models, using the technique of 'maximum pseudolikelihood'.

```
data(swedishpines)
ppm(swedishpines ~1, Strauss(r=7))

Stationary Strauss process

First order term:
      beta
0.02583902

Interaction: Strauss process
interaction distance:   7
Fitted interaction parameter gamma:     0.1841
```

Fitting Gibbs models

The model can include both spatial trend and interpoint interaction.

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```
data(japanesepines)
ppm(japanesepines ~polynom(x,y,3), Strauss(r=0.07))
```

Fitting Gibbs models

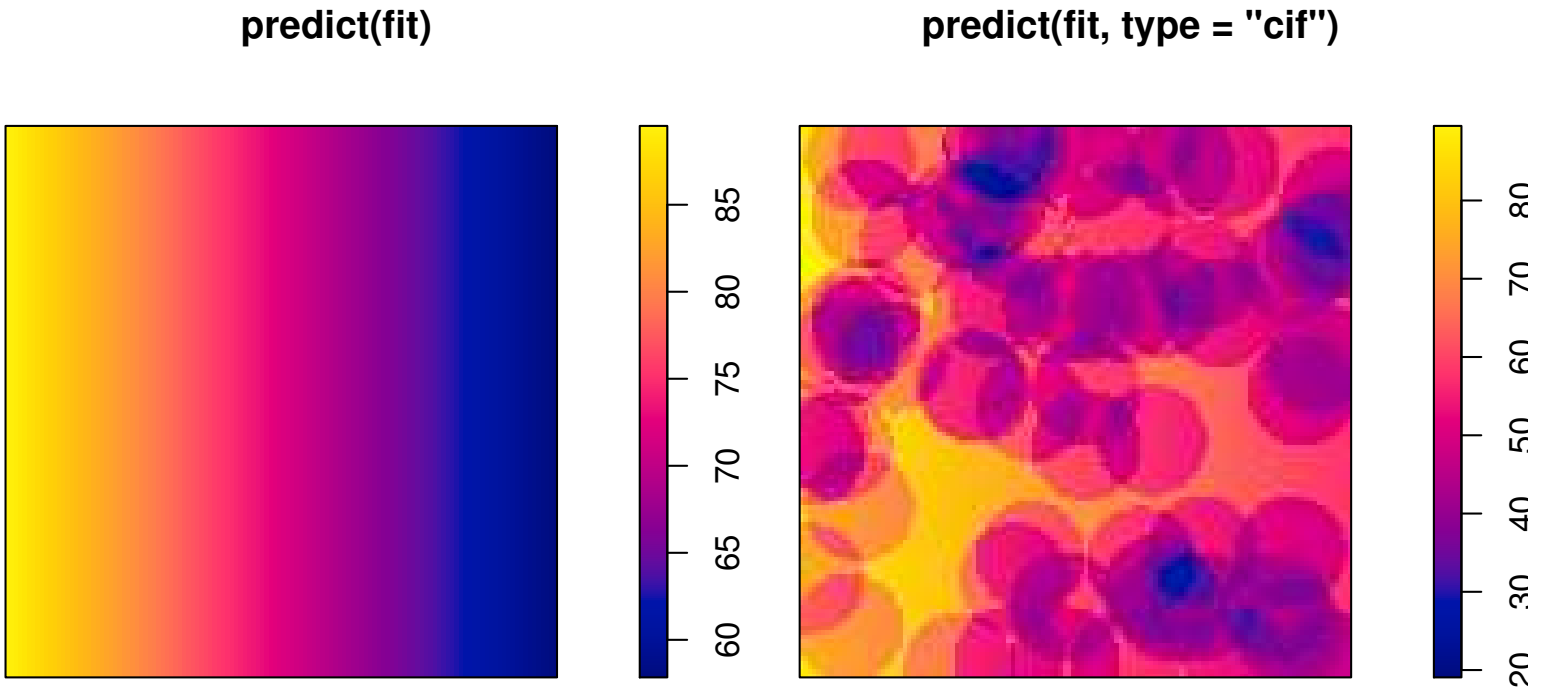
The model can include both spatial trend and interpoint interaction.

```
data(japanesepines)
ppm(japanesepines ~polynom(x,y,3), Strauss(r=0.07))
Nonstationary Strauss process
Trend formula: ~polynom(x, y, 3)
Fitted coefficients for trend formula:
            (Intercept)     polynom(x, y, 3)[x]     polynom(x, y, 3)[y]
              0.4925368              22.0485400              -9.1889134
  polynom(x, y, 3)[x^2]   polynom(x, y, 3)[x.y]   polynom(x, y, 3)[y^2]
             -14.6524958             -41.0222232              50.2099917
  polynom(x, y, 3)[x^3] polynom(x, y, 3)[x^2.y] polynom(x, y, 3)[x.y^2]
              3.4935300               5.4524828              23.9209323
  polynom(x, y, 3)[y^3]
             -38.3946389
Interaction: Strauss process
interaction distance:   0.1
Fitted interaction parameter gamma:     0.5323
```

Plotting a fitted model

When we `plot` or `predict` a fitted Gibbs model, the first order trend $\beta(u)$ and/or the conditional intensity $\lambda(u \mid \mathbf{x})$ are plotted.

```
fit <- ppm(japanesepines ~x, Strauss(r=0.1))
plot(predict(fit))
plot(predict(fit, type="cif"))
```



Simulating the fitted model

A fitted Gibbs model can be simulated automatically using the Metropolis-Hastings algorithm (which only requires the conditional intensity).

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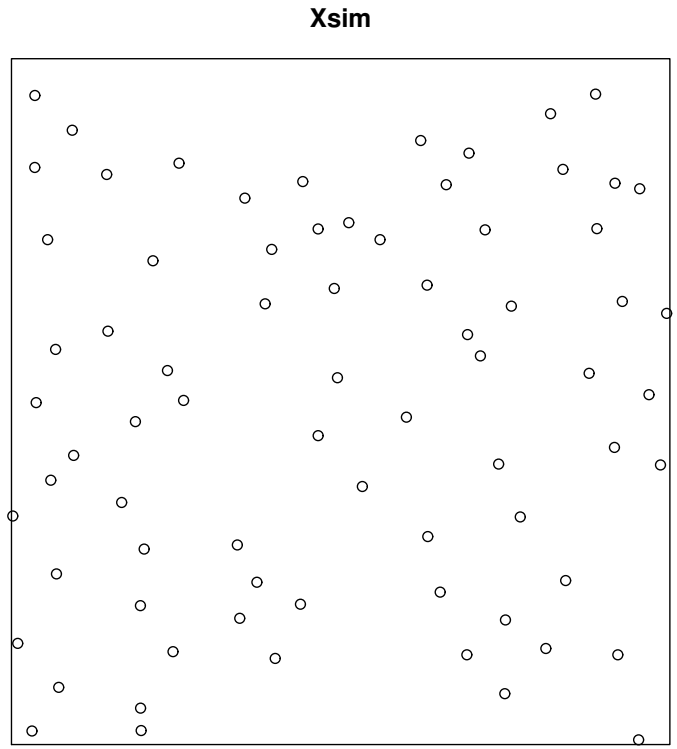
```
fit <- ppm(swedishpines ~1, Strauss(r=7))
Xsim <- simulate(fit)
plot(Xsim)
```

Simulating the fitted model

A fitted Gibbs model can be simulated automatically using the Metropolis-Hastings algorithm (which only requires the conditional intensity).

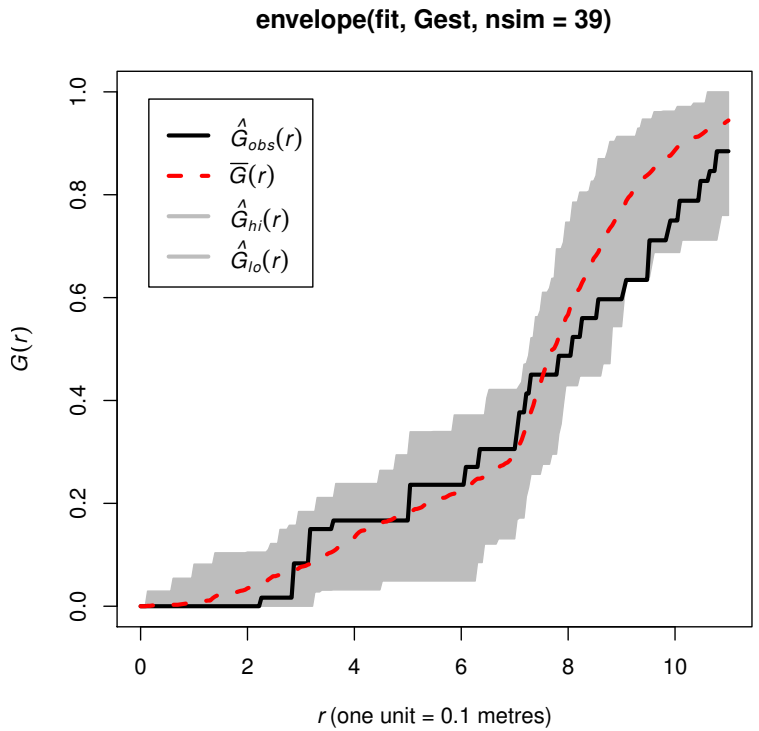
```
fit <- ppm(swedishpines ~1, Strauss(r=7))
Xsim <- simulate(fit)
plot(Xsim)
```



Simulation-based tests

Tests of goodness-of-fit can be performed by simulating from the fitted model.

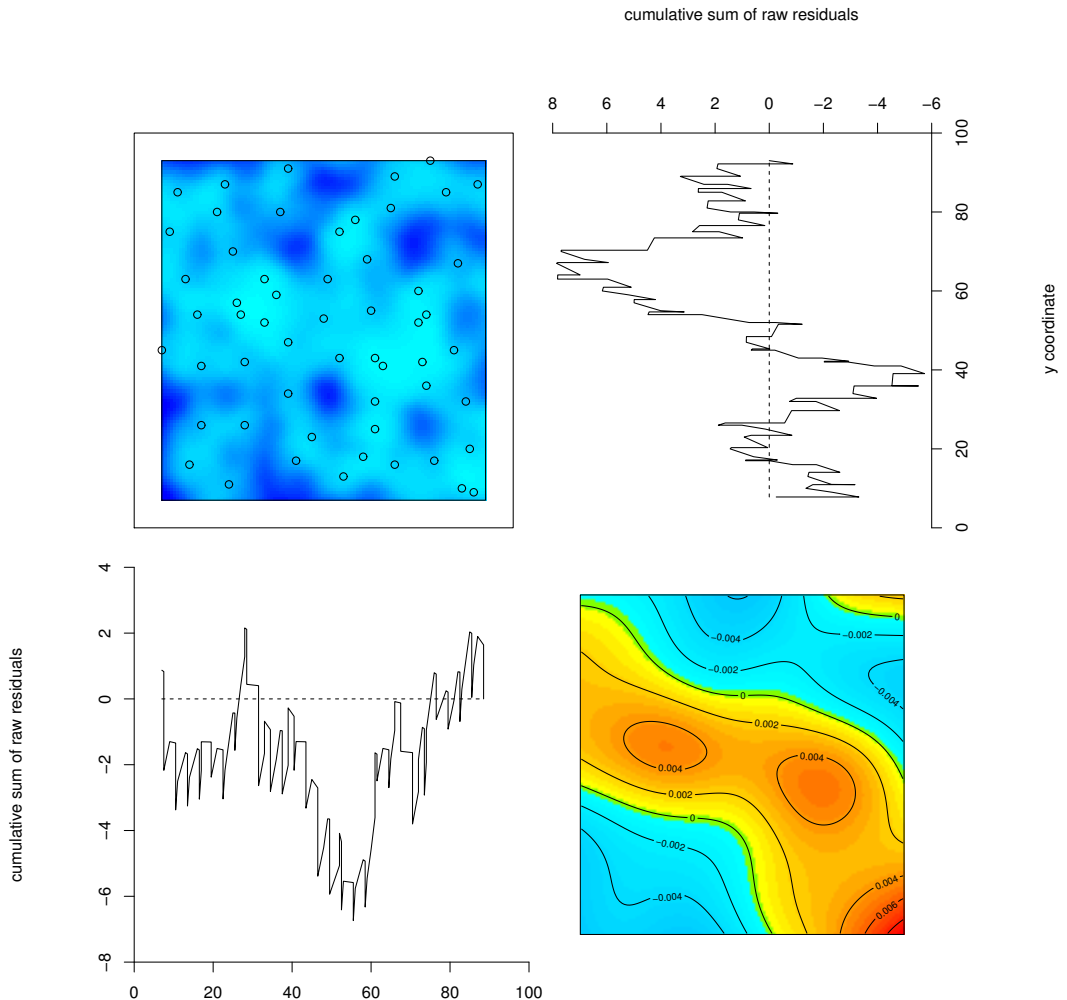
```
plot(envelope(fit, Gest, nsim=19))
```



Diagnostics

More powerful diagnostics are available.

```
diagnose.ppm(fit)
```



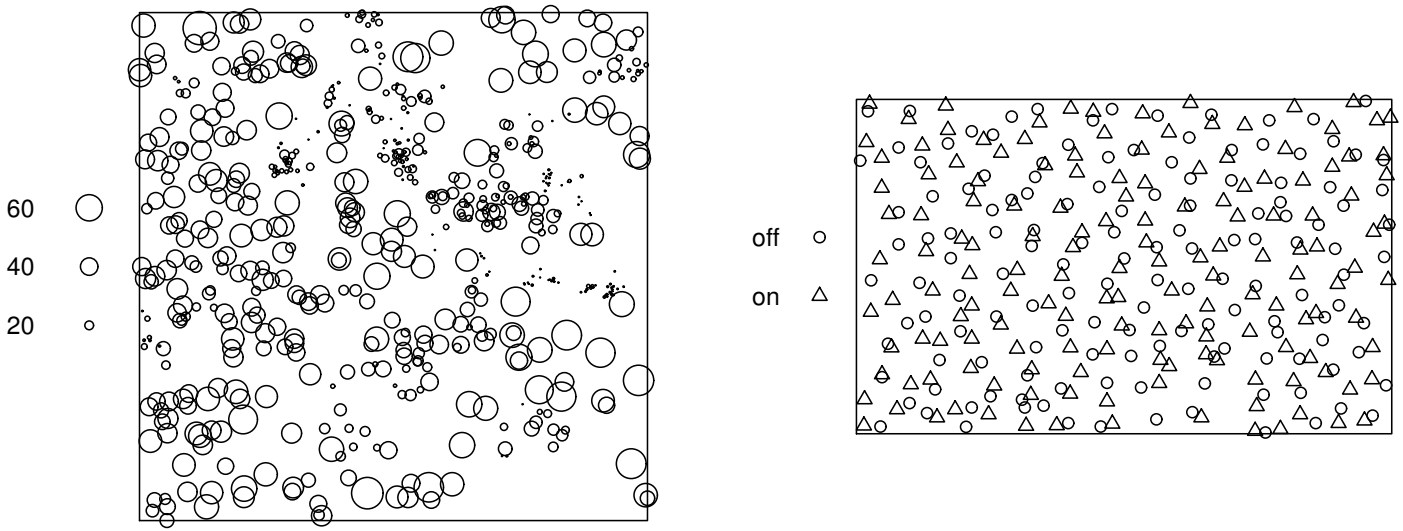
Marks

Marks

Each point in a spatial point pattern may carry additional information called a ‘mark’. It may be

a continuous variate: tree diameter, tree height

a categorical variate: label classifying the points into two or more different types (on/off, case/control, species, colour)



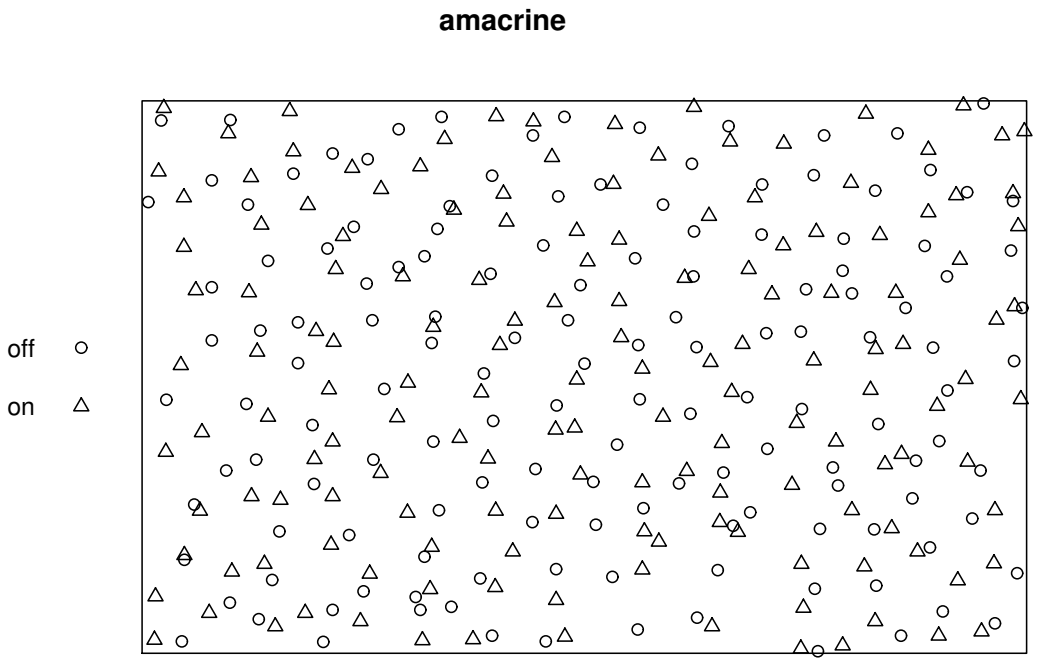
In `spatstat` version 1, the mark attached to each point must be a *single* value.

Categorical marks

Categorical marks

A point pattern with categorical marks is usually called “multi-type”.

```
> data(amacrine)
> amacrine
marked planar point pattern: 294 points
multitype, with levels = off    on
window: rectangle = [0, 1.6012] x [0, 1] units (one unit = 662 microns)
> plot(amacrine)
```



Multitype point patterns

```
summary(amacrine)
```

Multitype point patterns

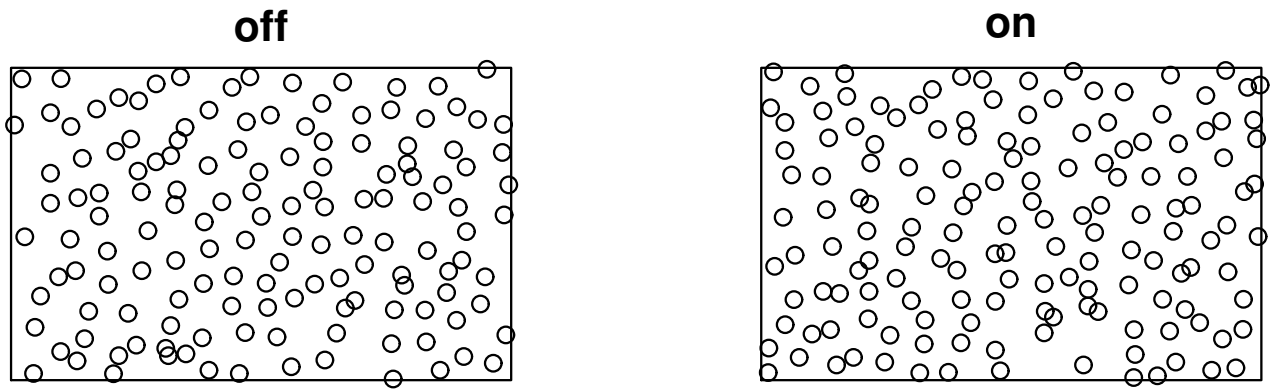
```
summary(amacrine)

Marked planar point pattern: 294 points
Average intensity 184 points per square unit (one unit = 662 microns)
Multitype:
    frequency proportion intensity
off       142      0.483      88.7
on        152      0.517      94.9

Window: rectangle = [0, 1.6012] x [0, 1] units
Window area =  1.60121 square units
Unit of length: 662 microns
```

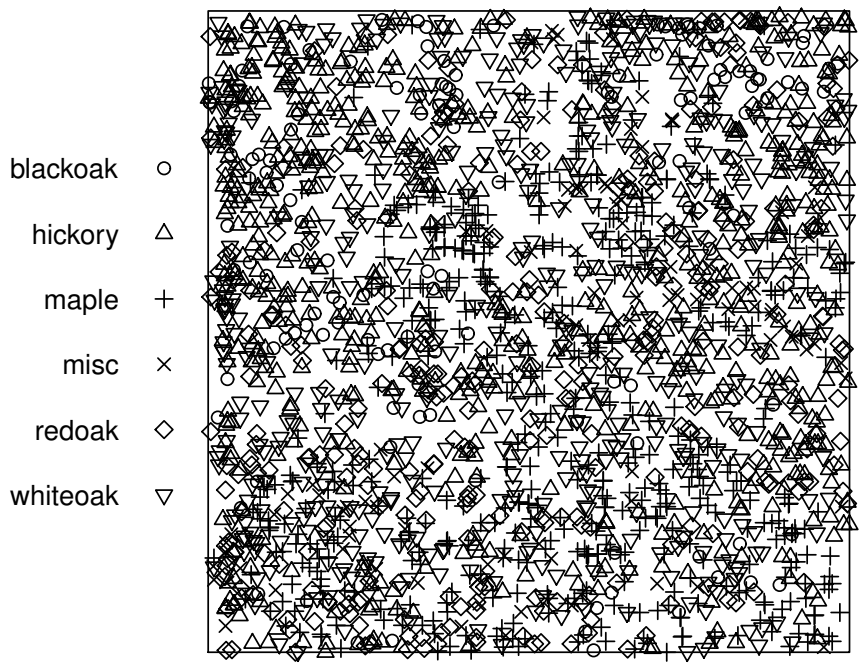
Intensity of multitype patterns

```
plot(split(amacrine))
```



Intensity of multitype patterns

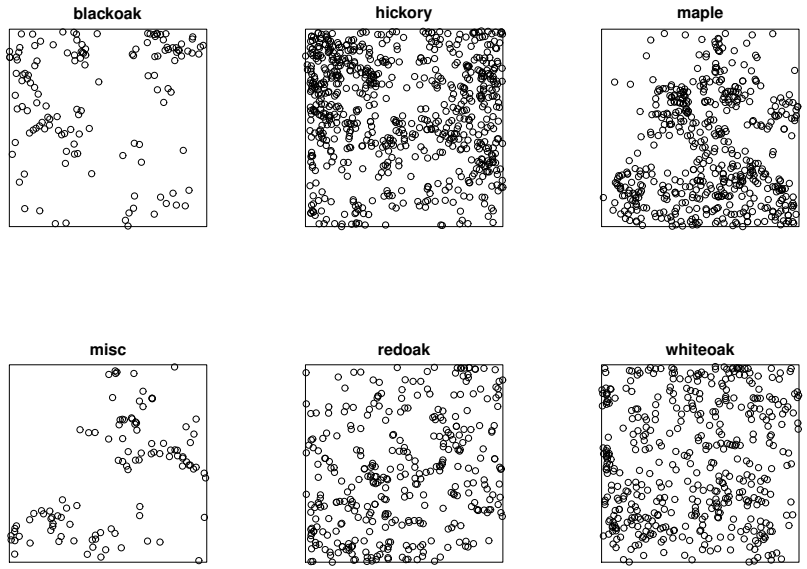
```
data(lansing)
summary(lansing)
plot(lansing)
```



Intensity of multitype patterns

"Segregation" occurs when the intensity depends on the mark (i.e. on the type of point).

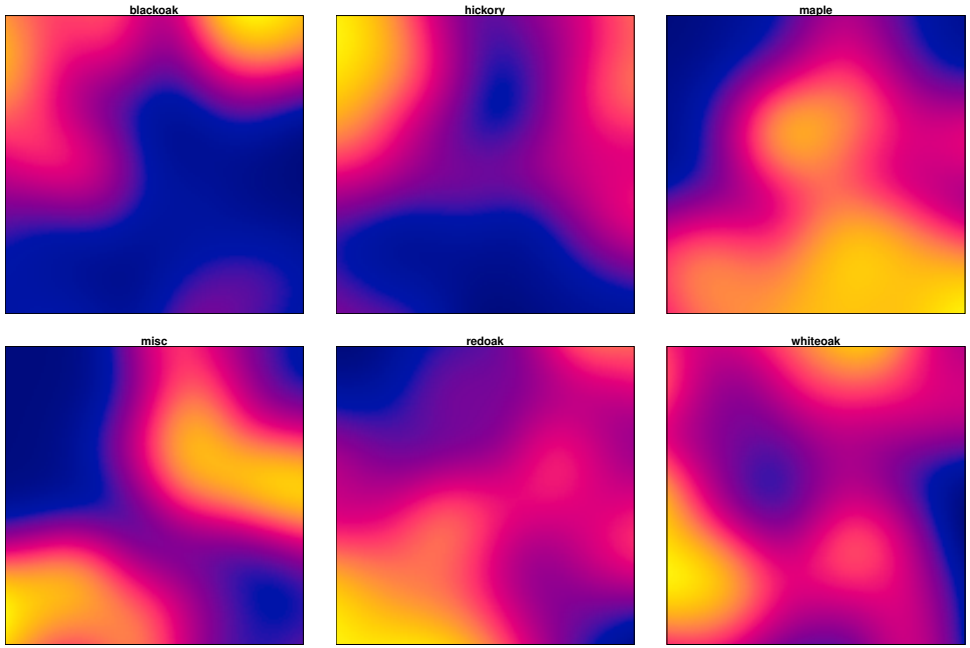
```
plot(split(lansing))
```



Intensity of multitype patterns

Let $\lambda(u, m)$ be the intensity function for points of type m at location u. This can be estimated by kernel smoothing the data points of type m.

```
plot(density(split(lansing)))
```



Segregation

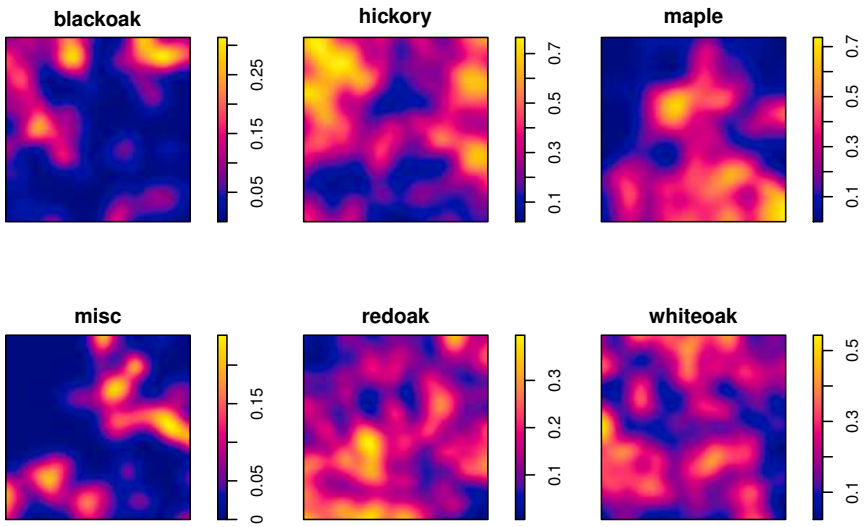
The probability that a point at location u has mark m is

$$p(m \mid u) = \frac{\lambda(u, m)}{\lambda(u)}$$

where $\lambda(u) = \sum_m \lambda(u, m)$ is the intensity function of points of all types.

Segregation

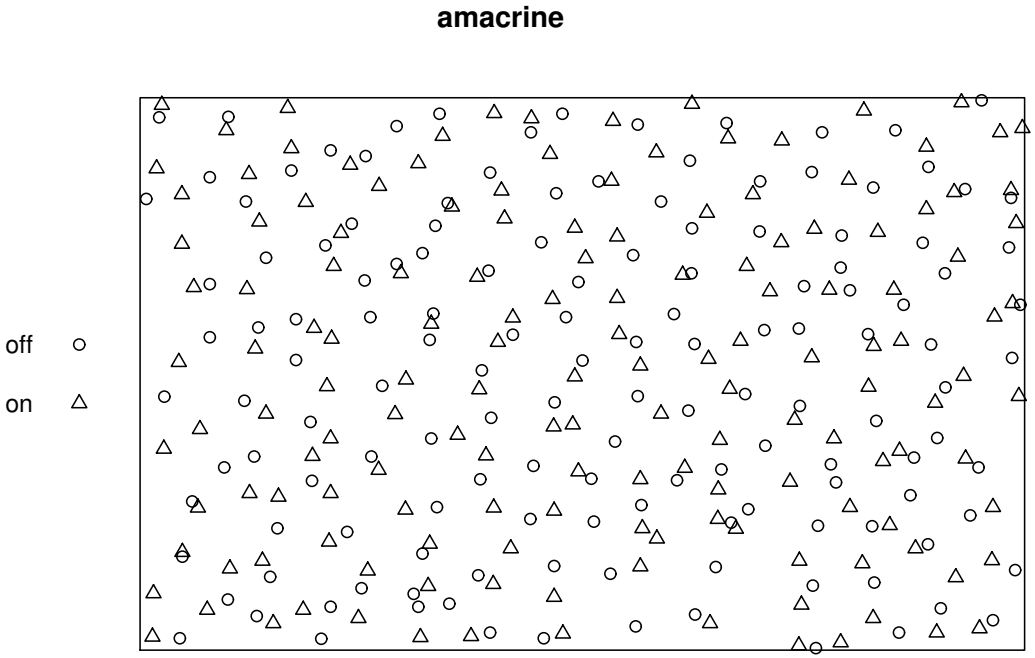
```
lansP <- relrisk(lansing)
plot(lansP)
```



Interaction between types

Interaction between types

In a multitype point pattern, there may be interaction between the points of *different* types, or between points of the *same* type.



Bivariate G-function

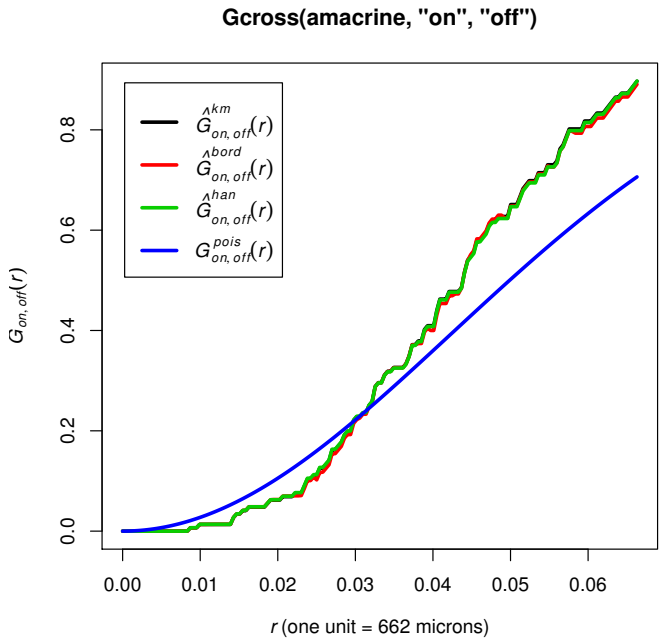
Assume the points of type i have uniform intensity λ_i, for all i.
For two given types i and j, the bivariate G-function G_{ij} is

$$G_{ij}(r) = P(R_{ij} \leq r)$$

where R_{ij} is the distance from a typical point of type i to the nearest point of type j.

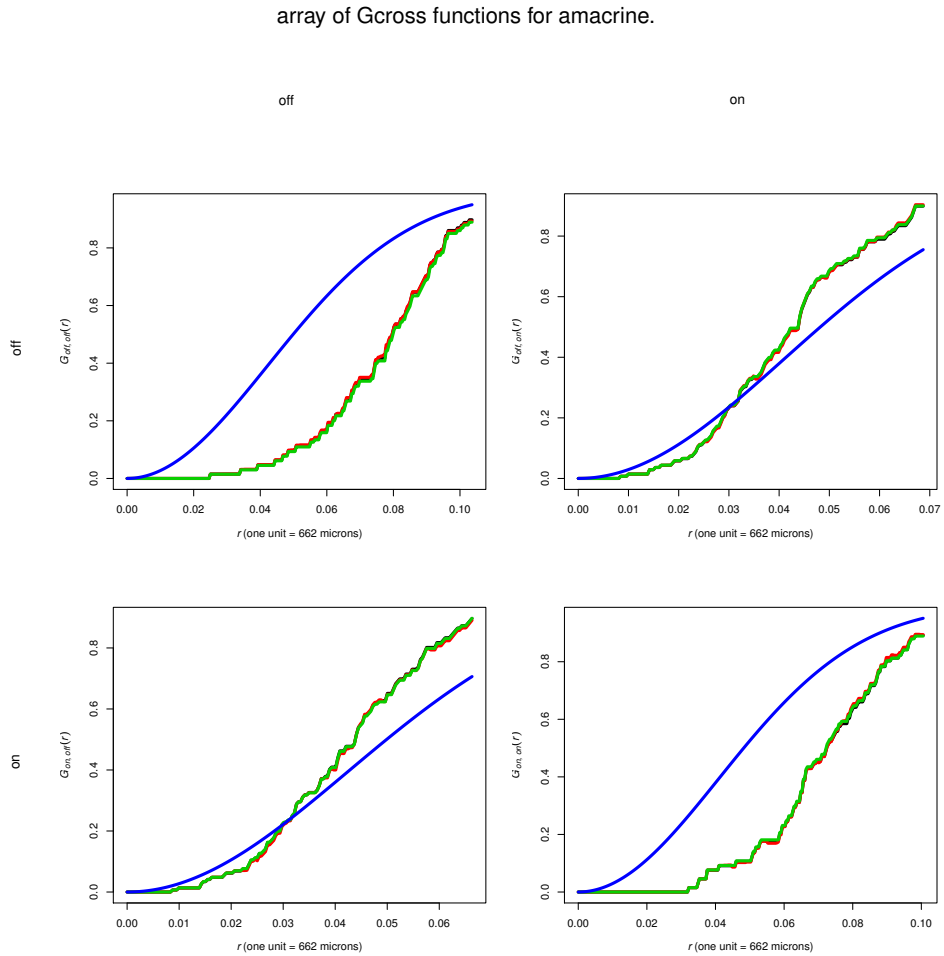
Bivariate G-function

```
plot(Gcross(amacrine, "on", "off"))
```



Bivariate G-function

```
plot(alltypes(amacrine, Gcross))
```



Fitting Poisson models

For a *multitype* point pattern:

COMMAND	INTERPRETATION

Fitting Poisson models

For a *multitype* point pattern:

COMMAND	INTERPRETATION
`ppm(X ~1)`	

Fitting Poisson models

For a *multitype* point pattern:

COMMAND	INTERPRETATION
`ppm(X ~1)`	$\log \lambda(u, m) = \beta$ constant.

Fitting Poisson models

For a *multitype* point pattern:

COMMAND	INTERPRETATION
`ppm(X ~1)`	$\log \lambda(u, m) = \beta$ constant. Equal intensity for points of each type.

Fitting Poisson models

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`ppm(X ~marks)`	

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`ppm(X ~marks)`	$\log \lambda(u, m) = \beta_m$

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`ppm(X ~marks + x)`	

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`ppm(X ~marks + x)`	$\log \lambda((x, y), m) = \beta_m + \alpha x$

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Fitting Poisson models

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`ppm(X ~marks + x + marks:x)`	

Fitting Poisson models

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`ppm(X ~1)`	$\log \lambda(u, m) = \beta$ constant. Equal intensity for points of each type.
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`ppm(X ~marks + x)`	$\log \lambda((x, y), m) = \beta_m + \alpha x$ Common spatial trend Different overall intensity for each type.
`ppm(X ~marks + x + marks:x)` `ppm(X ~marks * x)`	equivalent to

Fitting Poisson models

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`ppm(X ~marks + x + marks:x)` `ppm(X ~marks * x)`	equivalent to $\log \lambda((x, y), m) = \beta_m + \alpha_m x$

Fitting Poisson models

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`ppm(X ~marks + x + marks:x)` `ppm(X ~marks * x)`	equivalent to $\log \lambda((x, y), m) = \beta_m + \alpha_m x$ Different spatial trends for each type

Segregation test

Likelihood ratio test of segregation in Lansing Woods data:

Segregation test

Likelihood ratio test of segregation in Lansing Woods data:

```
fit0 <- ppm(lansing ~marks + polynom(x,y,3))
fit1 <- ppm(lansing ~marks * polynom(x,y,3))
anova(fit0, fit1, test="Chi")
```

Segregation test

Likelihood ratio test of segregation in Lansing Woods data:

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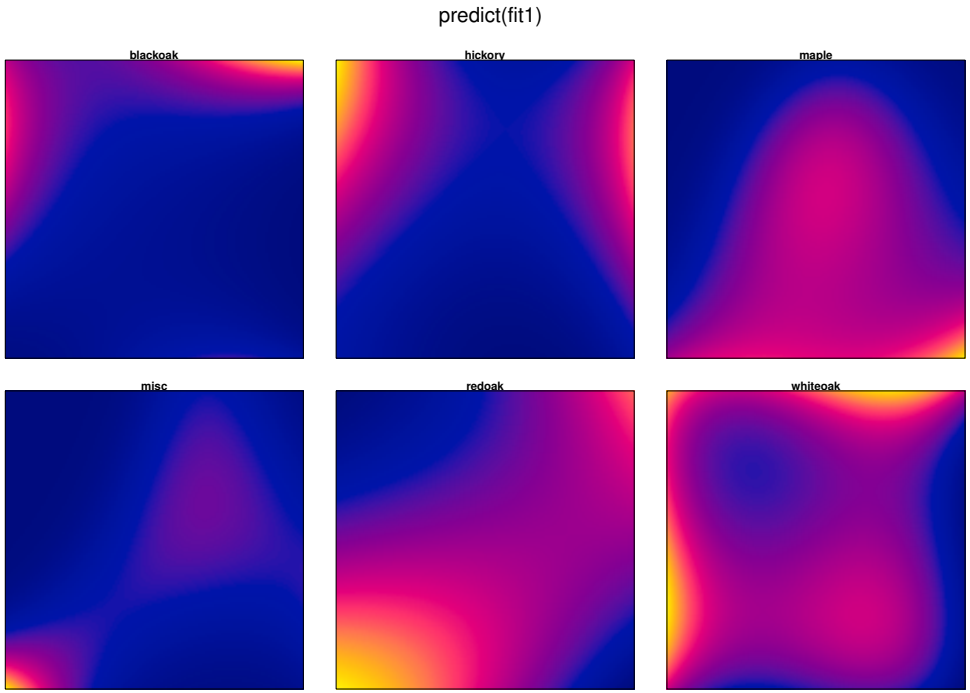
fit0 <- ppm(lansing ~marks + polynom(x,y,3))
fit1 <- ppm(lansing ~marks * polynom(x,y,3))
anova(fit0, fit1, test="Chi")
```

```
Analysis of Deviance Table

Model 1: ~marks + (x + y + I(x^2) + I(x * y) +
  I(y^2) + I(x^3) + I(x^2 * y) + I(x * y^2) + I(y^3))          Poisson
Model 2: ~marks * (x + y + I(x^2) + I(x * y) +
  I(y^2) + I(x^3) + I(x^2 * y) + I(x * y^2) + I(y^3))          Poisson
  Npar Df Deviance  Pr(>Chi)
1   15
2   60 45   612.57 < 2.2e-16 ***
```

Fitted intensity

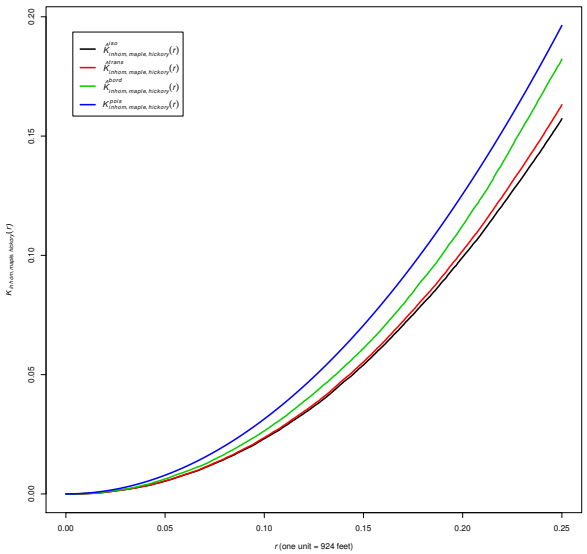
```
fit1 <- ppm(lansing ~marks * polynom(x,y,3))
plot(predict(fit1))
```



Inhomogeneous multitype K function

Inhomogeneous K function can be generalised to inhomogeneous multitype K function.

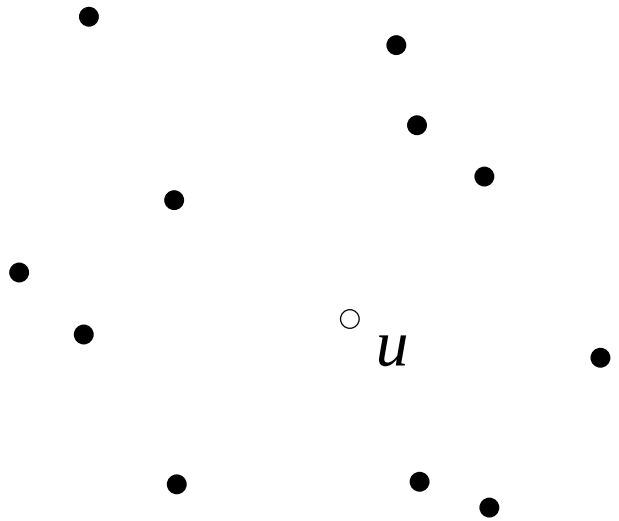
```
fit1 <- ppm(lansing ~marks * polynom(x,y,3))
lamb <- predict(fit1)
plot(Kcross.inhom(lansing, "maple","hickory",
      lamb$markmaple, lamb$markhickory))
```



Multitype Gibbs models

Conditional intensity

The conditional intensity $\lambda(u, m \mid \mathbf{x})$ is essentially the conditional probability of finding a point of type m at location u, given complete information about the rest of the process $\mathbf{x}$.



Multitype Strauss process

```
 >    ppm(amacrine ~marks, Strauss(r=0.04))

Stationary Strauss process

First order terms:
beta_off  beta_on
156.0724 162.1160

Interaction: Strauss process
interaction distance:   0.04
Fitted interaction parameter gamma:     0.4464
```

Multitype Strauss process

```
> rad <- matrix(c(0.03, 0.04, 0.04, 0.02), 2, 2)
> ppm(amacrine ~ marks,
        MultiStrauss(radii=rad,types=c("off", "on")))

Stationary Multitype Strauss process

First order terms:
beta_off  beta_on
120.2312 108.8413

Interaction radii:
     off   on
off 0.03 0.04
on  0.04 0.02
Fitted interaction parameters gamma_ij:
       off     on
off 0.0619 0.8786
on  0.8786 0.0000
```

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