Machine_Learning

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22/07/2017

Machine Learning

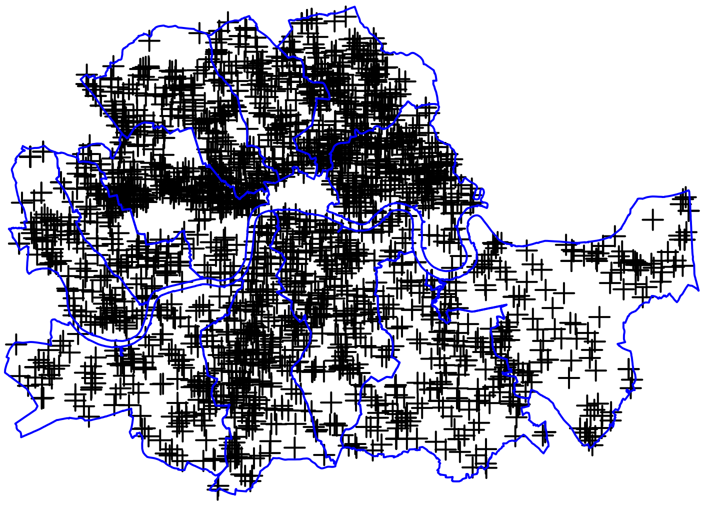
Spatial analysis using point pattern analysis

Point pattern analysis is the evaluation of the pattern, or distribution, of a set of points on a surface. It can refer to the actual spatial or temporal location of these points or also include data from point sources.

The first steps are to load addional libraries `raster`, `gridExtra`, `spatstat` and `tidyverse`, then ensure that the same coordinate reference system (CRS) is used for both crime points and borough polygons - WGS84 was selected. The crime data for the inner boroughs for 2016 is filtered to include only burglaries in November 2016 as this method did not function with the full unfiltered dataset. The coordinates for the crime locations and boroughs need to be obtained, these are then plotted to check the process has worked. The bulk of the workflow in this section is based on.

```
library(raster)
library(gridExtra)
library(spatstat)
library(tidyverse)
library(dplyr)
library(ggplot2)
library(readr)
library(ggplot2)
library(lubridate)
library(scales)
library(rgdal)
library(broom)
library(classInt)
library(KernSmooth)
library(RColorBrewer)
library(leaflet)
library(sp)
library(maptools)
library(rgdal)
library(rgeos)

boroughs <- readOGR(dsn = "statistical-gis-boundaries-london/ESRI", "London_Borough_Excluding_MHW", ver

wgs.84       <- "+proj=longlat +datum=WGS84"
central <- boroughs %>%
  subset(NAME %in% c('Camden','Greenwich','Hackney', 'Hammersmith and Fulham','Islington', 'Kensington a

crime16 <- readRDS('crime16.rds')
burglary16.2 <- crime16 %>%
  filter(crime_type == "burglary") %>%
  filter(month == 11)

coords <- SpatialPoints(burglary16.2[,c("longitude","latitude")])
burglary16.2 <- SpatialPointsDataFrame(coords, burglary16.2)
```

```r
proj4string(burglary16.2) <- CRS(wgs.84)
burglary16.2 <- spTransform(burglary16.2, CRS(proj4string(central)))
plot(burglary16.2)
plot(central, border = "blue", add = T)
```



```r
xy <- coordinates(burglary16.2)
dim(xy)
```

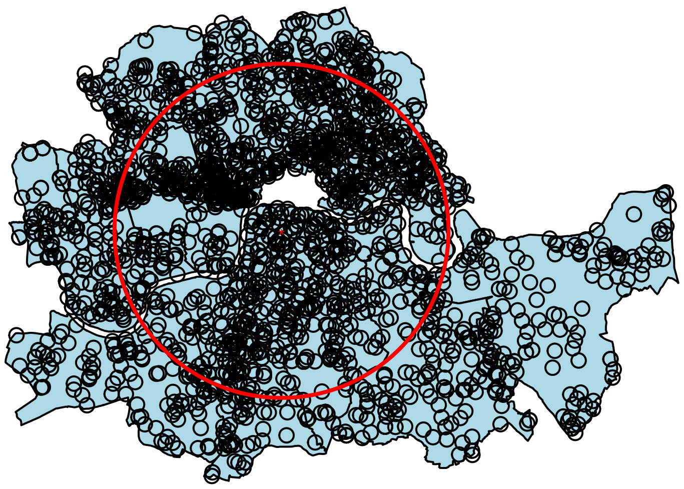
```
## [1] 2414    2
```

```r
xy <- unique(xy)
dim(xy)
```

```
## [1] 1925    2
```

Duplicated crime locations must be removed for this technique to be correctly executed. Due to the ‘map points’ previously mentioned, many locations are duplications. When these are removed the dataset reduces from 2414 to 1925 unique sets of coordinates. Basic statistics are calculated, mean centre and standard distance for the crime locations, and plotted with a summary circle created by dividing the circle into 360 points and computing the bearing in radians. The crime location density is then calculated as 6.4 per km2.

```r
mc <- apply(xy, 2, mean)
sd <- sqrt(sum((xy[,1] - mc[1])^2 + (xy[,2] - mc[2])^2) / nrow(xy))
plot(central, col='light blue')
points(burglary16.2) #The city of London gap is very clear
points(cbind(mc[1], mc[2]), pch='*', col='red', cex=0.5)
bearing <- 1:360 * pi/180
cx <- mc[1] + sd * cos(bearing)
cy <- mc[2] + sd * sin(bearing)
circle <- cbind(cx, cy)
lines(circle, col='red', lwd=2)
```



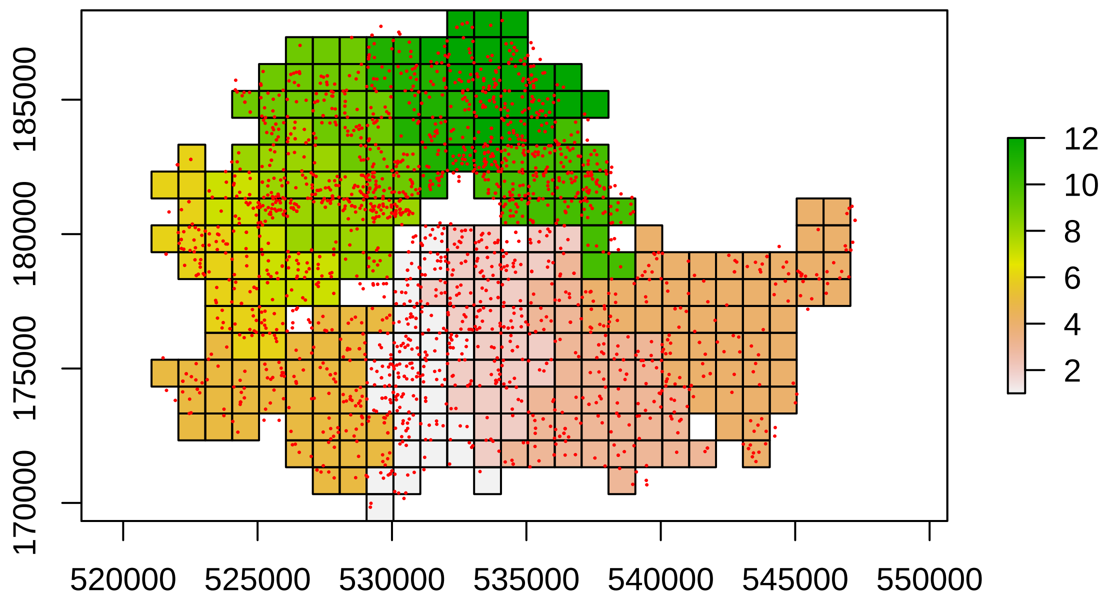
```r
CityArea <- sum(area(central))
dens <- nrow(xy) / CityArea
```

Quadrat analysis was then applied whereby you divide your study area into subsections of equal size, count the frequency of points in each subsection and then calculate the frequency of points in each subsection. Extent for the raster is obtained from the borough polygon, and then an arbitrary resolution is assigned of 1000. Cells are identified which lie within the borough boundary, then rasterize is used to determine frequency of locations in each quadrat.

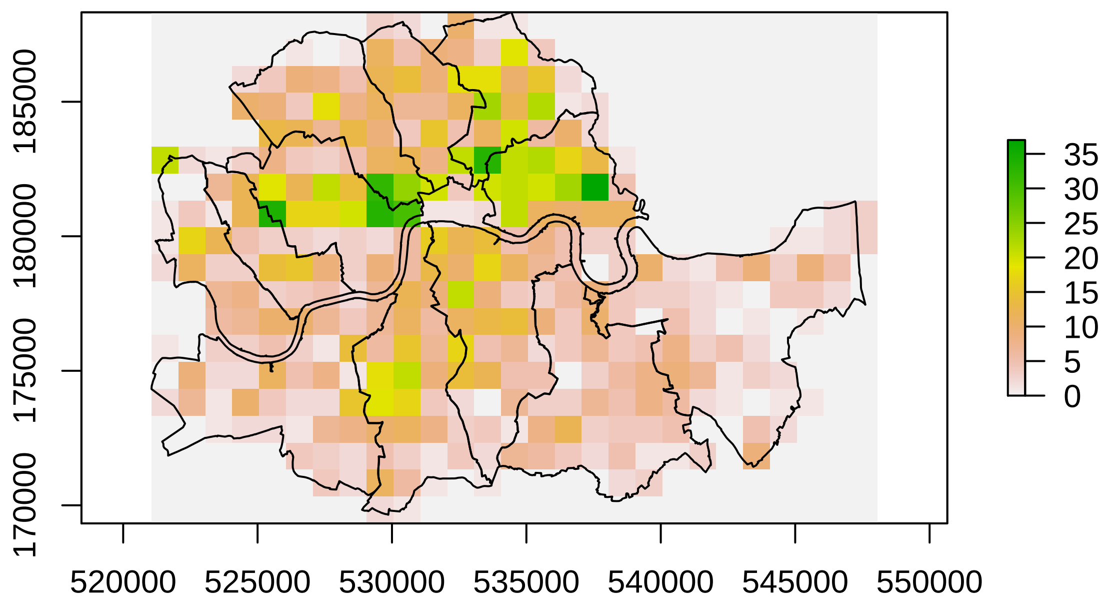
```r
r <- raster(central)
res(r) <- 1000
r
```

```
## class       : RasterLayer
## dimensions  : 19, 27, 513  (nrow, ncol, ncell)
## resolution  : 1000, 1000  (x, y)
## extent      : 521054.9, 548054.9, 169327.4, 188327.4  (xmin, xmax, ymin, ymax)
## coord. ref. : +proj=tmerc +lat_0=49 +lon_0=-2 +k=0.999601272 +x_0=400000 +y_0=-100000 +datum=OSGB36
```

```r
r <- rasterize(central, r)
plot(r)
quads <- as(r, 'SpatialPolygons')
plot(quads, add=TRUE)
points(burglary16.2, col='red',cex=0.1)
```



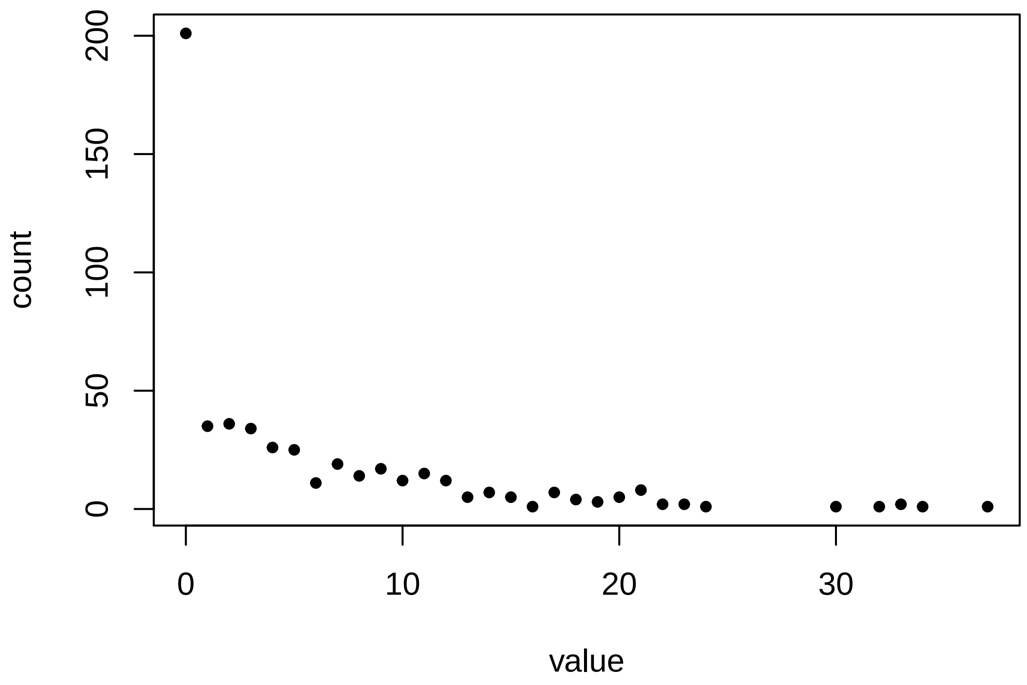
```r
nc <- rasterize(coordinates(burglary16.2), r, fun='count', background=0)
plot(nc)
plot(central, add=TRUE)
```



```r
f <- freq(nc, useNA='no')
head(f)
```

```
##      value count
## [1,]     0   201
## [2,]     1    35
## [3,]     2    36
## [4,]     3    34
## [5,]     4    26
## [6,]     5    25
```

```r
plot(f, pch=20)
```



```r
quadrats <- sum(f[,2])
cases <- sum(f[,1] * f[,2])
mu <- cases / quadrats
mu
```

```
## [1] 4.705653
```

```r
ff <- data.frame(f)
colnames(ff) <- c('K', 'X')
ff$Kmu <- ff$K - mu
ff$Kmu2 <- ff$Kmu^2
ff$XKmu2 <- ff$Kmu2 * ff$X
head(ff)
```

```
##   K   X       Kmu        Kmu2       XKmu2
## 1 0 201 -4.705653 22.14317036 4450.777242
## 2 1  35 -3.705653 13.73186432  480.615251
## 3 2  36 -2.705653  7.32055827  263.540098
## 4 3  34 -1.705653  2.90925223   98.914576
## 5 4  26 -0.705653  0.49794619   12.946601
## 6 5  25  0.294347  0.08664014    2.166004
```

This indicates that the 201 quadrats with no crime locations at all include the null ones that lie outside the boroughs. There are 5 quadrats with over 30 different crime locations. The average number of crime locations per quadrat is 4.7. Statistics can also be calculated using the quadrat data.

```r
s2 <- sum(ff$XKmu2) / (sum(ff$X)-1)
VMR <- s2 / mu
```

The observed variance s2 is 41.5362375 and the variance to mean ratio (VMR) is 8.8268806. This is a unit-less statistic describing the spatial arrangement of points. In general stratified distributions ~ 0, random distributions = 1 and clustered distributions a VMR of above 1. This distribution is highly clustered.

Distance based measurements will be carried out requiring a planar coordinate based system. A `dist` object is created and then coerced to a matrix, the distances from each point to itself are removed. To get the minimum distance to another event `apply` can be used.

```
d <- dist(xy)
dm <- as.matrix(d)
dm[1:5, 1:5]
```

```
##          1         2         3         4         5
## 1    0.000 2328.9164 3490.7732 3418.9726 2069.8328
## 2 2328.916    0.0000 1171.4764 1120.9239  828.9643
## 3 3490.773 1171.4764    0.0000  155.9122 1798.5964
## 4 3418.973 1120.9239  155.9122    0.0000 1802.5113
## 5 2069.833  828.9643 1798.5964 1802.5113    0.0000
```

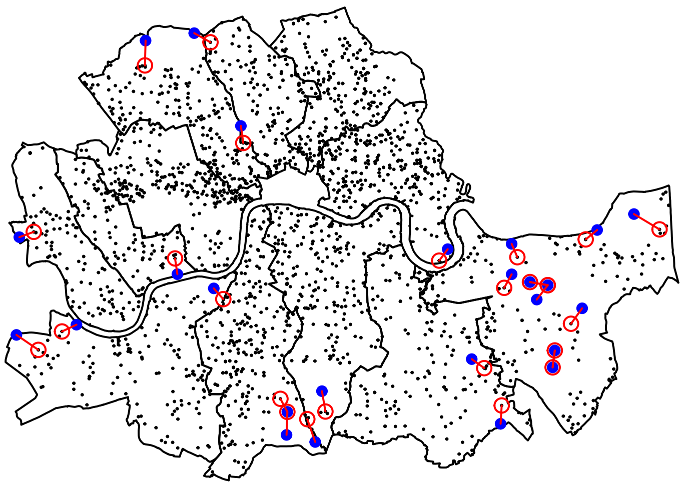
```
diag(dm) <- NA
dm[1:5, 1:5]
```

```
##          1         2         3         4         5
## 1       NA 2328.9164 3490.7732 3418.9726 2069.8328
## 2 2328.916        NA 1171.4764 1120.9239  828.9643
## 3 3490.773 1171.4764        NA  155.9122 1798.5964
## 4 3418.973 1120.9239  155.9122        NA 1802.5113
## 5 2069.833  828.9643 1798.5964 1802.5113        NA
```

```
dmin <- apply(dm, 1, min, na.rm=TRUE)
mdmin <- mean(dmin)
wdmin <- apply(dm, 1, which.min)
```

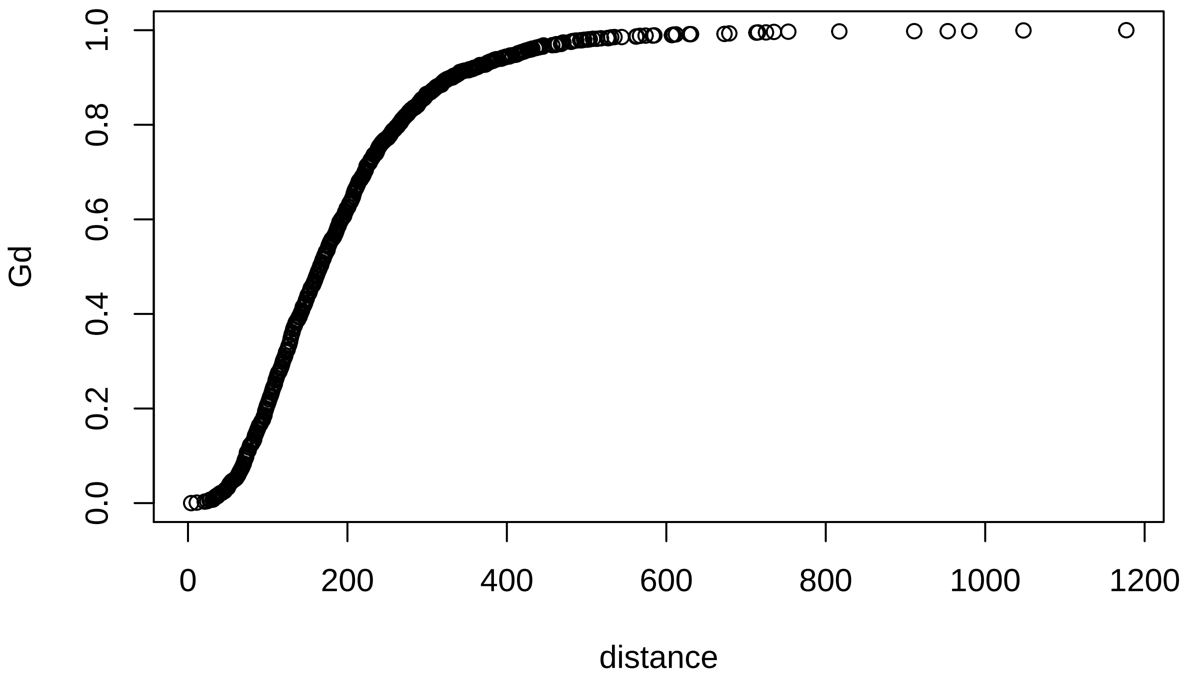
The mean nearest neighbour distance is 190.0353488 metres. The top 25 most isolated (from their nearest neighour) cases can be identified and plotted.

```
plot(central)
points(burglary16.2, cex=.1)
ord <- rev(order(dmin))
far25 <- ord[1:25]
neighbours <- wdmin[far25]
points(xy[far25, ], col='blue', pch=20)
points(xy[neighbours, ], col='red')

for (i in far25) {
  lines(rbind(xy[i, ], xy[wdmin[i], ]), col='red')
}
```

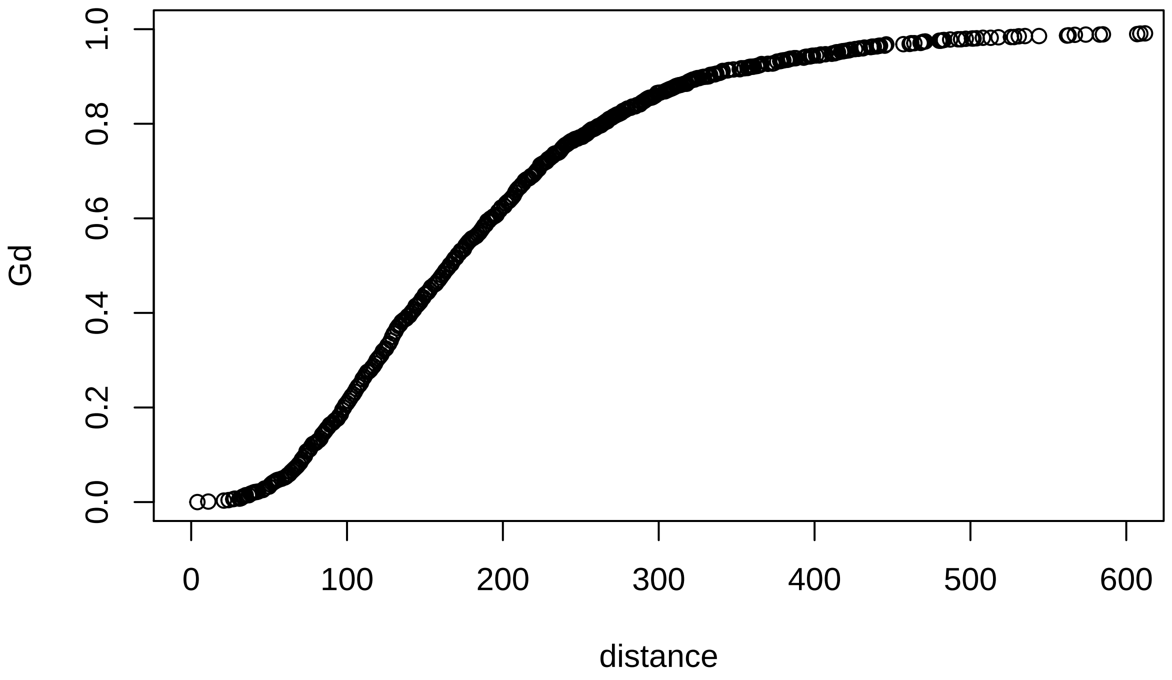


The G function is a cumulative frequency distribution of the nearest neighbor distance. It is the probability for a specified distance, that the nearest neighbor distance to another event in the pattern will be less than the specified distance. The maximum distance to a nearest neighbour is 1176.9604373 metres. The unique distances need to be calculated for the x-axis and how many cases there are with distances smaller than each x. These are then normalised between 0 and 1.

```
distance <- sort(unique(round(dmin)))
Gd <- sapply(distance, function(x) sum(dmin < x))
Gd <- Gd / length(dmin)
plot(distance, Gd)
```



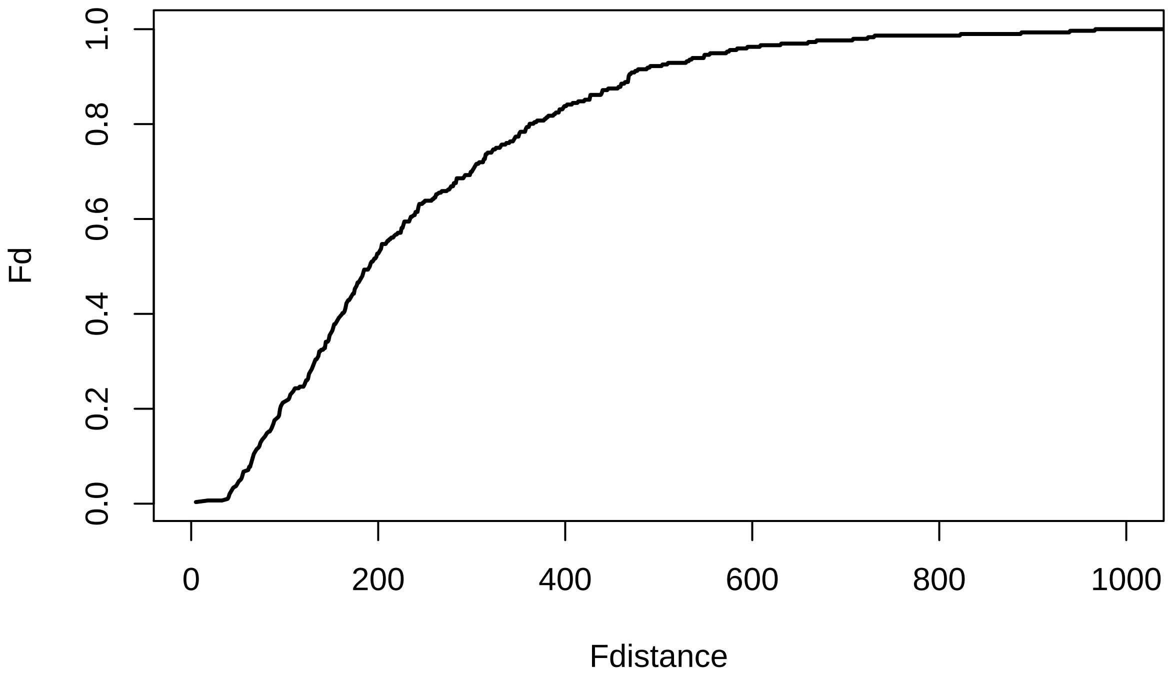
```
plot(distance, Gd, xlim=c(0,600))
```



With evenly-spaced events G(d) should rise gradually up to the distance at which most events are spaced, and then increase rapidly. For clustered events G(d) rises rapidly at short distances, and then levels off at larger d-values. The distribution is more clustered than evenly spaced.

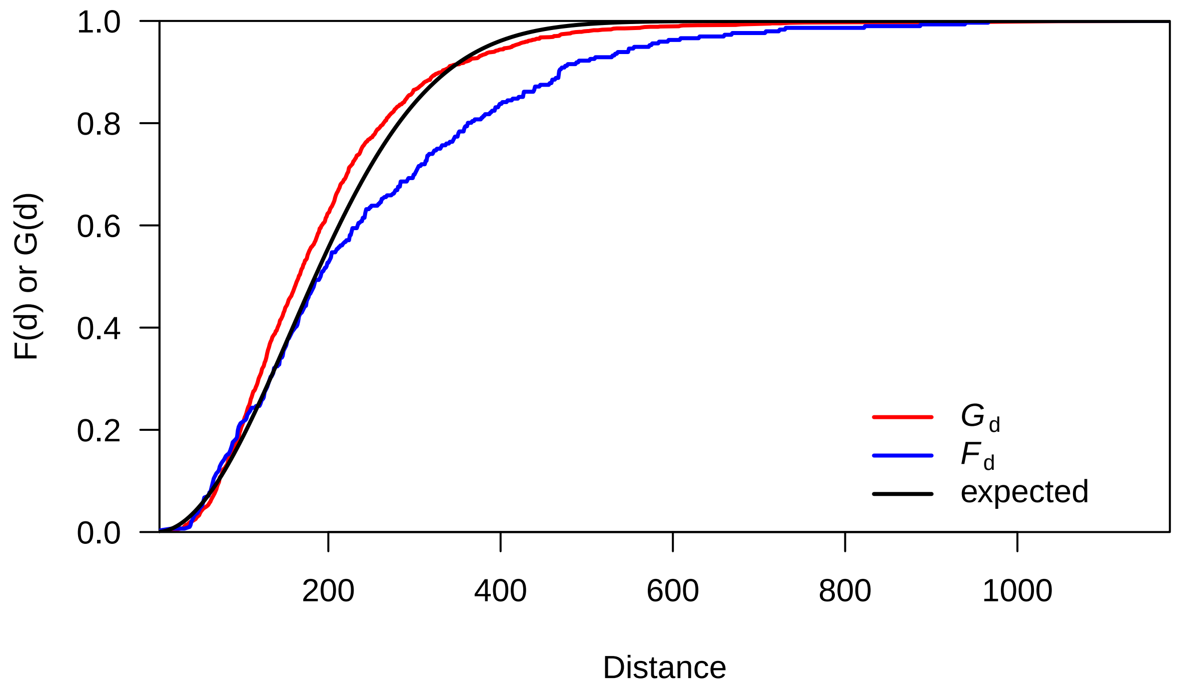
The centres of previously defined raster cells are used to compute the F function. The distance from all crime locations to these cell centres is calculated, then a similar process to the G function is followed.

```
p <- rasterToPoints(r)
d2 <- pointDistance(p[,1:2], xy, longlat=FALSE)
Fdistance <- sort(unique(round(d2)))
mind <- apply(d2, 1, min)
Fd <- sapply(Fdistance, function(x) sum(mind < x))
Fd <- Fd / length(mind)
plot(Fdistance, Fd, type='l', lwd=2, xlim=c(0,1000))
```

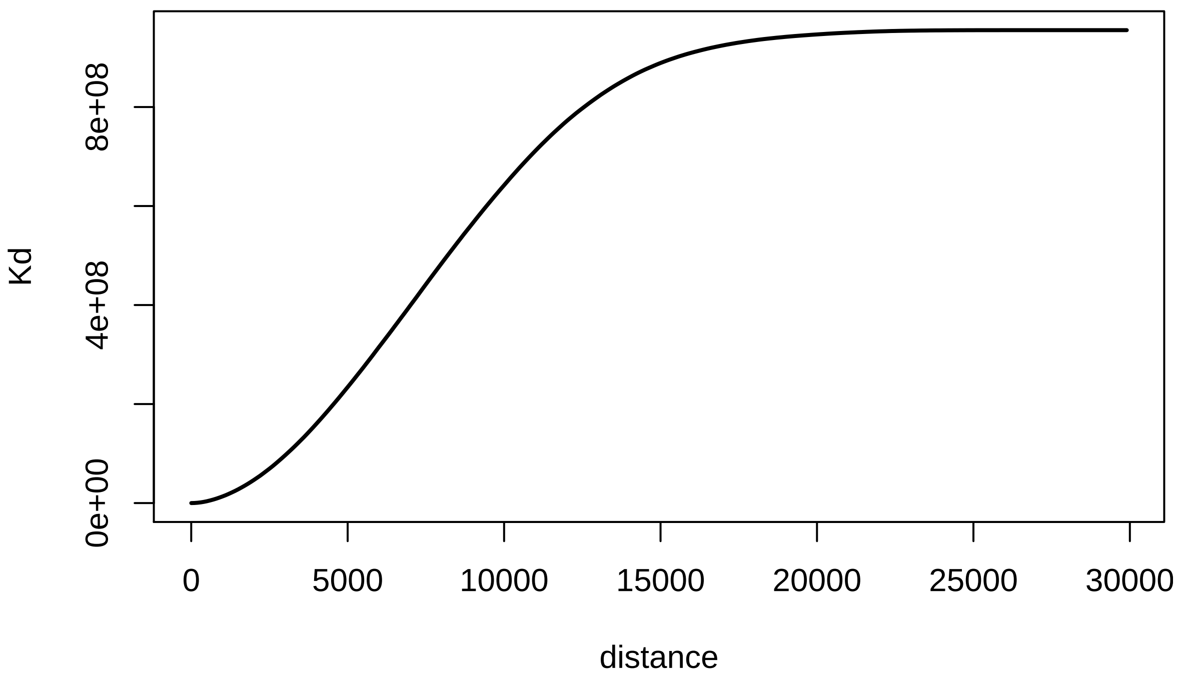


For Evenly-spaced events F(d) should rise rapidly up to the distance at which most events are spaced and then level off (more nearest neighbors at small distances from randomly placed points). For clustered events F(d) rises rapidly at short distances, and then levels off at larger d-values; again indicating a highly clustered distribution in the dataset. The expected distribution can be computed, then all three functions plotted together. K is calculated using the original distance matrix `d`.

```
ef <- function(d, lambda) {
  E <- 1 - exp(-1 * lambda * pi * d^2)
}
expected <- ef(0:2000, dens)

plot(distance, Gd, type='l', lwd=2, col='red', las=1,
     ylab='F(d) or G(d)', xlab='Distance', yaxs="i", xaxs="i")
lines(Fdistance, Fd, lwd=2, col='blue')
lines(0:2000, expected, lwd=2)

legend(800, .3, c(expression(italic("G")["d"]), expression(italic("F")["d"]), 'expected'),
       lty=1, col=c('red', 'blue', 'black'), lwd=2, bty="n")
```



```r
distance <- seq(1, 30000, 100)
Kd <- sapply(distance, function(x) sum(d < x))
Kd <- Kd / (length(Kd) * dens)
plot(distance, Kd, type='l', lwd=2)
```



Next the spatstat package is used to make a Kernel Density raster. SpatialPolygons are coerced to an object of class “owin” (observation window) and coordinates extracted from SpatialPointsDataFrame. The kernel density was calculated - the number of points per km2 - then plotted. A marked point pattern object (ppp) is created, the marks must be coerced to a factor variable.

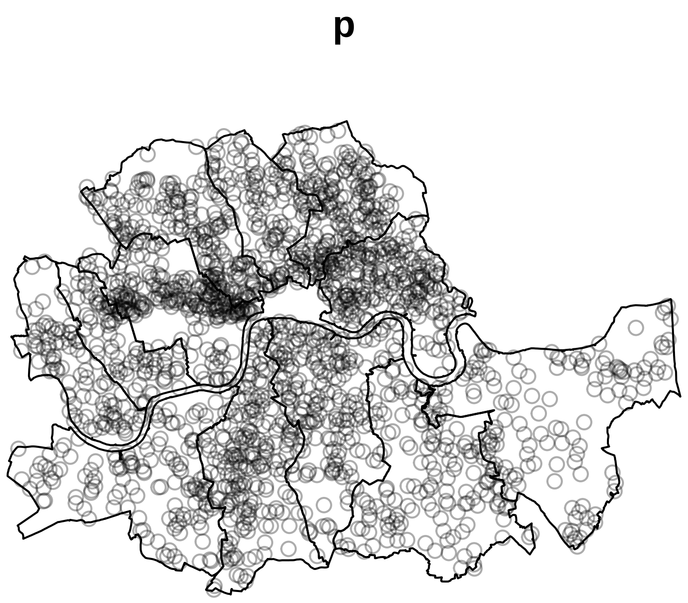
```r
cityOwin <- as.owin(central)
class(cityOwin)
```

```
## [1] "owin"
```

```r
pts <- coordinates(xy)
p <- ppp(pts[,1], pts[,2], window=cityOwin)
p
```

```
## Planar point pattern: 1925 points
## window: polygonal boundary
## enclosing rectangle: [521054.9, 547612] x [169648, 188327.4] units
```

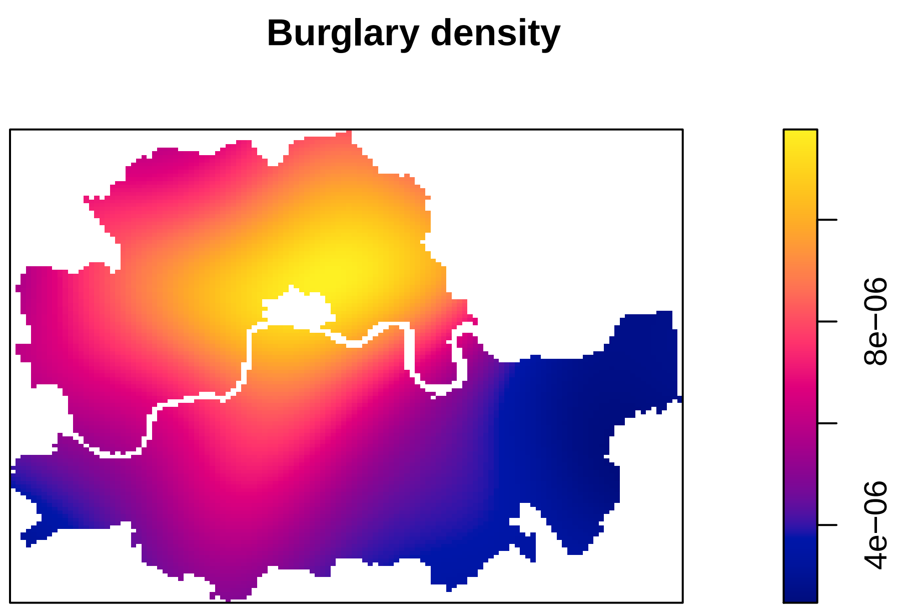
```r
plot(p)
```



```r
ds <- density(p)
class(ds)
```

```
## [1] "im"
```

```r
plot(ds, main='Burglary density')
```



```
burglary16.2$fcat <- as.factor(burglary16.2$crime_type)
burglary16.2 <- remove.duplicates(burglary16.2)

w <- as.owin(central)
xy <- coordinates(burglary16.2)
mpp <- ppp(xy[,1], xy[,2], window = w, marks=burglary16.2$fcat)
spp <- split(mpp)
```

K-plots with an envelope were produced for burglary.

```
spatstat.options(checksegments = FALSE)
kburglary <- Kest(spp$"burglary")
keburglary <- envelope(spp$"burglary", Kest)

par(mfrow=c(1,2))
plot(kburglary, xlim=c(0,2500))
png("kburglary.png")
plot(keburglary)
png("keburglary.png")
```

In order to determine if population density is a good predictor of burglary, a Kolmogorov-Smirnov (‘kstest’) test was carried out using population density as a covariate:

```
KS.burglary <- kstest(spp$burglary, ds)
KS.burglary
```

This gives the following result: Spatial Kolmogorov-Smirnov test of CSR in two dimensions data: covariate ‘ds’ evaluated at points of ‘spp$burglary’ and transformed to uniform distribution under CSR D = 0.21068, p-value < 2.2e-16 alternative hypothesis: two-sided

This function performs a goodness-of-fit test of a Poisson point process model fitted to point pattern data. The observed distribution of the values of a spatial covariate at the data points, and the predicted distribution of the same values under the model, are compared. The null hypothesis is that 2 independent samples are drawn from the same continuous distribiton. The output reports maximum difference between the two cumulative distributions (D), and calculates a P value from that and the sample sizes. The P value is small (2.2e-16) so it is concluded that the two groups were sampled from populations with different distributions and the null hypothesis is rejected.

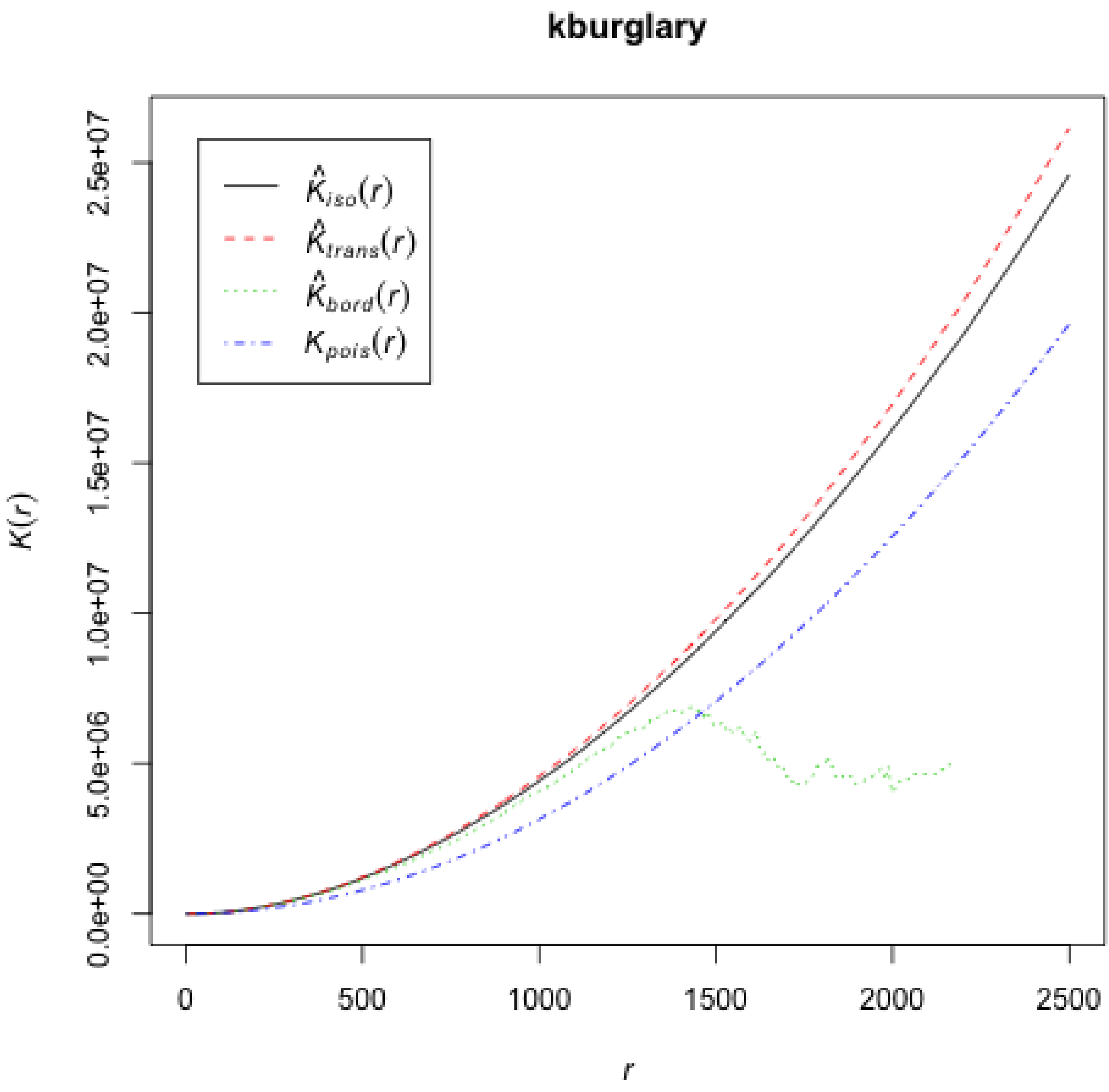


Figure 1: kburglary plot

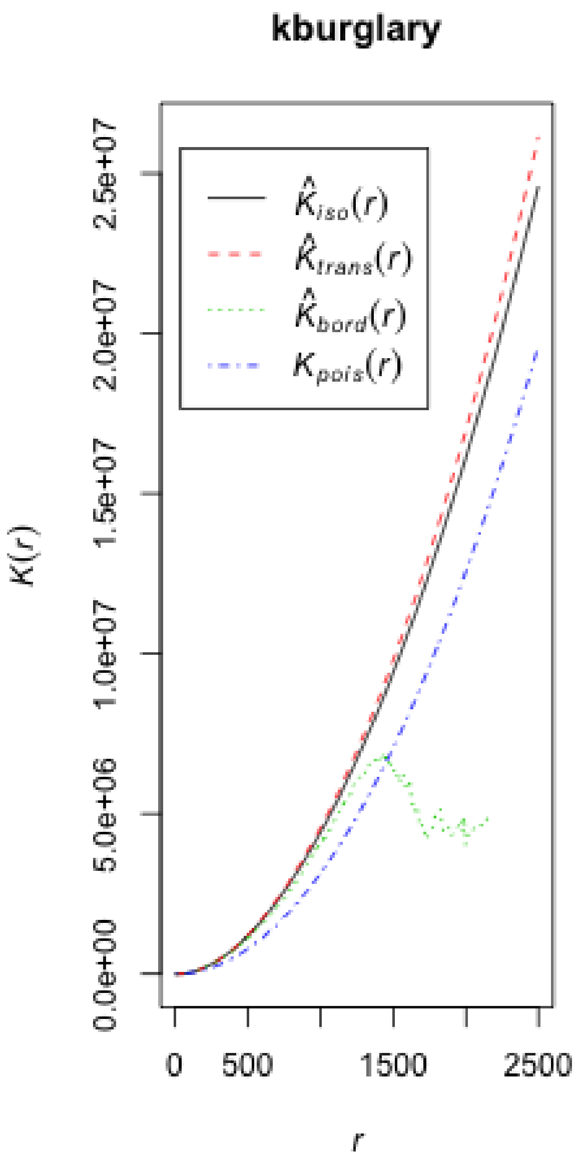


Figure 2: keburglary plot