

R Notebook

[Code ▼](#)

Point Pattern Analysis

Following code contains several methods for evaluating the spatial distribution of a discrete point pattern, in this case coal mines within the Uinta coal region in western Colorado. Kernel density estimations, the quadrant counts of the coal mine point pattern was mapped. The Hopkins-Skellam and Clak Evans tests statisitcs measure the randomness in the points and test for clustering.

Import Libraries and Read Files

[Hide](#)

```
library(sf)
library(spatstat)
```

[Hide](#)

```
boundary <- st_read('~/GitHub/502Project/Data/uinta_buff_1500ft.shp')
```

```
Reading layer `uinta_buff_1500ft' from data source
`C:\Users\Jessi\OneDrive\Documents\GitHub\502Project\Data\uinta_buff_1500ft.shp'
using driver `ESRI Shapefile'
Simple feature collection with 1 feature and 1 field
Geometry type: MULTIPOLYGON
Dimension:      XY
Bounding box:   xmin: 150608.3 ymin: 4284734 xmax: 333779.1 ymax: 4477811
Projected CRS: NAD83 / UTM zone 13N
```

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```
shapefile <- st_read("~/GitHub/502Project/Data/coal_mines_Uinta.shp")
```

```
Reading layer `coal_mines_Uinta' from data source
`C:\Users\Jessi\OneDrive\Documents\GitHub\502Project\Data\coal_mines_Uinta.shp'
using driver `ESRI Shapefile'
Simple feature collection with 296 features and 63 fields
Geometry type: POINT
Dimension:      XY
Bounding box:   xmin: 159585.4 ymin: 4285405 xmax: 330132.3 ymax: 4461288
Projected CRS: NAD27 / UTM zone 13N
```

Plot Data

[Hide](#)

```
coordinates <- st_coordinates(shapefile)
par(mfrow = c(1, 1), mar = c(0.1, 0.1, 0.1, 0.1) + 0.1, cex = 0.6) # Adjust cex as needed
mines <- ppp(coordinates[,1], coordinates[,2], window=as.owin(boundary), check=TRUE)
```

Warning: 22 points were rejected as lying outside the specified window

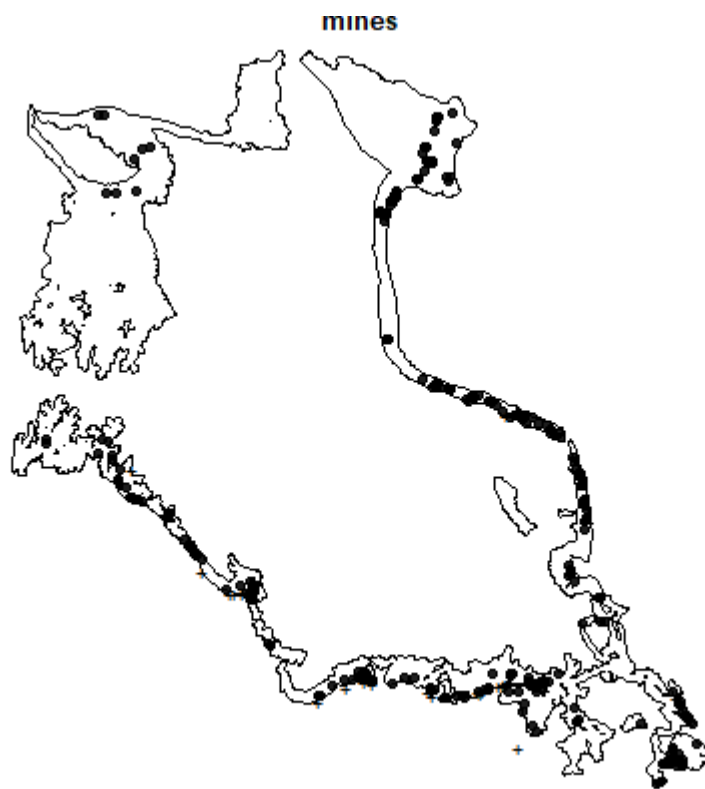
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```
print(plot(mines, pch = 19))
```

Symbol map with constant values

pch: 19

cols: #000000DE



Clark Evans Statistic

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```
clarkevans.test(mines, clipregion = as.owin(boundary), alternative="clustered")
```

Clark-Evans test
CDF correction
Z-test

data: mines
R = 0.34841, p-value < 2.2e-16
alternative hypothesis: clustered (R < 1)

Hide

```
clarkevans.test(mines, clipregion = as.owin(boundary))
```

Clark-Evans test
CDF correction
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data: mines
R = 0.34841, p-value < 2.2e-16
alternative hypothesis: two-sided

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```
clarkevans.test(mines, clipregion = as.owin(boundary), alternative="clustered")
```

Clark-Evans test
CDF correction
Z-test

data: mines
R = 0.34841, p-value < 2.2e-16
alternative hypothesis: clustered (R < 1)

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```
clarkevans.test(mines, clipregion = as.owin(boundary), correction="cdf", nsim=99)
```

Clark-Evans test
CDF correction
Z-test

data: mines
R = 0.34841, p-value < 2.2e-16
alternative hypothesis: two-sided

Hopskel

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```
hopskel(mines)
```

```
[1] 0.009725984
```

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```
hopskel.test(mines, alternative="clustered")
```

```
Hopkins-Skellam test of CSR  
using F distribution
```

```
data: mines  
A = 0.011562, p-value < 2.2e-16  
alternative hypothesis: clustered (A < 1)
```

Intensity

Source: <https://www.paulamoraga.com/book-spatial/intensity-estimation.html> (<https://www.paulamoraga.com/book-spatial/intensity-estimation.html>)

The `density()` (<https://rdr.io/pkg/terra/man/density.html>) function of **spatstat** can be used to obtain a kernel estimate of the intensity of a point pattern. These include the type of kernel (`kernel`) and the smoothing bandwidth (`sigma`). By default, `density()` (<https://rdr.io/pkg/terra/man/density.html>) uses a Gaussian kernel and a bandwidth determined by a simple rule of thumb that depends only on the size of the window. Here, we use the `density()` (<https://rdr.io/pkg/terra/man/density.html>) function to estimate the intensity of the point pattern of tree locations that is in the `japanesepines` data from **spatstat**

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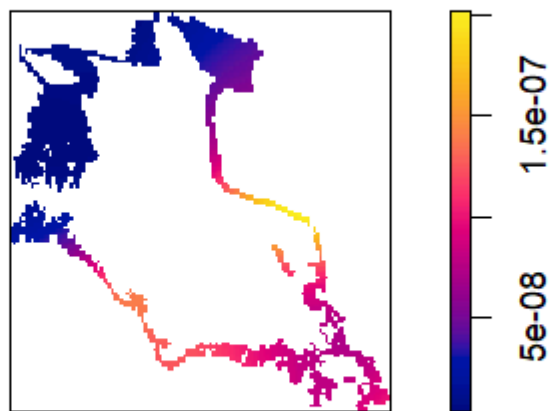
```
lambdahat <- density(mines)  
attr(lambdahat, "sigma")
```

```
[1] 22896.34
```

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```
plot(lambdahat, main = "Default bandwidth")
```

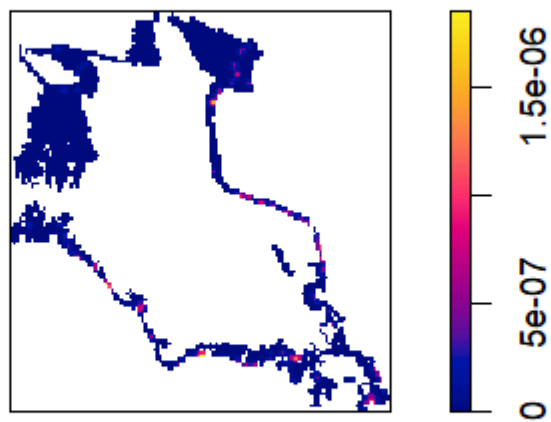
Default bandwidth



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```
plot(density(mines, sigma = 1000))
```

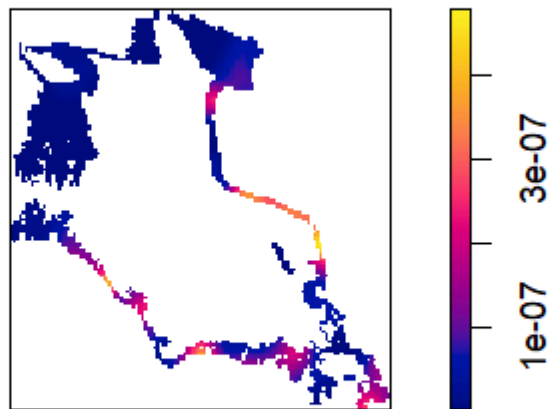
density(mines, sigma = 1000)



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```
plot(density(mines, sigma = 5000))
```

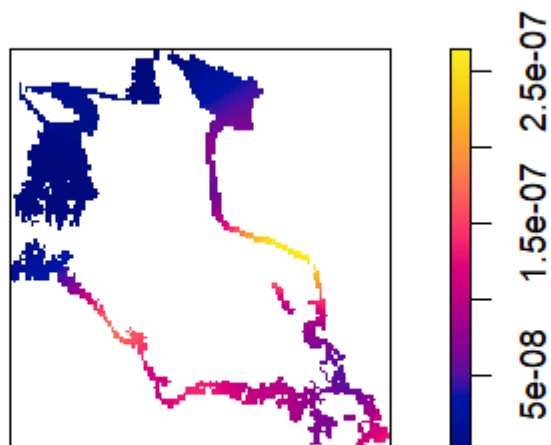
density(mines, sigma = 5000)



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```
plot(density(mines, sigma = 15000))
```

density(mines, sigma = 15000)



Quadrant Test

<<https://www.rdocumentation.org/packages/spatstat/versions/1.64-1/topics/quadrat.test>
(<https://www.rdocumentation.org/packages/spatstat/versions/1.64-1/topics/quadrat.test>)

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```
par(mfrow = c(1, 1), mar = c(0.1, 0.1, 0.1, 0.1) + 0.1, cex = 0.6) # Adjust cex as needed

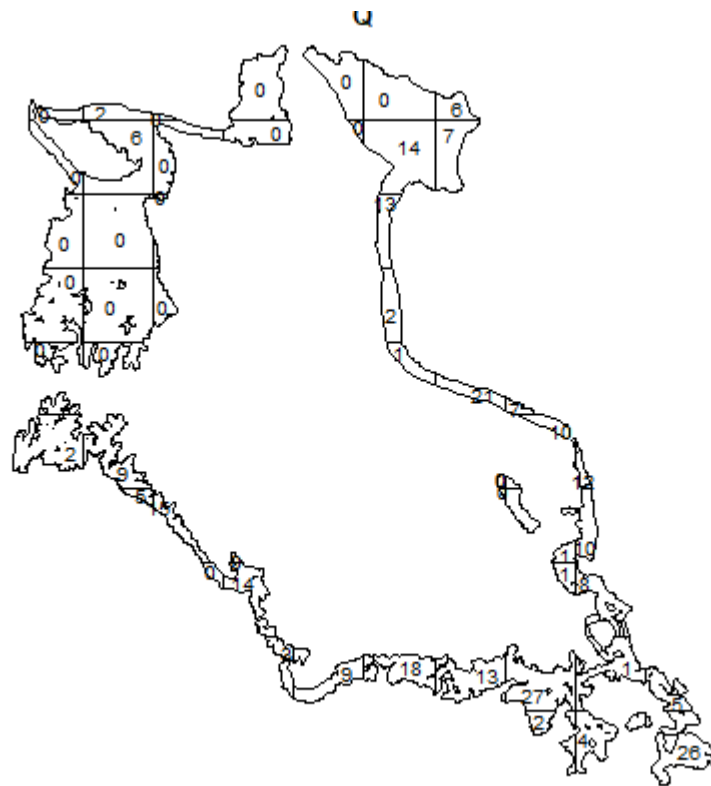
color_scheme <- colorRampPalette(c("blue", "red"))

# Perform your plot
Q <- quadratcount(mines, nx = 10, ny = 10)
plot(mines, pch=10, cols="grey70", main=NULL)
```



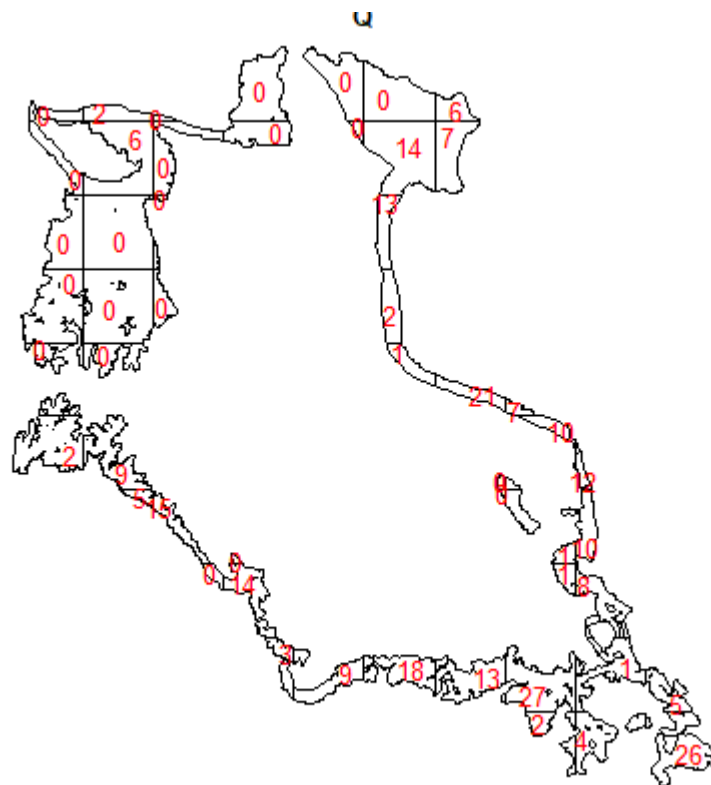
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```
plot(Q, pch="-")
```



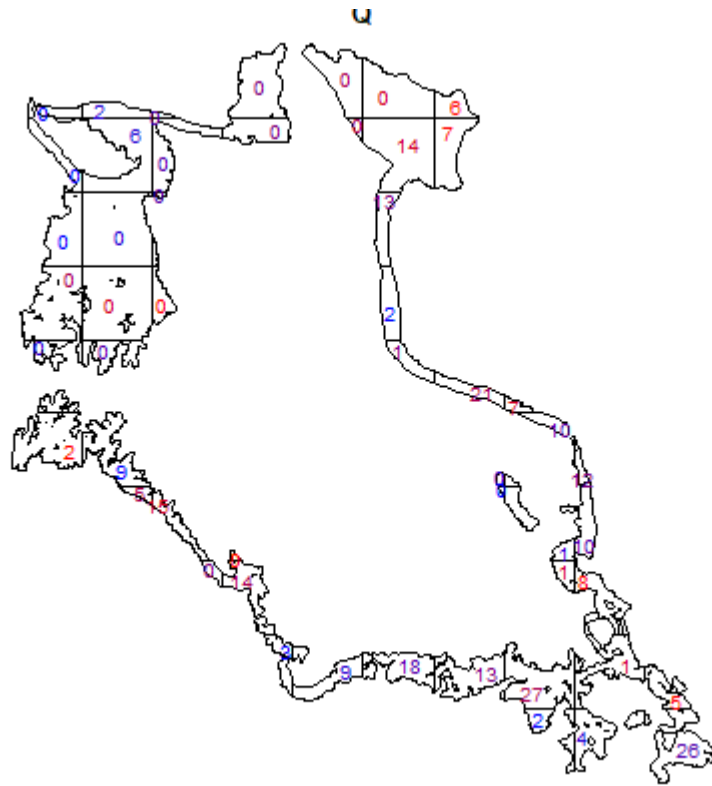
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```
plot(Q, col="red", cex=1.2)
```



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```
plot(Q, lty = 1, col = color_scheme(7))
```

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```
# Reset graphical parameters
#par(mfrow = c(1, 1), mar = c(5, 4, 4, 2) + 0.1, cex = 1)
```

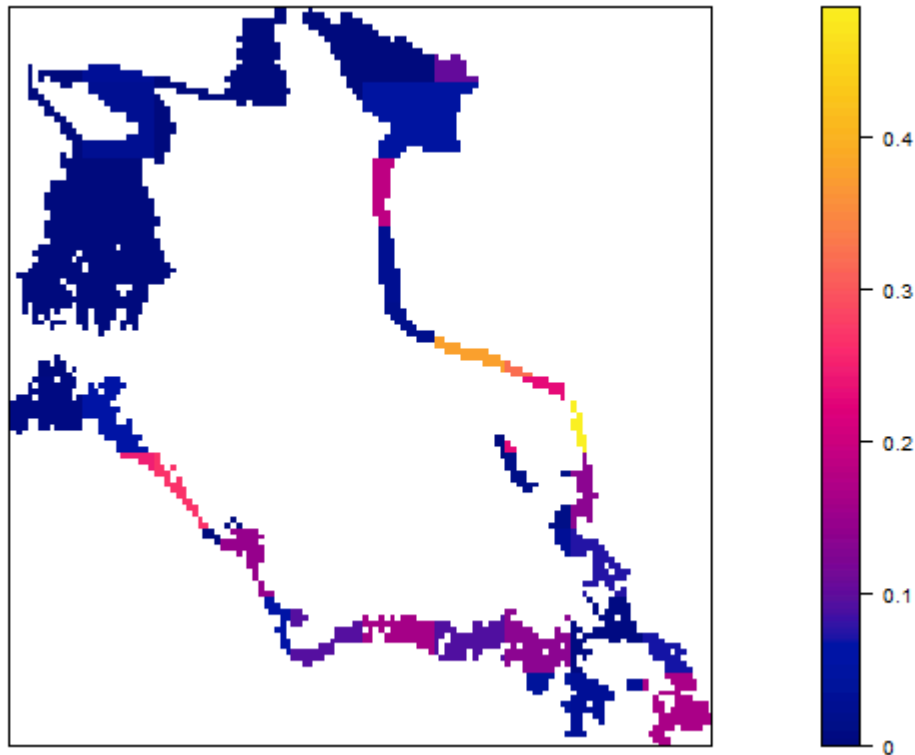
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```
par(mfrow = c(1, 1), mar = c(0.1, 0.1, 0.1, 0.1) + 0.1, cex = 0.6) # Adjust cex as needed

mines.km <- rescale(mines, 1000, "km")
Qkm <- quadratcount(mines.km, nx = 10, ny = 10)

# Plot the density

plot(intensity(Qkm, image=TRUE), main=NULL, las=1, interpolate = TRUE)
```



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```
#plot(Qkm, add=TRUE)
# Plot density raster
#plot(mines.km, pch=20, cex=0.6, col=rgb(0,0,0,.5), add=TRUE) # Add points
```

To test H_0 : CSR or regular vs. H_1 : clustered, we use `alternative = "clustered"`. If the pattern is clustered, the observed X^2 statistic will be large, and the p-value is calculated as the area to the right of the observed X^2

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```
quadrat.test(Q, alternative = "clustered")
```

Warning: Some expected counts are small; chi^2 approximation may be inaccurate

Chi-squared test of CSR using quadrat counts

```
data:
X2 = 612.04, df = 51, p-value < 2.2e-16
alternative hypothesis: clustered

Quadrats: 52 tiles (irregular windows)
```

Finally, we test H_0 : CSR vs. H_1 : no CSR (regular or clustered) using the default value `alternative = "two.sided"`. If the pattern is regular or clustered, the observed X^2 statistic will be near 0 or large. The p-value is calculated as 2 times the minimum of the area to the left of the observed X^2 and the area to the right of the observed

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```
quadrat.test(Q, alternative = "two.sided") # default
```

Warning: Some expected counts are small; chi² approximation may be inaccurate

Chi-squared test of CSR using quadrat counts

data:

X2 = 612.04, df = 51, p-value < 2.2e-16

alternative hypothesis: two.sided

Quadrats: 52 tiles (irregular windows)