proc_using_spatstat

Frances Lin

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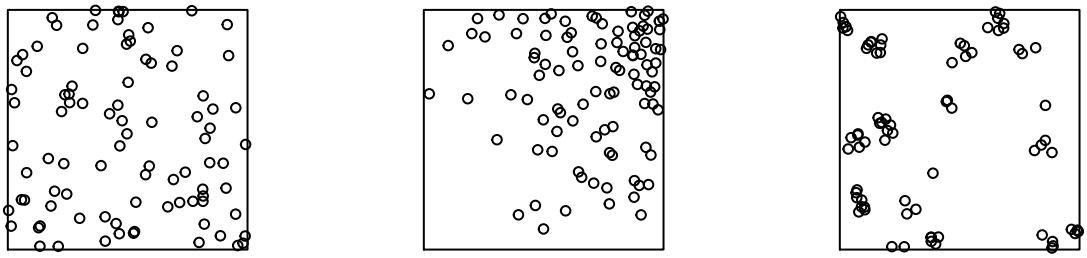
```
library(spatstat)
library(tidyverse)
library(here)
```

```
par(mfrow=c(1, 3))
plot(rpoispp(lambda = 100, win=square(1)), main="") #plot_2D_HPP
plot(rpoispp(lambda = function(x, y) 400*x*y, win=square(1)), main="") #plot_2D_NPP
plot(rMatClust(kappa = 20, r = 0.05, mu = 5), main="") #plot_2D_Matern
```



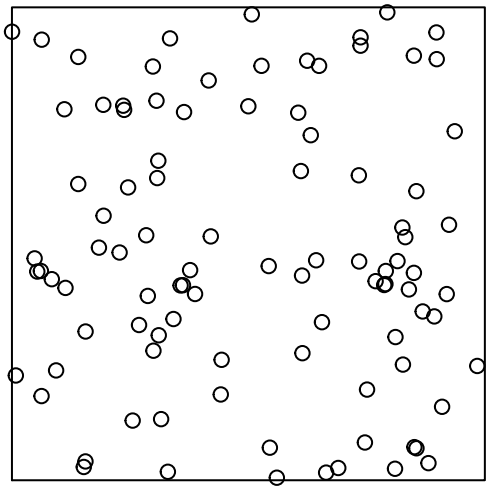
```
#HPP (rate = 100)
#NPP (intensity = 400*x*y)
#Matern (kappa = 20, r = 0.05, mu = 5)
```

```
# Check to see how to use the function
?rpoispp
# Check to see how this is written
#View(rpoispp)
```

```
# Plot a homogeneous Poisson process
# p.1334 of https://mran.microsoft.com/snapshot/2016-04-25/web/packages/spatstat/spatstat.pdf
# https://spatstat.org/SSAI2017/solutions/solution04.html

par(mfrow=c(1, 1))
plot_2D_HPP <- plot(rpoispp(lambda = 100, win=square(1)),main = "HPP (rate = 100)")
```

HPP (rate = 100)



```
plot_2D_HPP
```

```
## Symbol map with no parameters
```

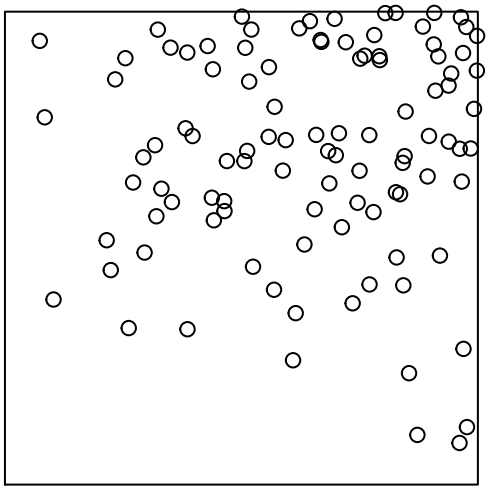
```
#plot(rpoispp(lambda = 50, win=square(1)),main = "HPP (rate = 50)")
#plot(rpoispp(lambda = 10, win=square(1)),main = "HPP (rate = 10)")
```

```
# Plot a homogeneous Poisson process
# p.33 of https://spatstat.org/resources/spatstatJSSpaper.pdf

#lmbda_function <- function(x, y) 400*x
#so that they have the same expected # of events but why ???

par(mfrow=c(1, 1))
plot_2D_NPP <- plot(rpoispp(lambda = function(x, y) 400*x*y, win=square(1)), main = "NPP (intensity = 4
```

NPP (intensity = 400*x*y)



```
plot_2D_NPP
```

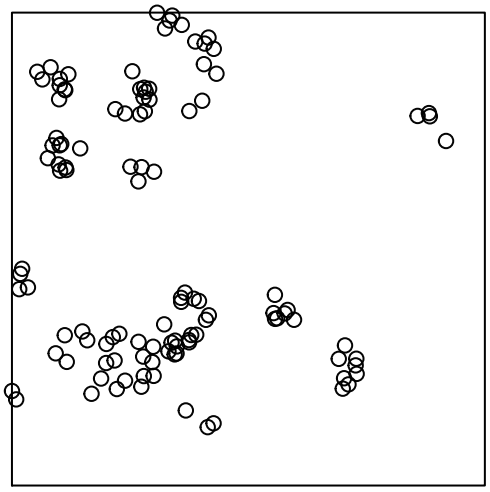
```
## Symbol map with constant values
## cols: #000000FF
```

```
#plot(rpoispp(lambda = function(x, y) 50*x, win=square(1)), main = "NPP (intensity = 50*x)")
#plot(rpoispp(lambda = function(x, y) 10*x, win=square(1)), main = "NPP (intensity = 10*x)")
```

```
?rMatClust
#kappa = intensity
#scale = radius of the clusters
#mu = mean # of points per cluster
```

```
plot_2D_Matern <- plot(rMatClust(kappa = 20, r = 0.05, mu = 5), main = "Matern (kappa = 20, r = 0.05, mu
```

Matern (kappa = 20, r = 0.05, mu = 5)



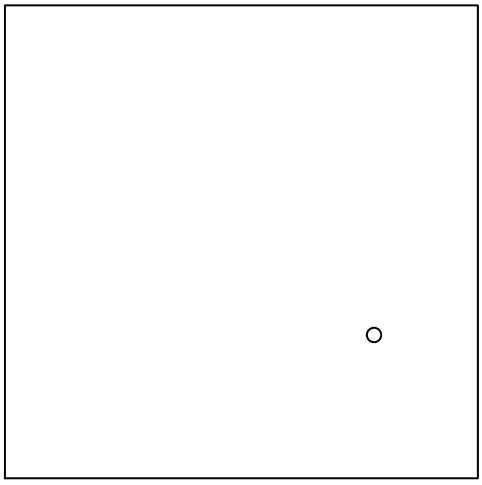
```
plot_2D_Matern
```

```
## Symbol map with constant values
## cols: #000000FC
```

```
?rMaternII
# kappa = intensity
# r = inhibition distance
```

```
# Plot a Matern I process #Inhibition
par(mfrow=c(1, 1))
plot(rMaternI(kappa = 100, r = 0.1), main = "Matern I (kappa = 100, r = 0.05)")
```

Matern I (kappa = 100, r = 0.05)



```
#plot(rMaternI(kappa = 50, r = 0.05), main = "Matern I (kappa = 50, r = 0.05)")
#plot(rMaternI(kappa = 10, r = 0.05), main = "Matern I (kappa = 10, r = 0.05)")
points <- rMaternI(kappa = 100, r = 0.07)
length(points)
```

```
## [1] 5
```

```
pairdist(points)
```

```
##            [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
##  [1,] 0.0000000 0.3906581 0.2912976 0.4167192 0.6274946 0.1669887
##  [2,] 0.3906581 0.0000000 0.1677863 0.1576277 0.2372641 0.3753469
##  [3,] 0.2912976 0.1677863 0.0000000 0.1255424 0.3720229 0.3492435
##  [4,] 0.4167192 0.1576277 0.1255424 0.0000000 0.2788529 0.4610372
##  [5,] 0.6274946 0.2372641 0.3720229 0.2788529 0.0000000 0.6031366
##  [6,] 0.1669887 0.3753469 0.3492435 0.4610372 0.6031366 0.0000000
##  [7,] 0.5172131 0.8101161 0.6467672 0.7362993 1.0125683 0.6779360
##  [8,] 0.6782062 0.3189587 0.3914974 0.2689923 0.1643380 0.6920240
##  [9,] 0.7011073 0.4048243 0.4122022 0.2909771 0.3193702 0.7512622
## [10,] 0.3555549 0.2953640 0.3722763 0.4378620 0.4706503 0.2180891
## [11,] 0.2309862 0.4514329 0.2896188 0.3899748 0.6597523 0.3930069
## [12,] 0.7331683 0.3455699 0.4953448 0.4091016 0.1311274 0.6865604
## [13,] 0.8360457 0.7004195 0.6138968 0.5445850 0.6985413 0.9495929
## [14,] 0.5404226 0.3246039 0.2657885 0.1711203 0.3597463 0.6150299
##            [,7]      [,8]      [,9]     [,10]     [,11]     [,12]
##  [1,] 0.5172131 0.6782062 0.7011073 0.3555549 0.2309862 0.7331683
##  [2,] 0.8101161 0.3189587 0.4048243 0.2953640 0.4514329 0.3455699
##  [3,] 0.6467672 0.3914974 0.4122022 0.3722763 0.2896188 0.4953448
##  [4,] 0.7362993 0.2689923 0.2909771 0.4378620 0.3899748 0.4091016
##  [5,] 1.0125683 0.1643380 0.3193702 0.4706503 0.6597523 0.1311274
##  [6,] 0.6779360 0.6920240 0.7512622 0.2180891 0.3930069 0.6865604
##  [7,] 0.0000000 0.9856244 0.9206811 0.8707660 0.3587120 1.1398921
##  [8,] 0.9856244 0.0000000 0.1617520 0.5984148 0.6530125 0.2548210
```

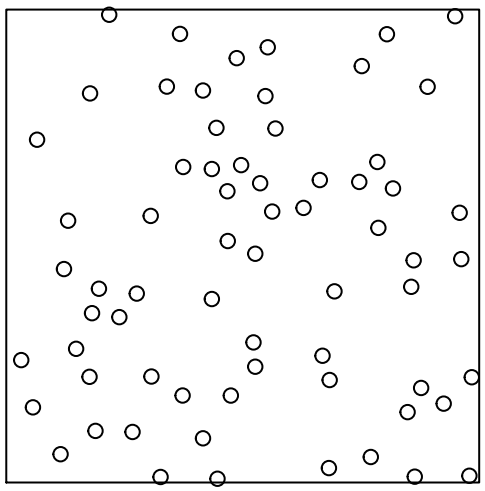
```
##  [9,] 0.9206811 0.1617520 0.0000000 0.6997377 0.6210708 0.4163871
## [10,] 0.8707660 0.5984148 0.6997377 0.0000000 0.5451840 0.5225156
## [11,] 0.3587120 0.6530125 0.6210708 0.5451840 0.0000000 0.7847486
## [12,] 1.1398921 0.2548210 0.4163871 0.5225156 0.7847486 0.0000000
## [13,] 0.8129779 0.5510076 0.3906689 0.9782639 0.6541301 0.8056111
## [14,] 0.7430319 0.2611692 0.1811042 0.6088889 0.4409126 0.4853320
##           [,13]     [,14]
##  [1,] 0.8360457 0.5404226
##  [2,] 0.7004195 0.3246039
##  [3,] 0.6138968 0.2657885
##  [4,] 0.5445850 0.1711203
##  [5,] 0.6985413 0.3597463
##  [6,] 0.9495929 0.6150299
##  [7,] 0.8129779 0.7430319
##  [8,] 0.5510076 0.2611692
##  [9,] 0.3906689 0.1811042
## [10,] 0.9782639 0.6088889
## [11,] 0.6541301 0.4409126
## [12,] 0.8056111 0.4853320
## [13,] 0.0000000 0.3761383
## [14,] 0.3761383 0.0000000
```

```
min(pairdist(points)[upper.tri(pairdist(points))])
```

```
## [1] 0.1255424
```

```
# Plot a Matern II process
par(mfrow=c(1, 1))
plot(rMaternII(kappa = 100, r = 0.05), main = "Matern II (kappa = 100, r = 0.05)")
```

Matern II (kappa = 100, r = 0.05)



```
#plot(rMaternII(kappa = 50, r = 0.05), main = "Matern II (kappa = 50, r = 0.05)")
#plot(rMaternII(kappa = 10, r = 0.05), main = "Matern II (kappa = 10, r = 0.05)")
```

```
# # Save out results
# write_rds(plot_2D_HPP, here("results", "plot_2D_HPP.jpeg"))
```

```
# # Error checking
# plot_2D_HPP <- readRDS(here("results", "plot_2D_HPP.jpeg"))
# plot_2D_HPP
```