# 04_proc_using_spatstat

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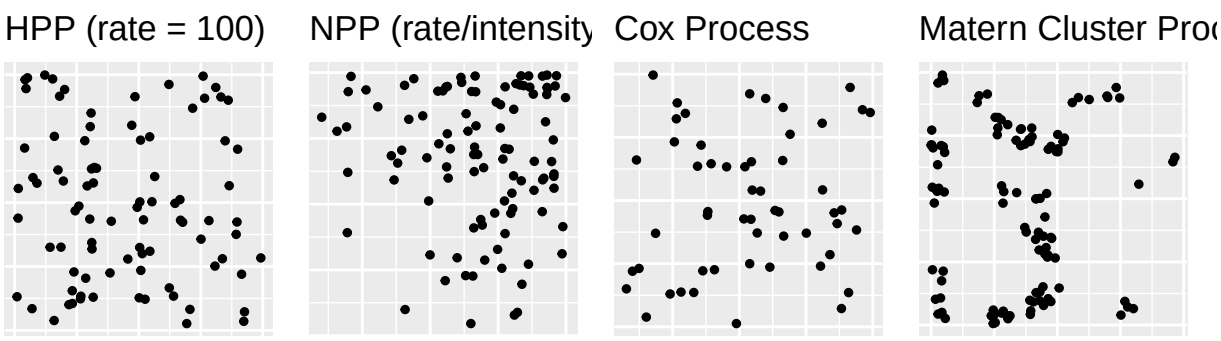
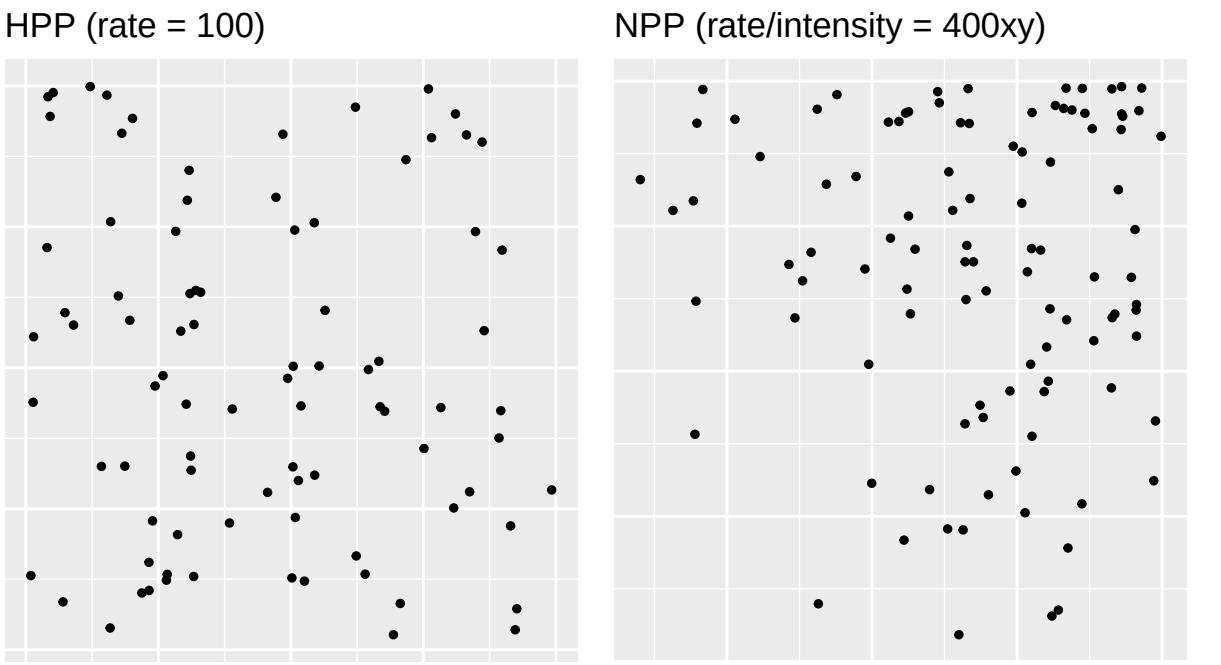
```
library(spatstat)
library(tidyverse)
library(here)
library(mvtnorm)
library(ggplot2)
library(patchwork)
```

```
# Because I like ggplot better
set.seed(1234)

# Extract x & y from ppp object (lists)
tmp1 <- rpoispp(lambda = 100, win=square(1))
tmp2 <- rpoispp(lambda = function(x, y) 400*x*y)
tmp3 <- rpoispp(lambda = rexp(n = 1, rate = 1/100))
tmp4 <- rMatClust(kappa = 20, r = 0.05, mu = 5)

# Create dataframes
df1 <- tibble(x = tmp1$x, y = tmp1$y)
df2 <- tibble(x = tmp2$x, y = tmp2$y)
df3 <- tibble(x = tmp3$x, y = tmp3$y)
df4 <- tibble(x = tmp4$x, y = tmp4$y)

n <- 1 # set size for geom_point

p1 <- ggplot(df1, aes(x=x, y=y)) + geom_point(size=n) +
  theme(axis.text.x=element_blank(), axis.ticks.x=element_blank(),
        axis.text.y=element_blank(), axis.ticks.y=element_blank(),
        axis.title=element_blank()) +
  labs(title="HPP (rate = 100)")

p2 <- ggplot(df2, aes(x=x, y=y)) + geom_point(size=n) +
  theme(axis.text.x=element_blank(), axis.ticks.x=element_blank(),
        axis.text.y=element_blank(), axis.ticks.y=element_blank(),
        axis.title=element_blank()) +
  labs(title="NPP (rate/intensity = 400xy)")

p3 <- ggplot(df3, aes(x=x, y=y)) + geom_point(size=n) +
  theme(axis.text.x=element_blank(), axis.ticks.x=element_blank(),
        axis.text.y=element_blank(), axis.ticks.y=element_blank(),
        axis.title=element_blank()) +
  labs(title="Cox Process")

p4 <- ggplot(df4, aes(x=x, y=y)) + geom_point(size=n) +
  theme(axis.text.x=element_blank(), axis.ticks.x=element_blank(),
        axis.text.y=element_blank(), axis.ticks.y=element_blank(),
        axis.title=element_blank()) +
  labs(title="Matern Cluster Process")
```

```
# Combine plots
p1 + p2 + p3 + p4 + plot_layout(ncol = 4) + coord_fixed(ratio = 1)
```

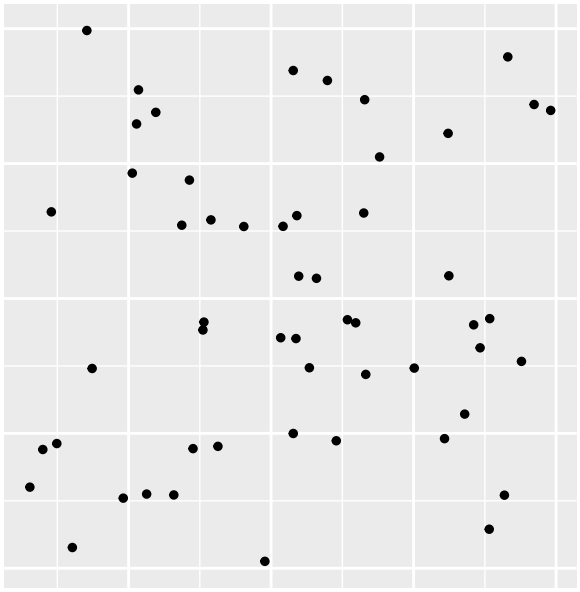



```
p1 + p2 + plot_layout(ncol = 2) + coord_fixed(ratio = 1)
```

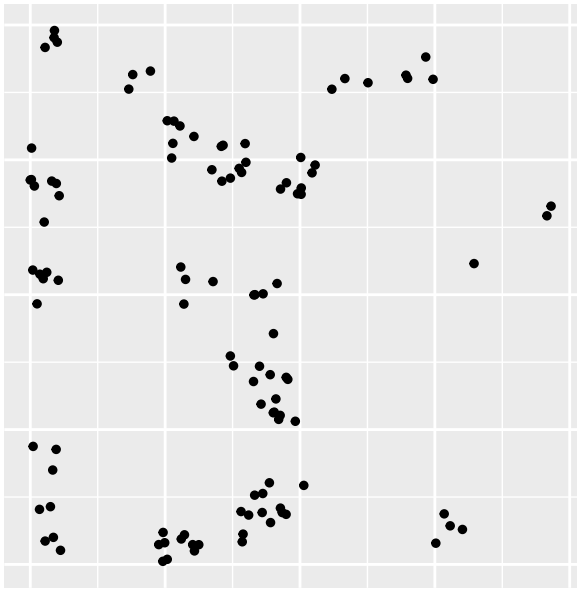



```
p3 + p4 + plot_layout(ncol = 2) + coord_fixed(ratio = 1)
```

Cox Process



Matern Cluster Process



```
# Save output and adjust size
png(file = '/Users/franceslinyc/Hawkes-Process-2021/results/plot_2D_All.png', width = 450*1, height = 45
p1 + p2 + plot_layout(ncol = 2) # + coord_fixed(ratio = 1)
```

```
# Save output and adjust size
png(file = '/Users/franceslinyc/Hawkes-Process-2021/results/plot_2D_All2.png', width = 450*1, height = 4
p3 + p4 + plot_layout(ncol = 2) #+ coord_fixed(ratio = 1)
```

```
# Cox?
#rmvnorm(1, c(0.5, 0.5))
```

```
# Cox?
#plot(rpoispp(lambda = function(x, y) 400*x*y, win = square(1)), main = "") #plot_2D_NPP
```

```
# # Cox?
# #fun <- function (x, y) x*y + rbeta(1, 1/5, 1/5)*400
# plot(rpoispp(lambda = rbeta(1, 1/5, 1/5)*150, win = square(1)), main = "")
```

```
# # Cox?
# plot(rpoispp(lambda = rnorm(n = 1, 50, 0.05)), main = "") #plot_2D_Cox
```

```
# # Plot HPP, NPP, Cox and Matern Processes
# set.seed(1234)
# par(mfrow=c(1, 4), mai = c(0.1, 0.1, 0.1, 0.1))
#
# plot(rpoispp(lambda = 100, win=square(1)), main = "HPP (rate = 100)") #plot_2D_HPP
# plot(rpoispp(lambda = function(x, y) 400*x*y, win = square(1)), main = "NPP (intensity = 400*x*y)") #
# plot(rpoispp(lambda = rexp(n = 1, rate = 1/100)), main = "Cox Process") #plot_2D_Cox
# plot(rMatClust(kappa = 20, r = 0.05, mu = 5), main = "Matern Process") #plot_2D_Matern
#
# #HPP (rate = 100)
```

```
# #NPP (intensity = 400*x*y)
# #Cox Process
# #Matern Process
# #Cox (intensity = exp(n = 1, rate = 1/100))
# #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)")
# plot_2D_HPP
# #plot(rpoispp(lambda = 50, win=square(1)),main = "HPP (rate = 50)")
# #plot(rpoispp(lambda = 10, win=square(1)),main = "HPP (rate = 10)")
```

```
# # Plot a nonhomogeneous 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 =
# plot_2D_NPP
# #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)")
```

```
# # Plot a Cox process
# # p.80 of https://darrylmcleod.com/wp-content/uploads/2016/06/Analysing-spatial-point-patterns-in-R.p
#
# lmbda <- rexp(n = 1, rate = 1/100)
# X <- rpoispp(lmbda)
# plot(X, main = "Cox (intensity = exp(n = 1, rate = 1/100))")
```

```
# ?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,
# plot_2D_Matern
```

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

```r
# # 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)")
# #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)
# pairdist(points)
# min(pairdist(points)[upper.tri(pairdist(points))])
```

```r
# # 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)")
# #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)")
```

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

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