Problem Set 3

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```
library (dplyr)

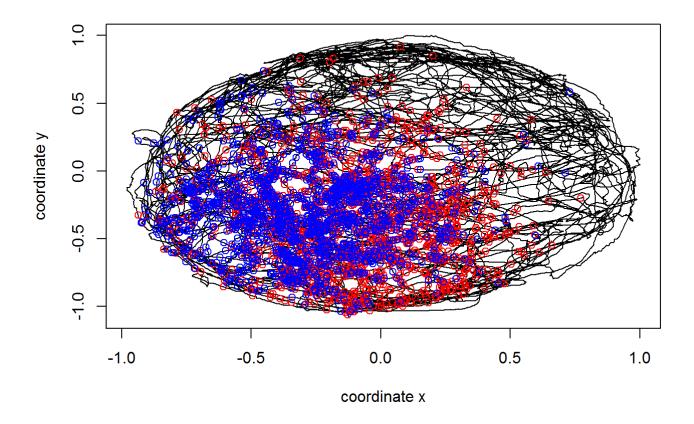
## ## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
## ## filter, lag

## The following objects are masked from 'package:base':
## ## intersect, setdiff, setequal, union

hipp_data <- read.csv("C:/YUKIHO/BU/MA 615/Classes/9.12.2016/class 9.12.2016/ma_568/Homework 3/hipp_data.csv")
```

```
plot(hipp_data$xN, hipp_data$yN, type='1', xlab="coordinate x", ylab="coordinate y")
hippl_data <- subset(hipp_data, spikes==1)
points(hippl_data$xN, hippl_data$yN, col='red')
hipp2_data <- subset(hipp_data, spikes2==1)
points(hipp2_data$xN, hipp2_data$yN, col='blue')</pre>
```



The plot shows that, both neuron's spikes are gathered in the left-bottom of the graph; thus we could say they are probably correlated.

```
m1 <- glm(spikes ~ xN + yN, poisson, hipp_data)
summary(m1)
```

```
##
## Call:
## glm(formula = spikes ~ xN + yN, family = poisson, data = hipp_data)
## Deviance Residuals:
##
      Min
                1Q Median
                                  3Q
                                          Max
## -0.5501 -0.3718 -0.2621 -0.1928
                                       2.6004
##
## Coefficients:
##
              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.24918
                          0. 02760 -117. 74
                                           <2e-16 ***
              -0.50623
## xN
                          0.04724 -10.72
                                           <2e-16 ***
## vN
              -1.18010
                          0.04477 - 26.36
                                           <2e-16 ***
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
## (Dispersion parameter for poisson family taken to be 1)
##
##
      Null deviance: 12311 on 41327 degrees of freedom
## Residual deviance: 11388 on 41325 degrees of freedom
## AIC: 15492
##
## Number of Fisher Scoring iterations: 6
```

All parameters are significant.

```
lambda <- function(x, y) {
  exp(m1$coefficients[1] + m1$coefficients[2] * x + m1$coefficients[3] * y)
  }

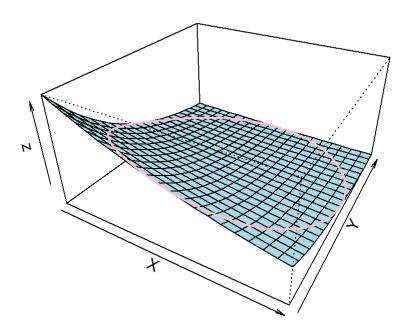
x2 <- y2 <- seq(-1, 1, .1)
?outer</pre>
```

```
## starting httpd help server ...
```

done

```
 z \leftarrow \text{outer}(x2, \ y2, \ \text{lambda})   \text{persp}(x2, \ y2, \ z, \ \text{theta} = 30, \ \text{phi} = 30, \ \text{expand} = 0.5, \ \text{col} = \text{"lightblue"}, \ \text{xlab="X"}, \ \text{ylab} = \text{"Y"}, \ \text{mai}   \text{n="Maximum Likelihood Model Indensity"}) \rightarrow \text{res}   \text{phi} \leftarrow \text{seq}(0, \ 2 * \text{pi}, \ \text{len} = 201)   \text{xr} \leftarrow \text{cos}(\text{phi})   \text{yr} \leftarrow \text{sin}(\text{phi})   \text{lines}(\text{trans3d}(\text{xr}, \ \text{yr}, \ \text{lambda}(\text{xr}, \ \text{yr}), \ \text{res}), \ \text{col} = \text{"pink"}, \ \text{lwd} = 2)
```

Maximum Likelihood Model Indensity



Due to the graph shows, the spatial firing properties are well captured.

```
hipp_data$xN2 <- (hipp_data$xN)^2
hipp_data$yN2 <- (hipp_data$yN)^2
m2 <- glm(spikes ~ xN2 + yN2 + xN + yN, poisson, hipp_data)
summary(m2)
```

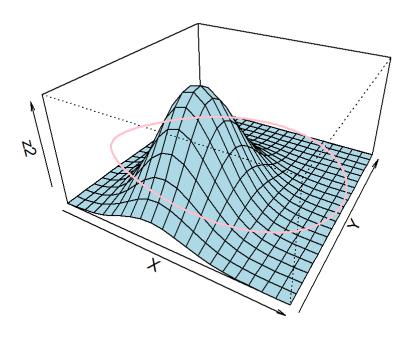
```
##
## Call:
## glm(formula = spikes \sim xN2 + yN2 + xN + yN, family = poisson,
##
       data = hipp data)
##
## Deviance Residuals:
##
      Min
                 1Q
                    Median
                                   3Q
                                          Max
## -0.7260 -0.3359 -0.1564 -0.0580
                                       3.5332
##
## Coefficients:
##
               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.82026
                          0. 03723 -48. 89
                                            <2e-16 ***
## xN2
               -5.81075
                          0.19772 -29.39
                                            <2e-16 ***
## yN2
               -3.66241
                          0. 13449 -27. 23
                                            <2e-16 ***
                          0.09165 -15.85
## xN
               -1.45219
                                            <2e-16 ***
## yN
              -2.40928
                          0.09536 -25.27
                                            <2e-16 ***
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
## (Dispersion parameter for poisson family taken to be 1)
##
##
      Null deviance: 12311.2 on 41327 degrees of freedom
## Residual deviance: 9141.5 on 41323 degrees of freedom
## AIC: 13249
##
## Number of Fisher Scoring iterations: 7
```

All significant.

```
lambda2 <- function (x, y) {
    exp(m2$coefficients[1] + m2$coefficients[2] * (x^2) + m2$coefficients[3] * (y^2) + m2$coefficients[4]
* x + m2$coefficients[5] * y)
    }

x2 <- y2 <- seq(-1, 1, .1)
    z2<- outer(x2, y2, lambda2)
    persp(x2, y2, z2, theta = 30, phi = 30, expand = 0.5, col = "lightblue", xlab="X", ylab = "Y", ma in="Maximum Likelihood Model Indensity") -> res
    phi <- seq(0, 2 * pi, len = 201)
    xr <- cos(phi)
    yr <- sin(phi)
    lines(trans3d(xr, yr, lambda(xr, yr), res), col = "pink", lwd = 2)</pre>
```

Maximum Likelihood Model Indensity



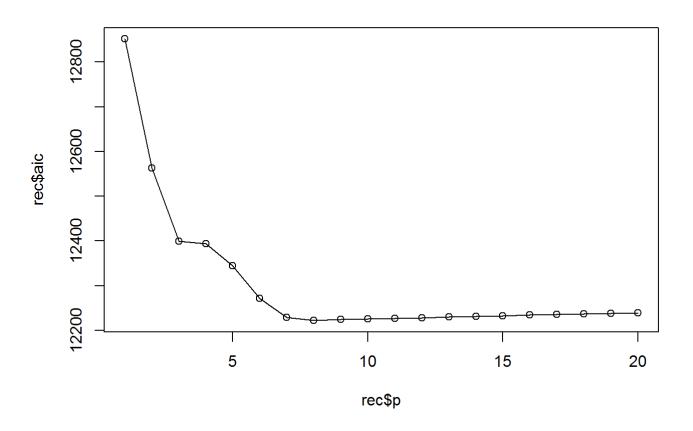


```
hipp_data_n <- hipp_data[, c("spikes", "xN", "yN", "xN2", "yN2", "spikes_hist1", "spikes_hist2", "spikes_hist3", "spikes_hist4", "spikes_hist5", "spikes_hist6", "spikes_hist7", "spikes_hist8", "spikes_hist9", "spikes_hist10", "spikes_hist11", "spikes_hist12", "spikes_hist13", "spikes_hist14", "spikes_hist15", "spikes_hist16", "spikes_hist17", "spikes_hist18", "spikes_hist19", "spikes_hist20")]

p <- aic <- c()

for (i in 6:25) {
    hipp_data_a <- hipp_data_n[, 1:i]
    m3 <- glm(spikes ~ ., poisson, hipp_data_a)
    aic <- c(aic, m3$aic)
    p <- c(p, i-5)
    }

rec <- data.frame("p"=p, "aic"=aic)
    plot(rec$p, rec$aic, type="1")
    points(rec$p, rec$aic)
```



```
subset(rec, aic==min(aic))
```

```
## p aic
## 8 8 12222.27
```

```
hipp_data_n2 <- hipp_data[, c("spikes", "xN", "yN", "xN2", "yN2", "spikes_hist1", "spikes_hist2", "spikes_hist3", "spikes_hist4", "spikes_hist5", "spikes_hist6", "spikes_hist7", "spikes_hist8", "spikes2_hist1", "spikes2_hist3", "spikes2_hist3", "spikes2_hist4", "spikes2_hist5", "spikes2_hist6", "spikes2_hist7", "spikes2_hist7", "spikes2_hist8", "spikes2_hist9", "spikes2_hist10", "spikes2_hist11", "spikes2_hist12", "spikes2_hist13", "spikes2_hist15", "spikes2_hist16", "spikes2_hist17", "spikes2_hist18", "spikes2_hist19", "spikes2_hist19", "spikes2_hist10", "spikes2_hist18", "spikes2_hist19", "spikes2_hist10", "spikes2_hist17", "spikes2_hist18", "spikes2_hist19", "spikes2_hist10", "spikes2
```

```
## p1 p2 aic2
## 1 8 1 12224.16
```

```
hipp_data_n3 <- select(hipp_data, spikes, xN, yN, xN2, yN2, spikes_hist1:spikes_hist20, spikes2_hist1:sp
ikes2 hist20)
p41 <- p42 <- aic4 <- c()
for (k in 6:25) {
  hipp data a <- hipp data n3[, 1:k] %>% select(-xN, -yN, -xN2, -yN2)
  m3 <- glm(spikes ~., poisson, hipp data a)
  aic4 <- c(aic4, m3$aic)
  p41 \leftarrow c(p41, k-5)
  p42 <- c (p42, 0)
  for (i in 26:45) {
    hipp_data_a <- hipp_data_n3[, c(1:k, 26:i)] %>% select(-xN, -yN, -xN2, -yN2)
    m3 <- glm(spikes ~., poisson, hipp data a)
    aic4 <- c(aic4, m3$aic)
    p41 \leftarrow c(p41, k-5)
    p42 <- c (p42, i-25)
    }
  }
rec4 <- data.frame("p1"=p41, "p2"=p42, "aic"=aic4)
subset(rec4, aic==min(aic))
```

```
## p1 p2 aic
## 420 20 20 13534.88
```

This does have a minimum aic. Almost every parameters are significant. The reason for why only when we fail to model the spatial component of the firing activity is that, in spatial component, the correlation between history and network interaction is more significant.

```
m0 <- glm(spikes ~ xN2 + yN2 + xN + yN + spikes_hist1 + spikes_hist2 + spikes_hist3 + spikes_hist4 + spikes_hist5 + spikes_hist6 + spikes_hist7 + spikes_hist8, poisson, hipp_data)
hipp_data[, "num"] <- 1:nrow(hipp_data)
hipp_data_zz <- subset(hipp_data, spikes==1)
Xi <- hipp_data_zz[, "num"]
```