# $Stats218\_HW1$

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```
library(networkdata)
library(sna)
library(network)
library(tidyverse)
```

#### Question 1

```
data(butland_ppi)
data(addhealth9)
data(tribes)
```

 $\mathbf{a})$ 

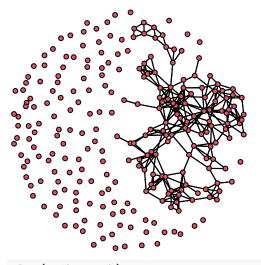
```
only_boy <- which(addhealth9$X[,"female"] == 0)
boys_match <- addhealth9$E[addhealth9$E[,1] %in% only_boy & addhealth9$E[,2] %in% only_boy,]
health_ntwk <- network(boys_match, directed = FALSE)
print(health_ntwk)</pre>
```

```
##
    Network attributes:
     vertices = 254
##
##
     directed = FALSE
##
     hyper = FALSE
##
     loops = FALSE
##
     multiple = FALSE
     bipartite = FALSE
##
##
     total edges= 273
##
       missing edges= 0
       non-missing edges= 273
##
##
## Vertex attribute names:
##
       vertex.names
##
## No edge attributes
```

```
pos_tribe <- tribes[,,"pos"]</pre>
tribe_ntwk <- network(pos_tribe, directed = FALSE)</pre>
print(tribe_ntwk)
## Network attributes:
##
     vertices = 16
##
     directed = FALSE
##
     hyper = FALSE
     loops = FALSE
##
     multiple = FALSE
##
##
     bipartite = FALSE
##
     total edges= 29
##
       missing edges= 0
##
       non-missing edges= 29
##
## Vertex attribute names:
##
       vertex.names
##
## No edge attributes
bl_ntwk <- network(butland_ppi, directed = FALSE)</pre>
print(bl_ntwk)
## Network attributes:
##
    vertices = 270
     directed = FALSE
##
##
     hyper = FALSE
##
     loops = FALSE
##
     multiple = FALSE
     bipartite = FALSE
##
     total edges= 716
##
       missing edges= 0
##
       non-missing edges= 716
##
## Vertex attribute names:
##
       vertex.names
##
## No edge attributes
```

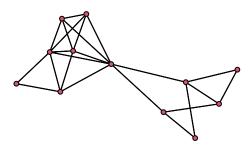
**b**)

plot(health\_ntwk)

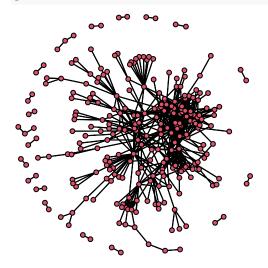


plot(tribe\_ntwk)





plot(bl\_ntwk)



c)
health\_degree <- degree(health\_ntwk, gmode = "graph") %>% table()
tribe\_degree <- degree(tribe\_ntwk, gmode = "graph") %>% table()
bl\_degree <- degree(bl\_ntwk, gmode = "graph") %>% table()
health\_degree

## .
## 0 1 2 3 4 5 6 7 8 9 10 11 13
## 136 8 10 16 29 22 10 11 8 1 1 1 1
tribe\_degree

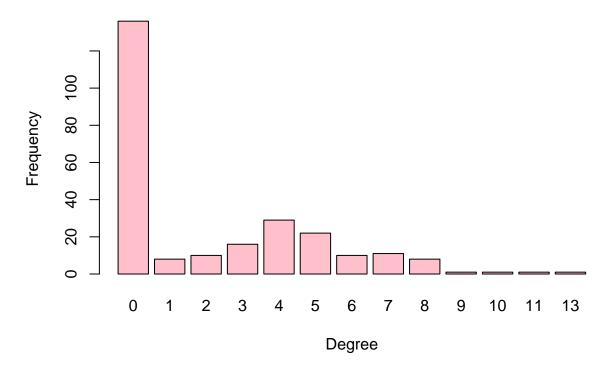
## . ## 2 3 4 5 6 7 ## 3 6 4 1 1 1

bl\_degree

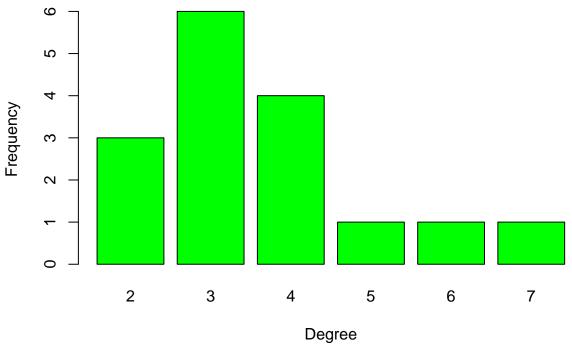
## . ## 1 2 3 4 5 6 7 8 10 11 12 13 14 15 16 17 18 19 20 22 ## 105 39 19 13 16 10 14 6 3 2 3 9 3 5 4 1 2 3 1 2 ## 23 27 28 30 32 33 34 36 ## 2 1 2 1 1 1 1 1

d)

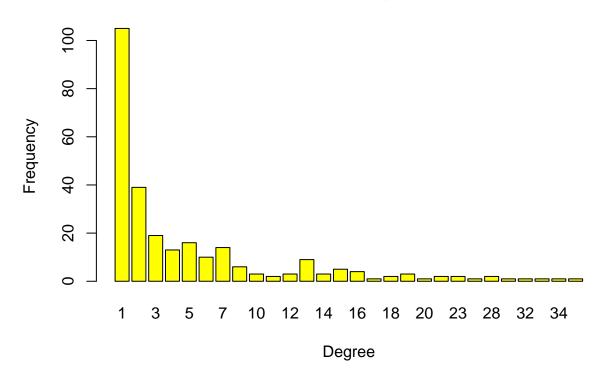
#### **Health Network Degree Distribution**



### **Tribe Network Degree Distribution**



### **Butland PPI Network Degree Distribution**



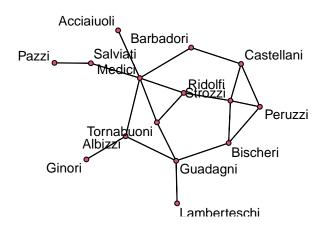
#### Question 2

```
data(florentine)
```

**a**)

```
network(flomarriage) %>%
plot(displaylabels = TRUE,
    label = network.vertex.names(flomarriage),
    label.cex = 0.8)
```

Pucci



b)

```
fm_degree <- degree(network(flomarriage), gmode = "graph")

cat("Familiy has the lowest degree: ",
    network.vertex.names(flomarriage)[fm_degree == min(fm_degree)],
    ". Its degree is ", min(fm_degree), ". \n")

## Familiy has the lowest degree: Pucci . Its degree is 0 .

cat("Familiy has the highest degree: ",
    network.vertex.names(flomarriage)[fm_degree == max(fm_degree)],
    ". Its degree is ", max(fm_degree), ". \n")</pre>
```

## Familiy has the highest degree: Medici . Its degree is 6 .

**c**)

```
fm_degree

## [1] 1 3 2 3 3 1 4 1 6 1 3 0 3 2 4 3

d)

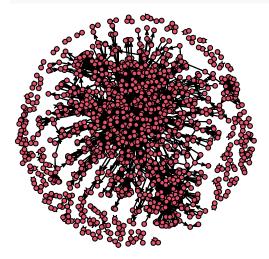
largest_fm <- which.max(component.dist(network(flomarriage))$csize)
largest_component <- component.dist(network(flomarriage))$membership == largest_fm
excluded <- network.vertex.names(flomarriage)[!largest_component]
cat("Family excluded from the largest component in the Florentine Marriage Network: ", excluded)</pre>
```

## Family excluded from the largest component in the Florentine Marriage Network: Pucci

### Question 3

**a**)

```
ccsb <- read.table("CCSB-Y2H.txt")
ccsb <- ccsb[ccsb[, 1] != ccsb[, 2], ]
ccsb_network <- network(ccsb[, 1:2], directed = TRUE)
plot(ccsb_network)</pre>
```



```
b)
out_degrees <- degree(ccsb_network, cmode = "outdegree")</pre>
in_degrees <- degree(ccsb_network, cmode = "indegree")</pre>
cat("Correlation between in-degree and out-degree:", cor(out_degrees, in_degrees), "\n")
## Correlation between in-degree and out-degree: -0.07393897
cat("Summary of total degrees:\n")
## Summary of total degrees:
summary(out_degrees + in_degrees)
##
      Min. 1st Qu. Median
                               Mean 3rd Qu.
                                               Max.
                                      3.000 85.000
##
     1.000
             1.000
                     1.000
                              2.662
barplot(table(out_degrees + in_degrees), main = "Protein Activity Network Degree Distribution",
        xlab = "Degree", ylab = "Frequency", col = "yellow")
```

## **Protein Activity Network Degree Distribution**

