

Seminar 2

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```
library("network")

## network: Classes for Relational Data
## Version 1.13.0.1 created on 2015-08-31.
## copyright (c) 2005, Carter T. Butts, University of California-Irvine
##           Mark S. Handcock, University of California -- Los Angeles
##           David R. Hunter, Penn State University
##           Martina Morris, University of Washington
##           Skye Bender-deMoll, University of Washington
## For citation information, type citation("network").
## Type help("network-package") to get started.

num_nodes <- 15

my_matrix<-matrix(round(runif(num_nodes*num_nodes)),
nrow = num_nodes,
ncol = num_nodes)

diag(my_matrix) <- 0

dim(my_matrix)

## [1] 15 15

my_network<-as.network(x = my_matrix,
directed = TRUE,
loops = FALSE,
matrix.type = "adjacency"
)

network.size(my_network)

## [1] 15

summary(my_network)

## Network attributes:
## vertices = 15
## directed = TRUE
```

```

## hyper = FALSE
## loops = FALSE
## multiple = FALSE
## bipartite = FALSE
## total edges = 99
## missing edges = 0
## non-missing edges = 99
## density = 0.4714286
##
## Vertex attributes:
## vertex.names:
## character valued attribute
## 15 valid vertex names
##
## No edge attributes
##
## Network edgelist matrix:
##      [,1] [,2]
## [1,]  7  1
## [2,]  8  1
## [3,]  9  1
## [4,] 10  1
## [5,] 12  1
## [6,]  1  2
## [7,]  3  2
## [8,]  5  2
## [9,]  7  2
## [10,] 8  2
## [11,] 9  2
## [12,] 10 2
## [13,] 12 2
## [14,] 15 2
## [15,]  1 3
## [16,]  2 3
## [17,]  5 3
## [18,]  6 3
## [19,]  7 3
## [20,] 11 3
## [21,] 12 3
## [22,]  1 4
## [23,]  2 4
## [24,]  7 4
## [25,] 14 4
## [26,]  1 5
## [27,]  2 5

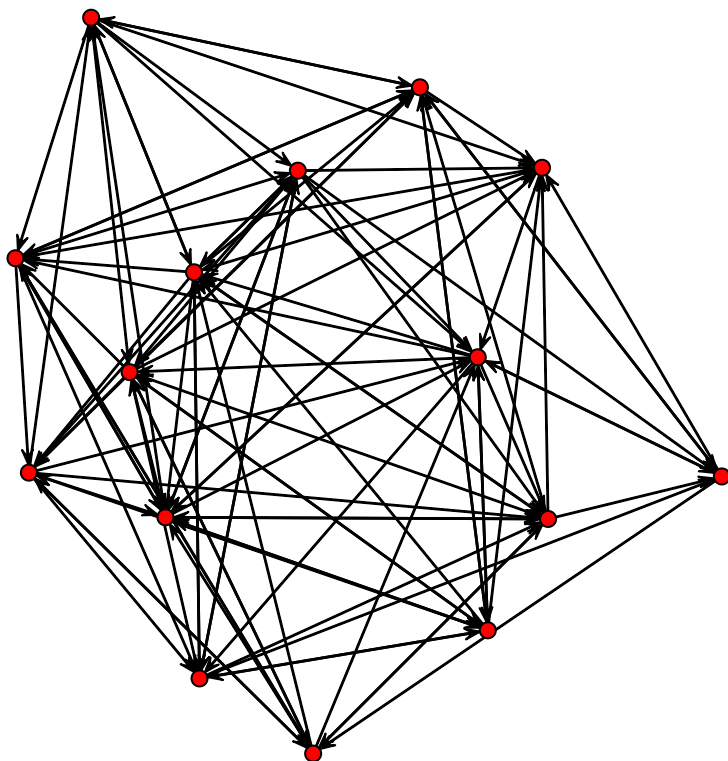
```

##	[28,]	4	5
##	[29,]	7	5
##	[30,]	9	5
##	[31,]	11	5
##	[32,]	1	6
##	[33,]	2	6
##	[34,]	4	6
##	[35,]	5	6
##	[36,]	8	6
##	[37,]	12	6
##	[38,]	13	6
##	[39,]	15	6
##	[40,]	3	7
##	[41,]	4	7
##	[42,]	5	7
##	[43,]	6	7
##	[44,]	8	7
##	[45,]	11	7
##	[46,]	12	7
##	[47,]	15	7
##	[48,]	2	8
##	[49,]	6	8
##	[50,]	10	8
##	[51,]	11	8
##	[52,]	14	8
##	[53,]	2	9
##	[54,]	4	9
##	[55,]	6	9
##	[56,]	7	9
##	[57,]	10	9
##	[58,]	12	9
##	[59,]	14	9
##	[60,]	15	9
##	[61,]	3	10
##	[62,]	4	10
##	[63,]	5	10
##	[64,]	6	10
##	[65,]	8	10
##	[66,]	11	10
##	[67,]	12	10
##	[68,]	1	11
##	[69,]	5	11
##	[70,]	6	11
##	[71,]	7	11
##	[72,]	8	11

```
## [73,]  9 11
## [74,]  1 12
## [75,]  3 12
## [76,]  9 12
## [77,] 10 12
## [78,] 13 12
## [79,]  3 13
## [80,]  5 13
## [81,]  6 13
## [82,] 11 13
## [83,] 14 13
## [84,]  1 14
## [85,]  3 14
## [86,]  4 14
## [87,]  7 14
## [88,]  8 14
## [89,]  9 14
## [90,] 10 14
## [91,] 13 14
## [92,]  2 15
## [93,]  3 15
## [94,]  4 15
## [95,]  5 15
## [96,]  8 15
## [97,] 10 15
## [98,] 13 15
## [99,] 14 15
```

```
par(mar=c(0,0,0,0))
```

```
plot(my_network)
```



```
library(foreign)
drugpaj <- read.paj('drugnet2.paj')
names(drugpaj)
```

```
## [1] "networks" "partitions"
```

```
names(drugpaj$networks)
```

```
## [1] "C:\\Users\\Ann\\Desktop\\drugnet.net"
```

```
names(drugpaj$partitions)
```

```
## [1] "C:\\Users\\Ann\\Desktop\\drugnet_gender.clu"
```

```
## [2] "C:\\Users\\Ann\\Desktop\\drugnet_ethnicity.clu"
```

```
drug <- drugpaj$networks[[1]]
class(drug)
```

```
## [1] "network"
```

```
drug
```

```
## Network attributes:
```

```
## vertices = 293
```

```
## directed = TRUE
```

```
## hyper = FALSE
```

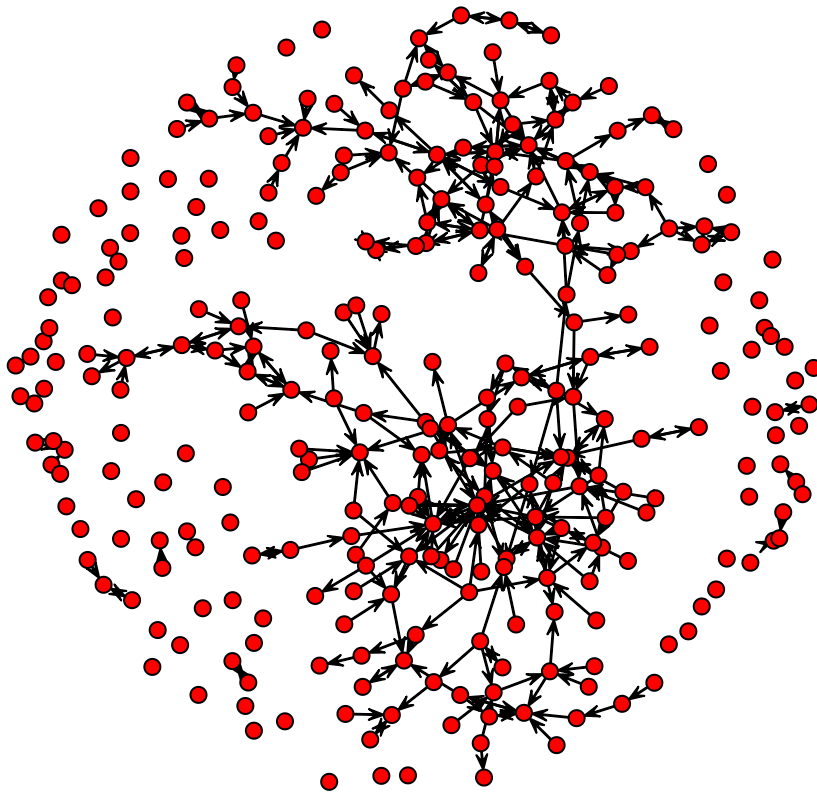
```
## loops = FALSE
```

```

## multiple = FALSE
## bipartite = FALSE
## title = C:\Users\Ann\Desktop\drugnet.net
## total edges= 337
##     missing edges= 0
##     non-missing edges= 337
##
## Vertex attribute names:
##     vertex.names x y z
##
## Edge attribute names:
##     C:\Users\Ann\Desktop\drugnet.net

```

```
plot(drug)
```



The network above displays the referrals of drug users. The one strange thing about that network is that a lot of people (units) are not connected at all. That might be explained by the hypothesis that a plenty of drug users come to using them not exactly from other drug users. The other interesting thing is that the most complex relations in many cases a one-way directed, moreover, that can happen through not only one unit, but through the line of them. That means, that there are might be some kind of hierarchy among drug users. But that is just a hypothesis.

```
network.size(drug)
```

```
## [1] 293
```

```
network.edgecount(drug)
```

```
## [1] 337
```

```
network.dyadcount(drug)
```

```
## [1] 85556
```

The numbers above represent some characteristics of the size of the network.

The first number (293) represent the total amount of the nodes. Nodes represent the units of the network, base on the connections between which the model is built. That means that there are 293 units in the sample.

The second number (337) represent the total amount of the edges in the model. Edges represent the connections between the units of the model. That means that there are 337 connections in the model.

The third number (85556) represent the total amount of all possible dyads the model. Dyad is the pair between two units. That means that the maximum amount of the dyads in the model is 85556.

```
names(drugpaj$partitions)
```

```
## [1] "C:\\Users\\Ann\\Desktop\\drugnet_gender.clu"
```

```
## [2] "C:\\Users\\Ann\\Desktop\\drugnet_ethnicity.clu"
```

```
gender <- drugpaj$partitions[[1]]
```

```
gender
```

```
## [1] 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 1 1 1 1 1 1 2 1 2 1 1 1 1 1 1 1
## [36] 1 2 1 1 1 1 1 1 1 1 2 2 1 1 1 1 2 1 2 1 1 1 1 1 2 1 2 1 1 1 1 1 1 1
## [71] 2 2 1 1 2 1 1 1 1 1 2 1 1 1 1 1 2 2 2 1 2 2 1 1 1 2 1 1 2 1 2 1 1 1 1
## [106] 1 1 1 1 1 2 2 1 1 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1
## [141] 1 1 1 1 2 1 1 2 1 2 2 1 1 1 1 2 1 1 2 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1
## [176] 1 1 2 1 1 1 1 1 2 1 1 1 1 0 1 1 1 1 1 2 1 1 1 0 1 2 0 2 1 2 2 1 1 2 1
## [211] 1 2 1 1 1 2 1 2 1 1 1 1 1 2 1 1 1 2 1 1 1 1 2 1 1 1 1 2 1 1 1 1 1 1 2
## [246] 1 2 2 2 2 1 1 1 1 1 2 2 2 1 0 0 2 2 2 2 2 2 0 2 2 2 2 2 2 2 2 2 1 2 2
## [281] 2 1 0 2 2 2 2 2 2 2 2 2 2
```

```
table(gender)
```

```
## gender
```

```
## 0 1 2
```

```
## 7 200 86
```

```
female <- ifelse(gender == 2, 1,
ifelse(gender == 1, 0, NA))
```

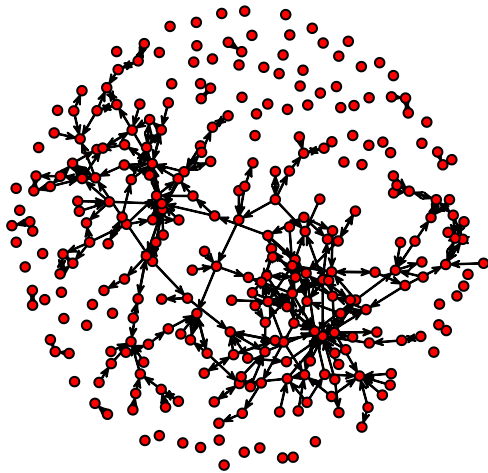
```
female
```

```
## [1] 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 0 0 0 0
## [24] 0 0 1 0 1 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 1
## [47] 1 0 0 0 0 1 0 1 0 0 0 0 0 0 1 0 1 0 0 0 0 0 0 0
## [70] 0 1 1 0 0 1 0 0 0 0 0 0 1 0 0 0 0 0 1 1 1 0 1 1
## [93] 0 0 0 1 0 0 1 0 1 0 0 0 0 0 0 0 0 0 0 1 1 0 0 0
## [116] 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0
## [139] 0 0 0 0 0 0 1 0 0 1 0 1 1 0 0 0 0 1 0 0 1 0 0
## [162] 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 1
## [185] 0 0 0 0 NA 0 0 0 0 0 1 0 0 0 NA 0 1 NA 1 0 1 1 0
## [208] 0 1 0 0 1 0 0 0 1 0 1 0 0 0 0 0 1 0 0 0 1 0 0
## [231] 0 0 1 0 0 0 0 1 0 0 0 0 0 0 1 0 1 1 1 1 0 0 0
## [254] 0 0 1 1 1 0 NA NA 1 1 1 1 1 1 NA 1 1 1 1 1 1 1 1
## [277] 1 0 1 1 1 0 NA 1 1 1 1 1 1 1 1 1 1
```

```
drug <- set.vertex.attribute(drug, 'female', value=c(female))
ethnicity <- drugpaj$partitions[[2]]
table(ethnicity)
```

```
## ethnicity
## 1 2 3 4
## 25 99 155 14
```

```
drug <- set.vertex.attribute(drug, 'ethnicity', value=c(ethnicity))
plot(drug)
```

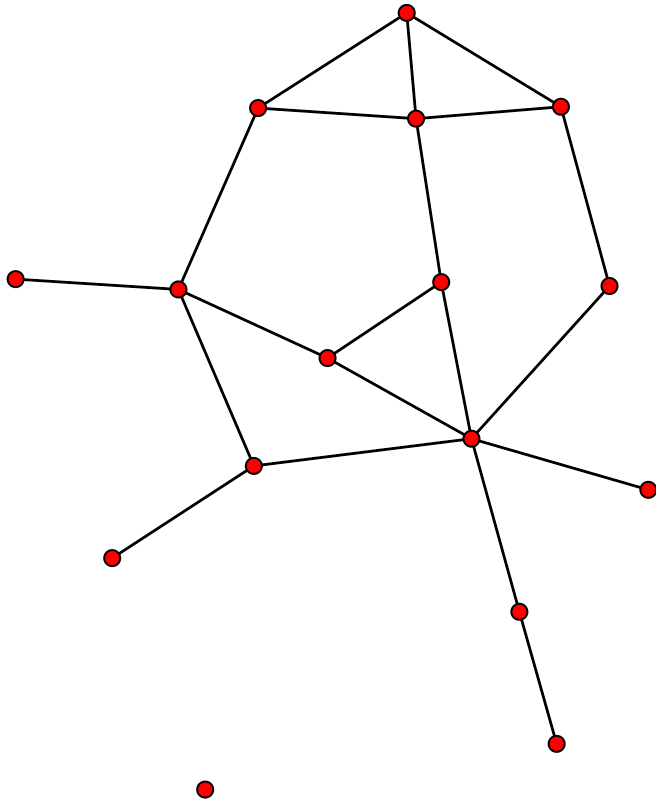


```
load('flo.Rdata')
```

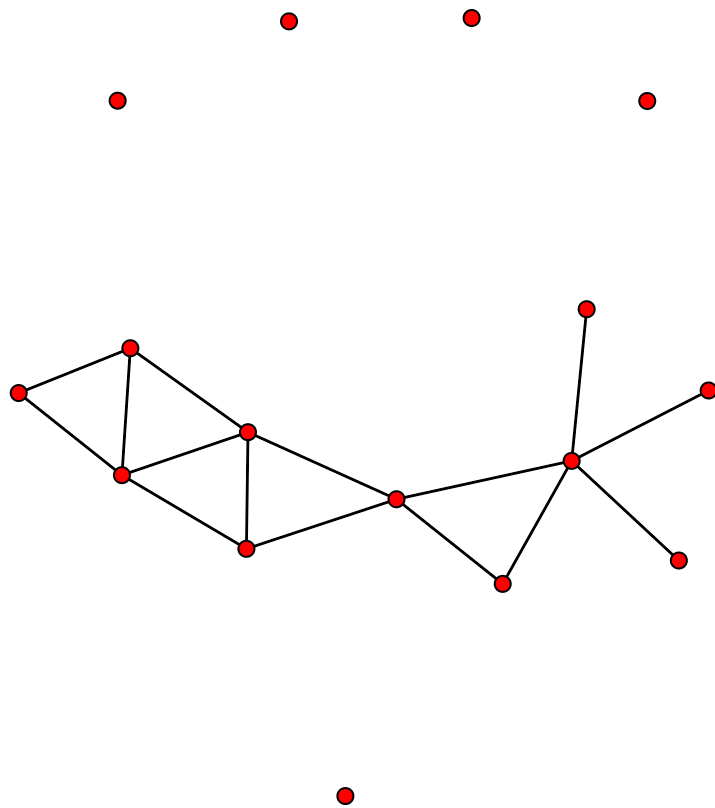
```
flo.marriage <- as.network(as.matrix(flo.marriage), directed=FALSE)
flo.biz <- as.network(as.matrix(flo.biz), directed=FALSE)
# Add attributes
set.vertex.attribute(flo.marriage, 'wealth', flo.att[,2])
```



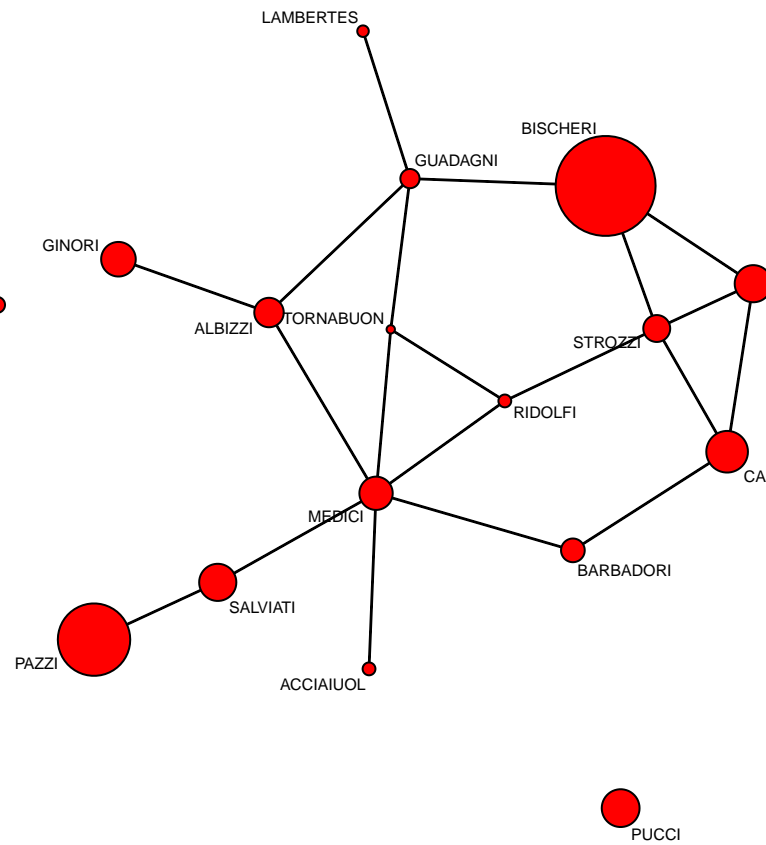
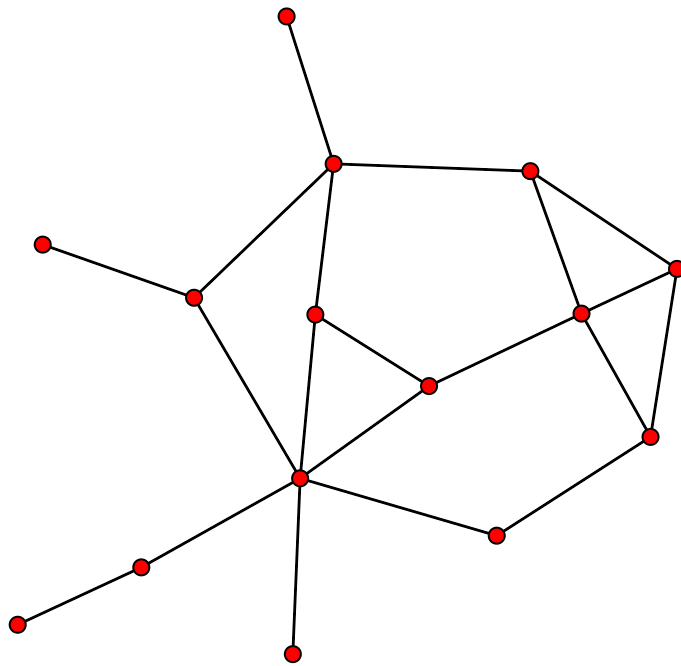
```
set.vertex.attribute(flo.biz, 'wealth', flo.att[,2])  
# Simple plots:  
par(mar=c(0,0,0,0))  
plot(flo.marriage)
```



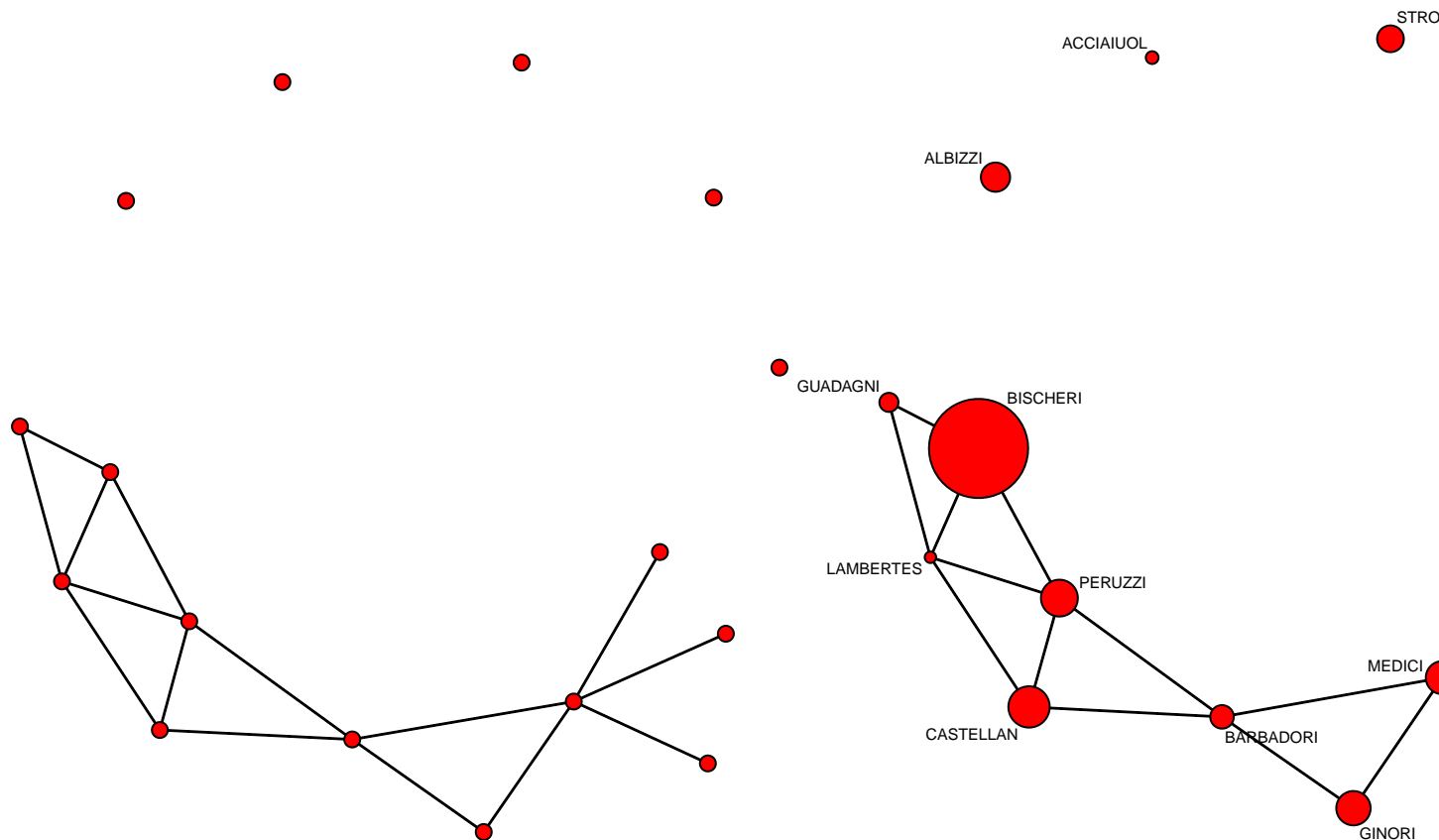
```
plot(flo.biz)
```



```
par(mar=c(0,0,0,0))
plot(flo.marriage,
vertex.cex=(get.vertex.attribute(flo.marriage, 'wealth')/25+.4),
displaylabels=TRUE,
label.cex=.5,
label.pos=0,
coord=plot(flo.marriage))
```



```
par(mar=c(0,0,0,0))
plot(flo.biz,
vertex.cex=(get.vertex.attribute(flo.biz, 'wealth')/25+.4),
displaylabels=TRUE,
label.cex=.5,
label.pos=0,
coord=plot(flo.biz))
```



```
flo.names <- scan('padgett.dat', what='character', skip=4, nlines=16)
flos <- read.table('padgett.dat', skip=41, col.names=flo.names)
flo.att <- read.table('padgw.dat',
col.names =c('WEALTH','NUM.PRIORS','NUM.TIES'), skip=25)
flo.att
```

##	WEALTH	NUM.PRIORS	NUM.TIES
## 1	10	53	2
## 2	36	65	3
## 3	27	38	4
## 4	146	74	29
## 5	55	0	14
## 6	44	12	9
## 7	20	22	18
## 8	8	21	14
## 9	42	0	14
## 10	103	53	54
## 11	48	0	7
## 12	49	42	32
## 13	10	35	5
## 14	48	0	7
## 15	32	0	9

```
## 16      3      0      1
```

```
flo.att <-cbind(flo.names,flo.att)
head(flo.att)
```

```
## flo.names WEALTH NUM.PRIORS NUM.TIES
## 1 ACCIAIUOL 10      53      2
## 2 ALBIZZI 36      65      3
## 3 BARBADORI 27      38      4
## 4 BISCHERI 146      74      29
## 5 CASTELLAN 55      0      14
## 6 GINORI 44      12      9
```

```
flo.marriage <-flos[1:16,]
dim(flo.marriage)
```

```
## [1] 16 16
```

```
row.names(flo.marriage) <-flo.names
flo.biz <- flos[17:32,]
row.names(flo.biz) <-flo.names
dim(flo.biz)
```

```
## [1] 16 16
```

```
flo.marriage[1:2,1:2]
```

```
## ACCIAIUOL ALBIZZI
## ACCIAIUOL 0 0
## ALBIZZI 0 0
```

```
flo.marriage[15:16,15:16]
```

```
## STROZZI TORNABUON
## STROZZI 0 0
## TORNABUON 0 0
```

```
flo.biz[1:2,1:2]
```

```
## ACCIAIUOL ALBIZZI
## ACCIAIUOL 0 0
## ALBIZZI 0 0
```

```
flo.biz[15:16,15:16]
```

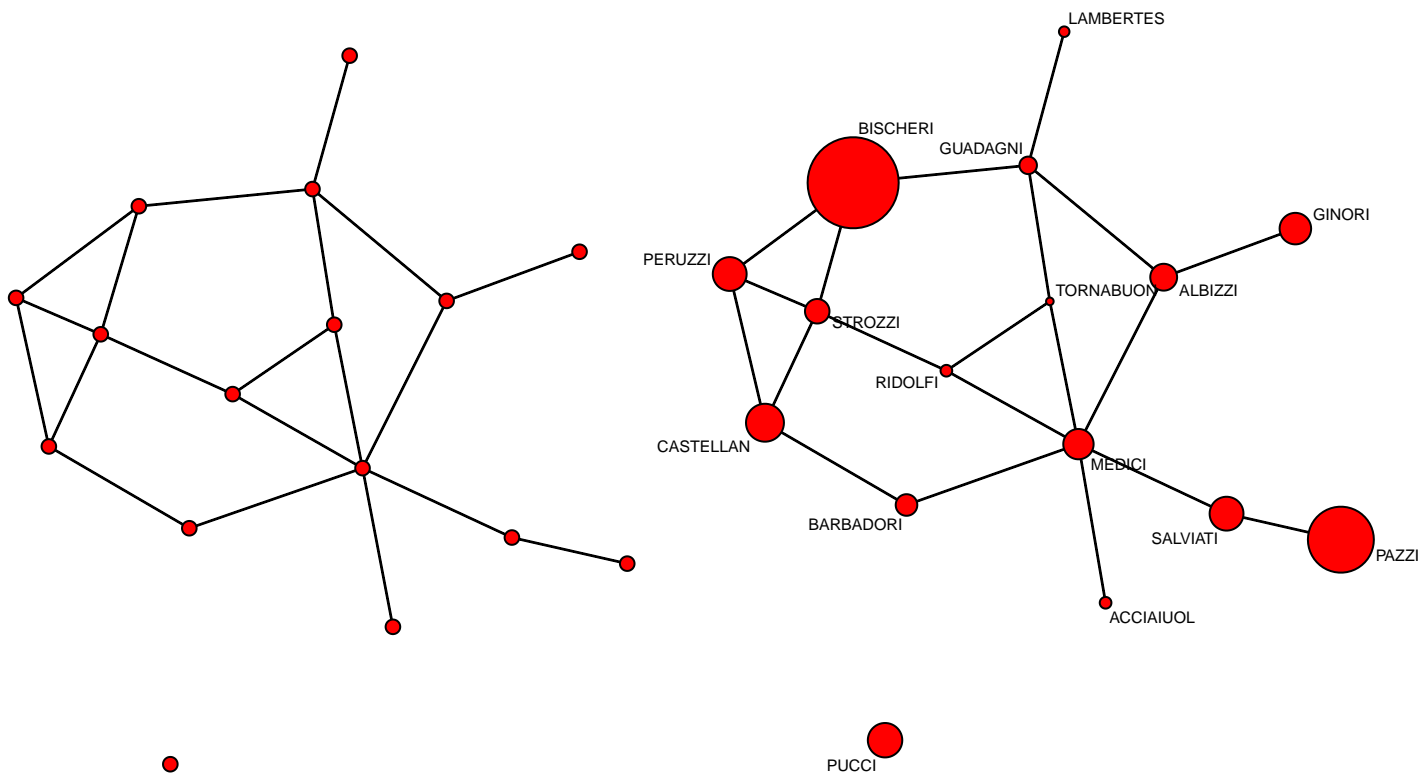
```
## STROZZI TORNABUON
## STROZZI 0 0
## TORNABUON 0 0
```

```

flo.marriage <- as.network(as.matrix(flo.marriage),directed=FALSE)
flo.biz <- as.network(as.matrix(flo.biz),directed=FALSE)
## add attributes
set.vertex.attribute(flo.marriage, 'wealth', flo.att[,2])
set.vertex.attribute(flo.biz, 'wealth', flo.att[,2])

par(mar=c(1,1,1,1))
plot(flo.marriage,
vertex.cex=(get.vertex.attribute(flo.marriage, 'wealth')/25+.4),
displaylabels=TRUE,
label.cex=.5,
label.pos=0,
coord=plot(flo.marriage))

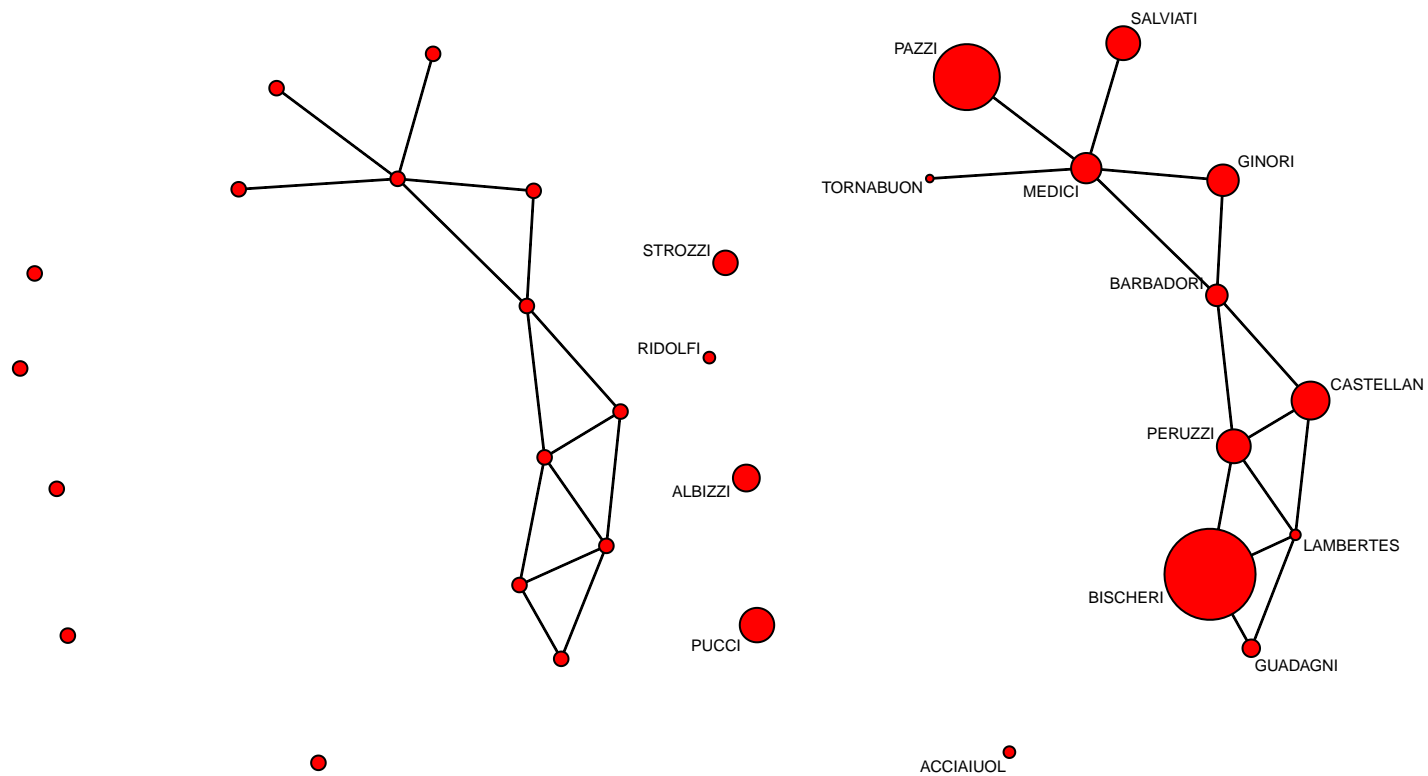
```



```

par(mar=c(1,1,1,1))
plot(flo.biz,
vertex.cex=(get.vertex.attribute(flo.biz, 'wealth')/25+.4),
displaylabels=TRUE,
label.cex=.5,
label.pos=0,
coord=plot(flo.biz))

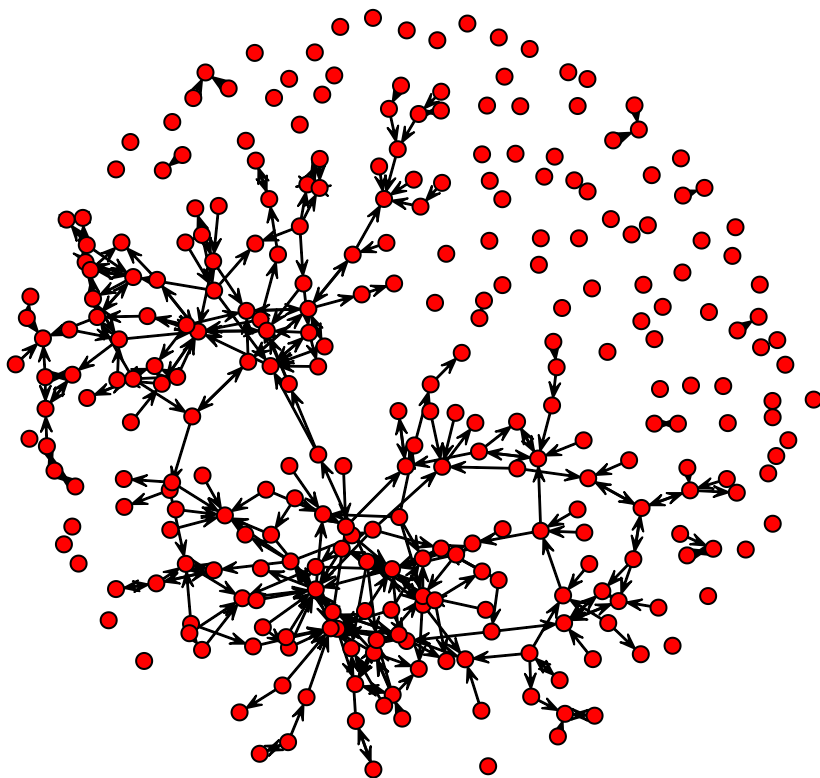
```



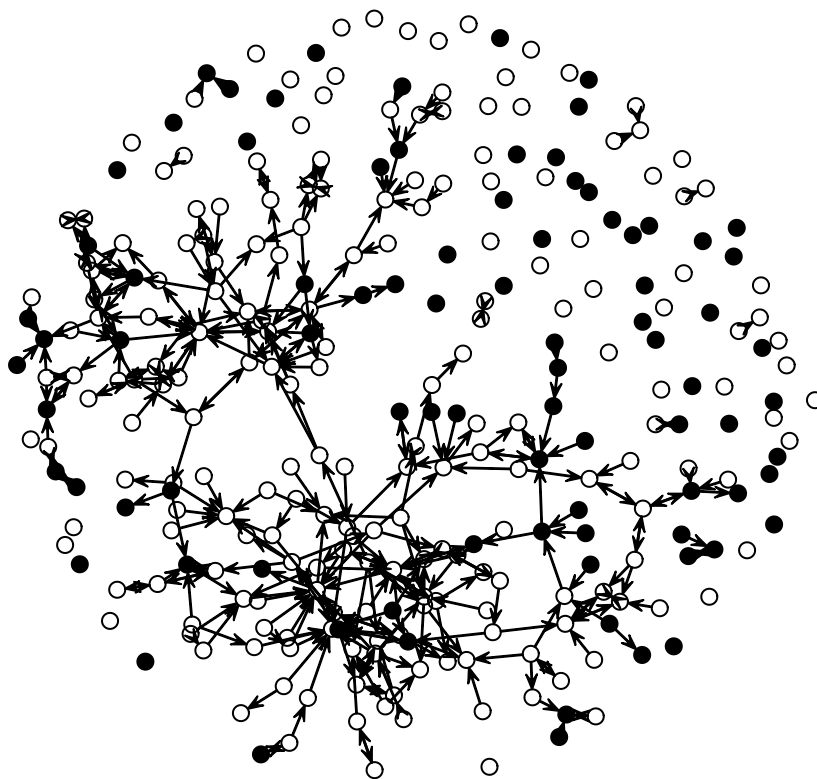
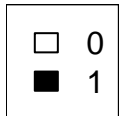
```
save(flo.marriage, flo.biz, file= 'floNets.Rdata')

drug.edges <- as.matrix(drug, matrix.type= 'edgelist')
write.csv(drug.edges, file= 'drugsEdgelist.csv',row.names=FALSE)

par(mar=c(0,0,0,0))
plot(drug,
     vertex.col=(female),
     displaylabels=FALSE,
     coord=plot(drug))
```

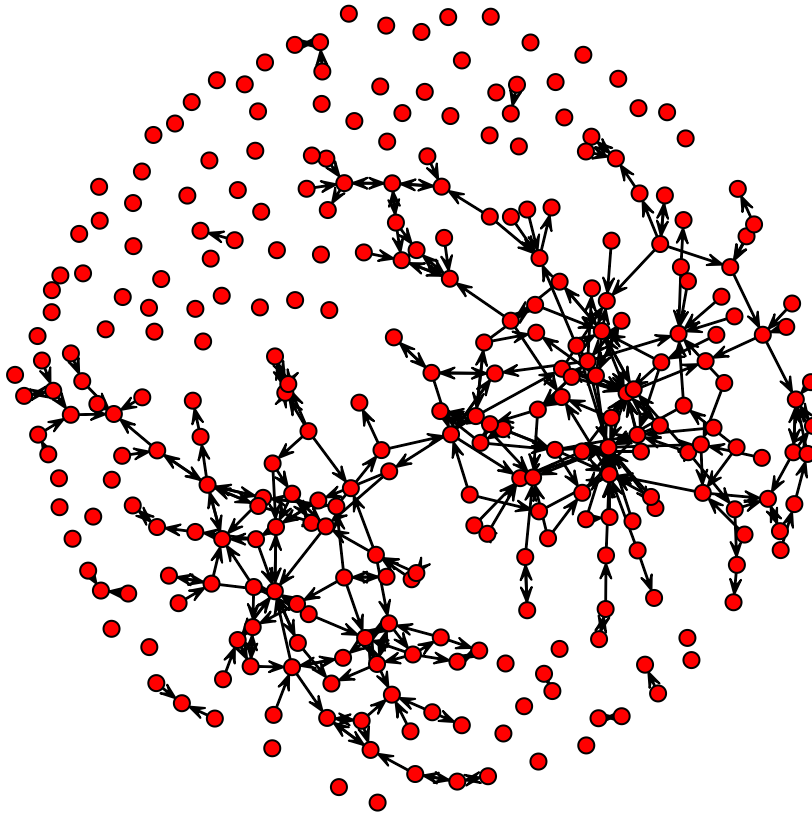


```
legend('topleft', legend = (sort(unique(female))), fill=(sort(unique(female))))
```

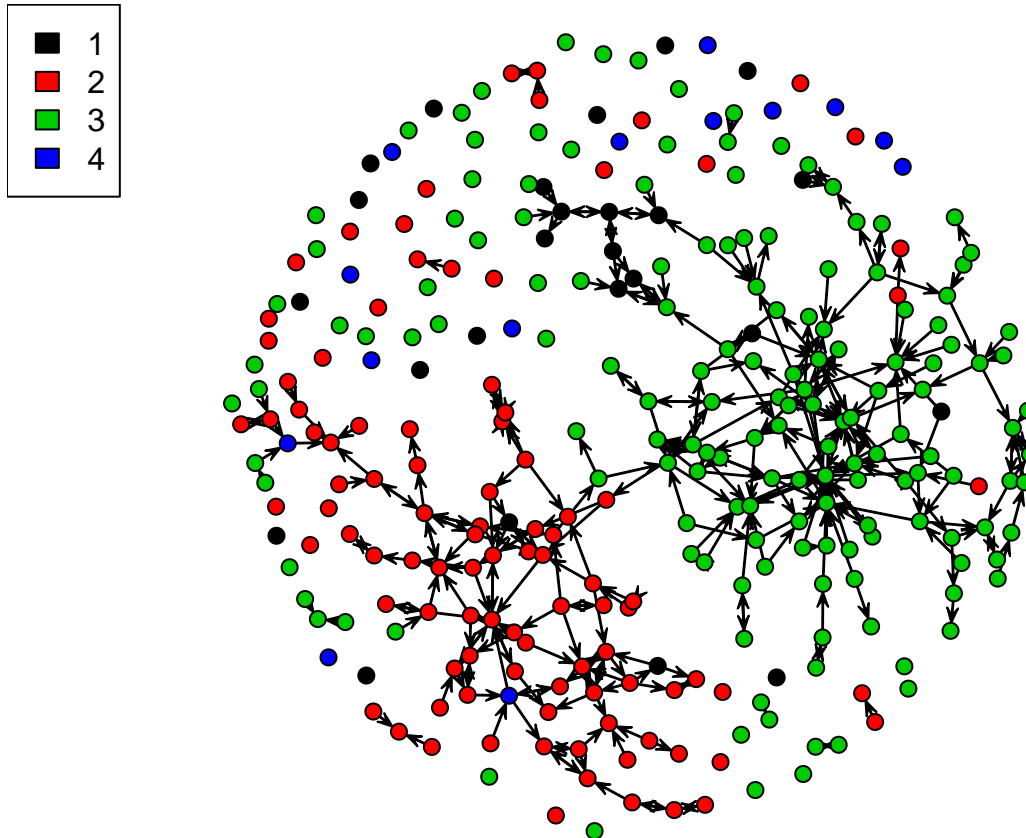


The network above represent the connections between drug users and includes their gender as attribute. Besides the fact that drug users are male, we can't make any relevant conclusions.

```
par(mar=c(0,0,0,0))
plot(drug,
      vertex.col=(get.vertex.attribute(drug, "ethnicity")),
      displaylabels=FALSE,
      coord=plot(drug))
```



```
legend('topleft', legend = (sort(unique((get.vertex.attribute(drug, "ethnicity"))))), fill=(sort(unique((get
```



The network above represent the connections between drug users and includes their ethnicity as attribute. Based on that network, we can tell that there is positive tendency between drug users of the same race, their ties are more close. I don't have the labels of the nodes, but I can suggest that the drug users might belong to the same either negroid or latinos ethnicity.