

# ChromosomeNetwork

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Getting the package igraph.

```
require(igraph)
```

```
## Loading required package: igraph
```

Reading the data set.

```
mydata <- read.csv("ChromosomeNetwork.csv")  
mydata
```

##	Mother	Father	X2nMother	X2nFather	CND	MNI	GR	GEOD	GEND
## 1	2709	2830J	68	66	2	3	28.0	134.2	0.636
## 2	2816	2893G	66	64	2	NA	86.0	223.3	0.545
## 3	2830D	2893C	66	64	2	1	72.0	117.6	0.716
## 4	2830D	2895K	66	66	0	1	88.0	105.7	0.432
## 5	2830D	2890A	66	67	1	2	57.0	134.2	0.636
## 6	2830J	2893C	66	64	2	3	91.0	117.6	0.508
## 7	2830J	2889D	66	66	0	0	96.0	133.7	0.455
## 8	2830J	2830D	66	66	0	0	90.0	0.0	0.508
## 9	2830N	2893D	65	62	3	NA	0.0	117.6	0.545
## 10	2865H	2893G	68	64	4	NA	0.0	51.7	0.727
## 11	2875G	2830N	62	65	3	NA	0.0	65.1	0.508
## 12	2875G	2880A	62	66	4	NA	0.0	3.7	0.598
## 13	2875G	2882A	62	66	4	NA	7.5	94.7	0.444
## 14	2875G	2893A	62	64	2	NA	1.0	71.0	0.663
## 15	2875G	2893D	62	62	0	NA	10.0	71.0	0.663
## 16	2875G	2895K	62	66	4	NA	20.0	79.1	0.542
## 17	2880A	2830N	66	65	1	NA	0.0	67.1	0.636
## 18	2880R	2830D	66	66	0	NA	0.0	67.1	0.481
## 19	2882A	2830D	66	66	0	3	50.0	130.1	0.636
## 20	2882A	2880A	66	66	0	NA	0.0	91.1	0.545
## 21	2882A	2893D	66	62	4	NA	0.0	29.3	0.545
## 22	2889A	2893C	68	64	4	NA	0.0	51.6	0.663
## 23	2889D	2895K	66	66	0	1	82.0	117.6	0.395
## 24	2890A	2895K	67	66	1	1	82.0	107.3	0.478
## 25	2890A	2889R	67	65	2	NA	2.0	13.9	0.417
## 26	2890A	2889D	67	66	1	NA	0.0	13.9	0.299
## 27	2890A	2895H	67	67	0	NA	0.0	107.3	0.534
## 28	2893G	2830J	64	66	2	NA	0.0	117.6	0.455
## 29	2893G	2830D	64	66	2	NA	25.0	117.6	0.754
## 30	2893A	2893D	64	62	2	NA	0.0	0.0	0.455
## 31	2893D	2882A	62	66	4	NA	0.0	29.3	0.545
## 32	2895H	2895K	67	66	1	NA	94.0	0.0	0.462
## 33	2895K	2890A	66	67	1	NA	0.0	107.3	0.478
## 34	2895K	2889D	66	66	0	3	14.0	117.6	0.395

```
## 35 2895K 2709 66 68 2 NA 0.0 107.3 0.523
## 36 2895K 2863M 66 67 1 NA 4.0 88.6 0.652
```

Getting network igraph format and plotting the first graph. Note: By doing this  $\log(E(g)\$GR+10)$ , the connections between circles look clearer.

```
g<-graph.data.frame(mydata, directed=F)
g
```

```
## IGRAPH UN-- 21 36 --
## + attr: name (v/c), X2nMother (e/n), X2nFather (e/n), CND (e/n),
## MNI (e/n), GR (e/n), GEOD (e/n), GEND (e/n)
```

```
V(g)
```

```
## Vertex sequence:
## [1] "2709" "2816" "2830D" "2830J" "2830N" "2865H" "2875G" "2880A"
## [9] "2880R" "2882A" "2889A" "2889D" "2890A" "2893G" "2893A" "28930"
## [17] "2895H" "2895K" "2893C" "2889R" "2863M"
```

```
E(g)
```

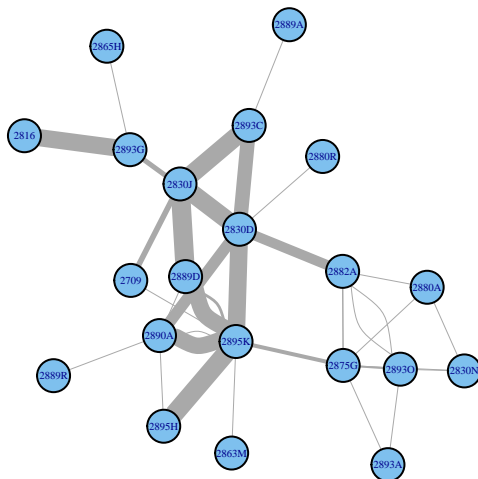
```
## Edge sequence:
##
## [1] 2830J -- 2709
## [2] 2893G -- 2816
## [3] 2893C -- 2830D
## [4] 2895K -- 2830D
## [5] 2890A -- 2830D
## [6] 2893C -- 2830J
## [7] 2889D -- 2830J
## [8] 2830J -- 2830D
## [9] 28930 -- 2830N
## [10] 2893G -- 2865H
## [11] 2875G -- 2830N
## [12] 2880A -- 2875G
## [13] 2882A -- 2875G
## [14] 2893A -- 2875G
## [15] 28930 -- 2875G
## [16] 2895K -- 2875G
## [17] 2880A -- 2830N
## [18] 2880R -- 2830D
## [19] 2882A -- 2830D
## [20] 2882A -- 2880A
## [21] 28930 -- 2882A
## [22] 2893C -- 2889A
## [23] 2895K -- 2889D
## [24] 2895K -- 2890A
## [25] 2889R -- 2890A
## [26] 2890A -- 2889D
## [27] 2895H -- 2890A
## [28] 2893G -- 2830J
```

```
## [29] 2893G -- 2830D
## [30] 2893D -- 2893A
## [31] 2893D -- 2882A
## [32] 2895K -- 2895H
## [33] 2895K -- 2890A
## [34] 2895K -- 2889D
## [35] 2895K -- 2709
## [36] 2863M -- 2895K
```

```
E(g)$GR
```

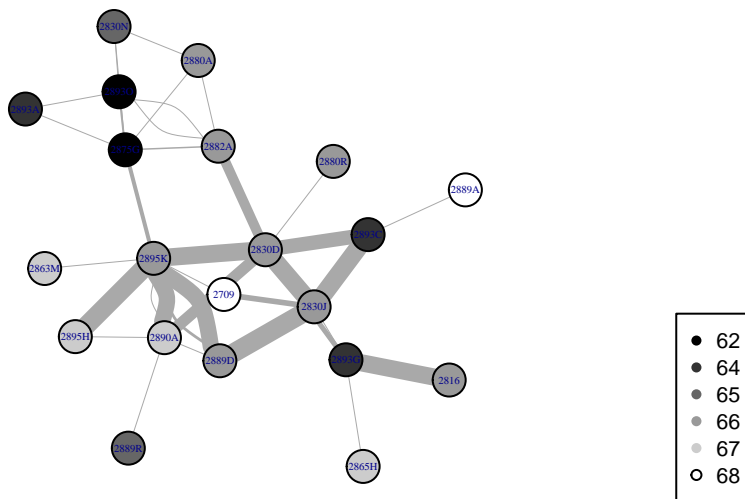
```
## [1] 28.0 86.0 72.0 88.0 57.0 91.0 96.0 90.0 0.0 0.0 0.0 0.0 7.5 1.0
## [15] 10.0 20.0 0.0 0.0 50.0 0.0 0.0 0.0 82.0 82.0 2.0 0.0 0.0 0.0
## [29] 25.0 0.0 0.0 94.0 0.0 14.0 0.0 4.0
```

```
V(g)$label.cex = 0.3
plot(g, layout = layout.auto, edge.width=(E(g)$GR)/10)
```



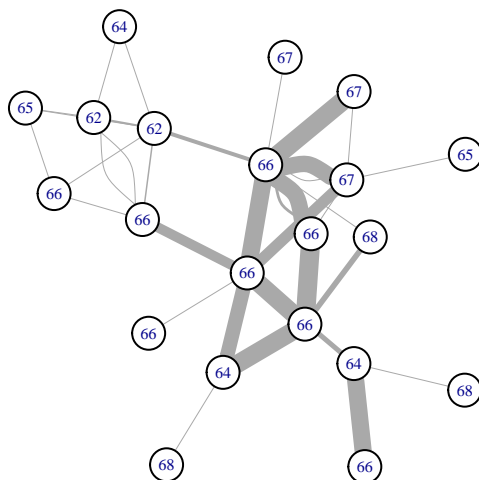
Now we are going to try to put the chromosome number information. 1. Putting chromosome number information in the vertex (it is not really necessary right now) 2. Putting gray scale in the vertex

```
g2 <- g
V(g2)$X2n <- c(68, 66, 66, 66, 65, 68, 62, 66, 66, 66, 68, 66, 67, 64, 64, 62, 67, 66, 64, 65, 67)
V(g2)$color <- c("white", "gray60", "gray60", "gray60", "gray40", "gray80", "black", "gray60", "gray60", "gray60", "gray60", "gray60", "gray60", "gray60", "gray60", "gray60", "gray60", "gray60", "gray60", "gray60")
V(g2)$label.cex = 0.3
plot(g2, layout = layout.auto, edge.width=(E(g)$GR)/10)
legend("bottomright", c("62", "64", "65", "66", "67", "68"), pch=c(16, 16, 16, 16, 16, 1), col=c("black", "gray20", "gray40", "gray60", "gray80", "black"))
```



Now the chromosome number in the vertices.

```
g3 <- g
V(g3)$name <- as.character(V(g2)$X2n)
V(g3)$color <- rep("white", 21)
V(g3)$label.cex = 0.5
plot(g3, edge.width=(E(g)$GR)/10)
```



Final important chunk

```
sessionInfo()
```

```
## R version 3.1.2 (2014-10-31)
## Platform: x86_64-pc-linux-gnu (64-bit)
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8      LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8     LC_NAME=C
##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
```

```
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] igraph_0.7.1
##
## loaded via a namespace (and not attached):
## [1] digest_0.6.4    evaluate_0.5.5  formatR_1.0     htmltools_0.2.6
## [5] knitr_1.9       rmarkdown_0.4.2 stringr_0.6.2   tools_3.1.2
## [9] yaml_2.1.13
```