What are social networks?

NETWORK ANALYSIS IN R

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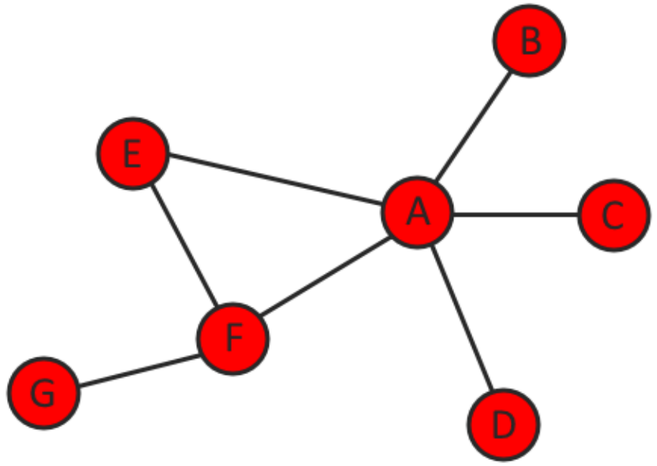
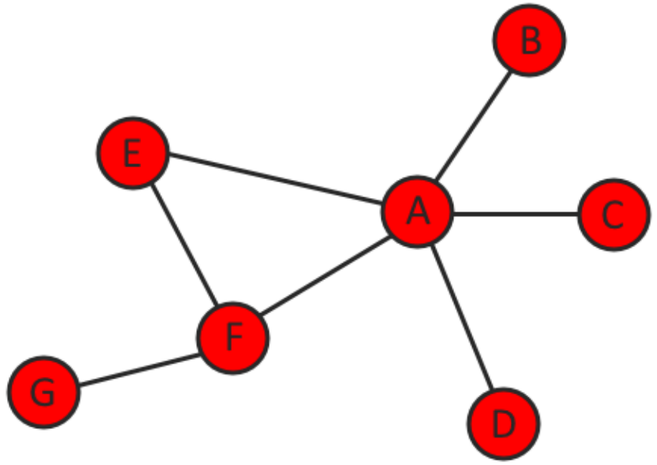
Network data: adjacency matrix



	A	B	C	D	E	F	G
A	0	1	1	1	1	1	0
B	1	0	0	0	0	0	0
C	1	0	0	0	0	0	0
D	1	0	0	0	0	0	0
E	1	0	0	0	0	1	0
F	1	0	0	0	1	0	1
G	0	0	0	0	0	1	0

Network data: edgelist



A	B
A	C
A	D
A	E
A	F
E	F
F	G

The igraph R package

A	B
A	C
A	D
A	E
A	F
E	F
F	G

```
library(igraph)
```

2 columns

```
g <- graph.edgelist(as.matrix(df),
                    directed = FALSE)

g
```

```
IGRAPH UN-- 7 7 --
+ attr: name (v/c)
+ edges (vertex names):
[1] A--B A--C A--D A--E A--F E--F F--G
```

7 vertices and 7 edges

Adding Vertex Attributes

```
g <- set_vertex_attr(
  g,
  "age",
  value = c(
    20,25,21,23,24,23,22
    )
  )
```

Adding Edge Attributes

```
g <- set_edge_attr(
  g,
  "frequency",
  value = c(
    2,1,1,1,3,2,4
    )
  )
```

Adding attributes II

edges.df

from	to	frequency
A	B	2
A	C	1
A	D	1
A	E	1
A	F	3
E	F	2
F	G	4

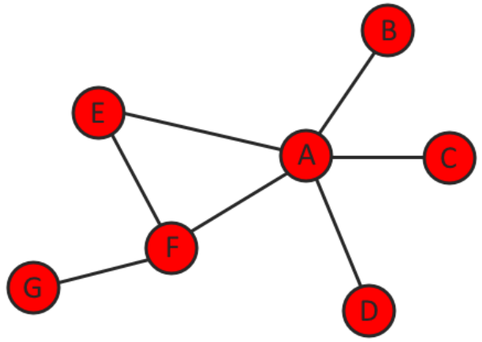
vertices.df

name	age
A	20
B	25
C	21
D	23
E	24
F	23
G	22

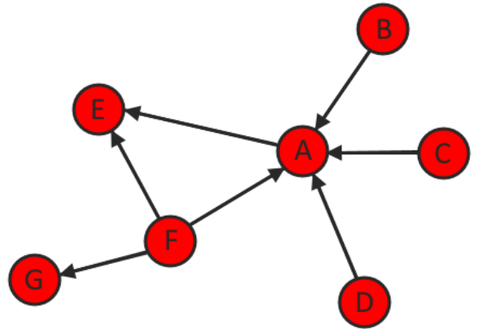
```
graph_from_data_frame(d = edges.df, vertices = vertices.df,
                      directed = FALSE)
```

Directionality

Undirected



Directed



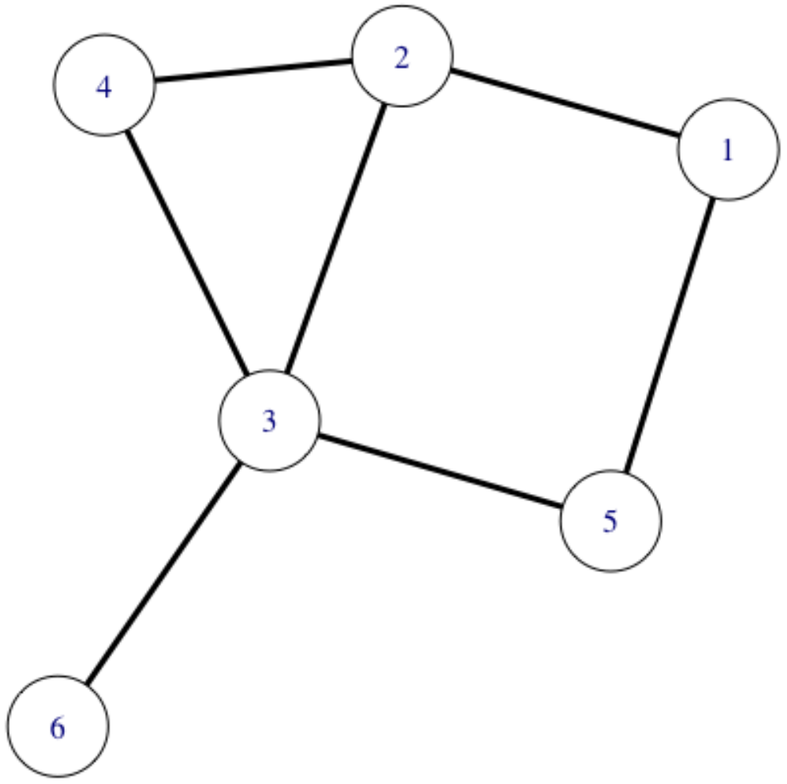
Undirected:

```
IGRAPH UN-- 7 7 --
+ attr: name (v/c)
+ edges (vertex names):
[1] A--B A--C A--D A--E A--F E--F F--G
```

Directed:

```
IGRAPH DN-- 7 7 --
+ attr: name (v/c)
+ edges (vertex names):
[1] A->E B->A C->A D->A F->A F->E F->G
```

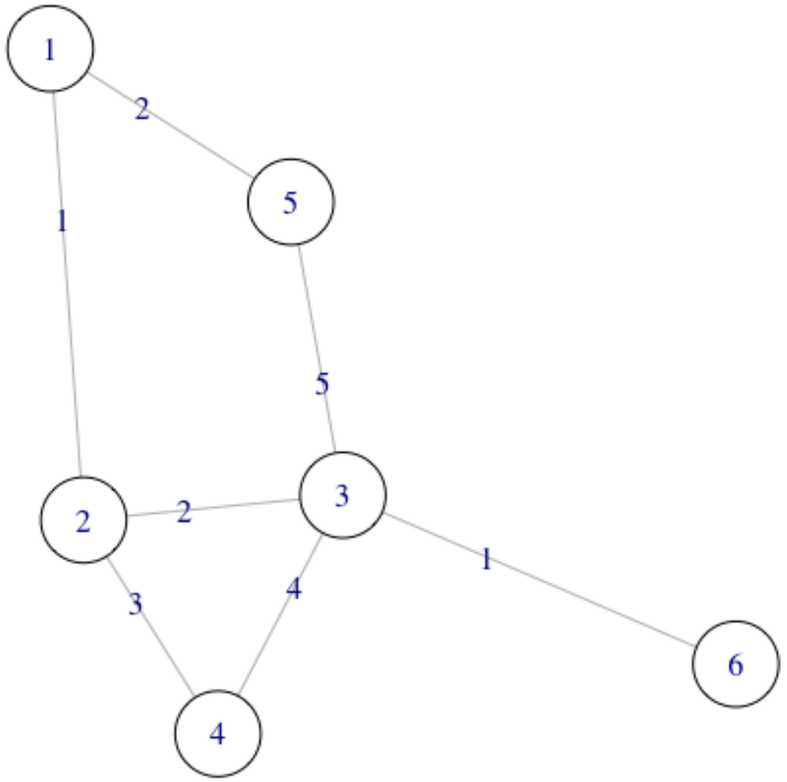
The adjacency matrix (part 1)




```
as_adjacency_matrix(g)
```

```
   1 2 3 4 5 6
1  0 1 0 0 1 0
2  1 0 1 1 0 0
3  0 1 0 1 1 1
4  0 1 1 0 0 0
5  1 0 1 0 0 0
6  0 0 1 0 0 0
```

The adjacency matrix (part 2)




```
as_adjacency_matrix(g,
                    attr="weight")
```

	1	2	3	4	5	6
1	0	1	0	0	2	0
2	1	0	2	3	0	0
3	0	2	0	4	5	1
4	0	3	4	0	0	0
5	2	0	5	0	0	0
6	0	0	1	0	0	0

A network as a data frame

```
as_data_frame(g, what = "both")
```

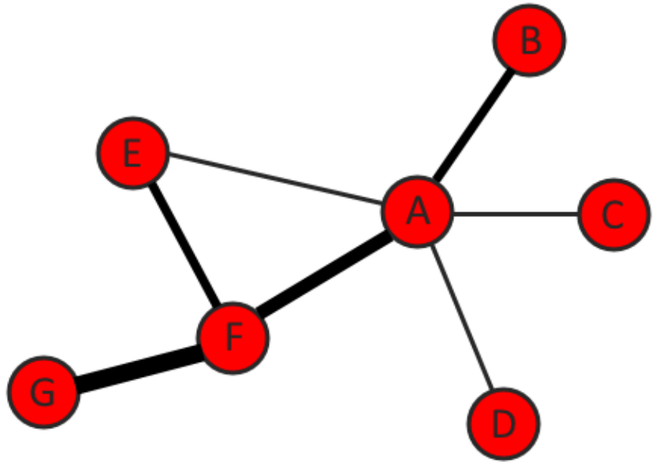
```
$nodes
  name
a    a
b    b
c    c
d    d
e    e
```

```
$ties
  from to weight
1    a  b      1
2    a  e      2
3    b  c      2
4    b  d      3
5    c  d      4
6    c  e      5
```

Mapping representations

```
# graph to matrix
A <- as_adjacency_matrix(g)

# matrix to graph
g <- graph_from_adjacency_matrix(A)
# graph to data frame
df = as_data_frame(g, what = "both")

# data frame to graph
g <- graph_from_data_frame(df$ties, vertices = df$nodes)
# matrix to data frame
df = as_data_frame(graph_from_adjacency_matrix(A), what = "both")

# data frame to matrix
A <- as_adjacency_matrix(graph_from_data_frame(df$ties,
     vertices = df$nodes))
```

Subsetting networks



[[filters the object and returns a data.frame but we can apply the same filter with a [and return igraph object.

```
E(g)[[inc('E')]]
```

```
+ 2/7 edges (vertex names):
  tail head tid hid frequency
4    E    A   5   1         1
6    F    E   6   5         2
```

```
E(g)[[frequency>=3]]
```

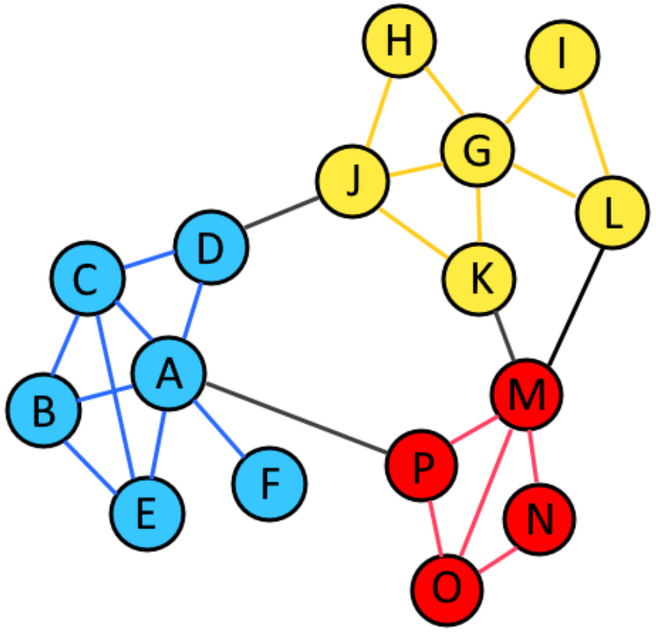
```
+ 2/7 edges (vertex names):
  tail head tid hid frequency
5    F    A   6   1         3
7    G    F   7   6         4
```

edges.df

from	to	frequency
A	B	2
A	C	1
A	D	1
A	E	1
A	F	3
E	F	2
F	G	4

```
# Create a new igraph object by deleting
edges that are less than 2 hours long
g2 <- delete_edges(g1, E(g1)[hours < 2])


# Assign largest cliques output to object 'lc'
lc <- largest_cliques(g)

# Create two new undirected subgraphs, each
# containing only the vertices of each largest
# clique.
gs1 <- as.undirected(subgraph(g, lc[[1]]))
gs2 <- as.undirected(subgraph(g, lc[[2]]))
```

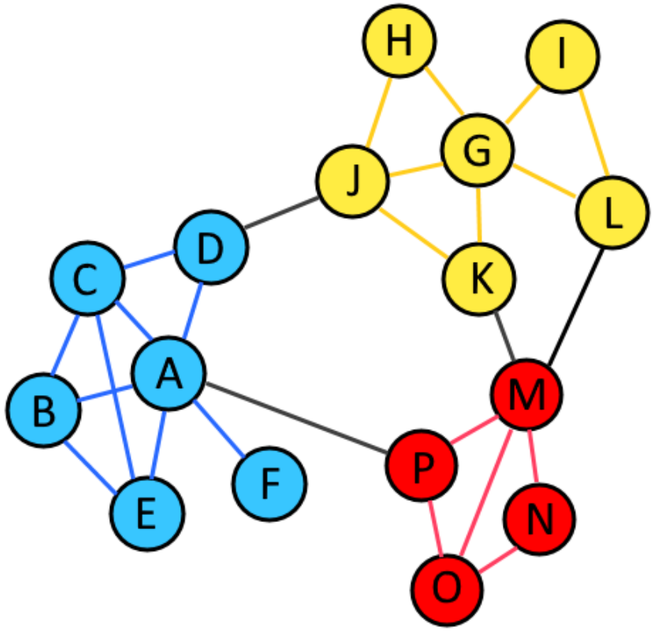
Fast-greedy detection




```
fastgreedy.community(g)
```

```
IGRAPH clustering fast greedy,
groups: 3, mod: 0.5
+ groups:
  $`1`
  [1] "A" "B" "C" "D" "E" "F"

  $`2`
  [1] "J" "G" "H" "I" "K" "L"

  $`3`
  [1] "M" "N" "O" "P"
```

Edge-betweenness detection




```
edge.betweenness.community(g)
```

```
IGRAPH clustering edge betweenness,
groups: 3, mod: 0.5
+ groups:
  $`1`
  [1] "A" "B" "C" "D" "E" "F"

  $`2`
  [1] "J" "G" "H" "I" "K" "L"

  $`3`
  [1] "M" "N" "O" "P"
```

Getting information from graph object

```
V(g)
```

```
+ 7/7 vertices, named:
[1] A B C D E F G
```

```
E(g)
```

```
+ 7/7 edges (vertex names):
[1] A--B A--C A--D A--E A--F E--F F--G
```

```
gorder(g)
```

```
[1] 7
```

```
gsize(g)
```

```
[1] 7
```

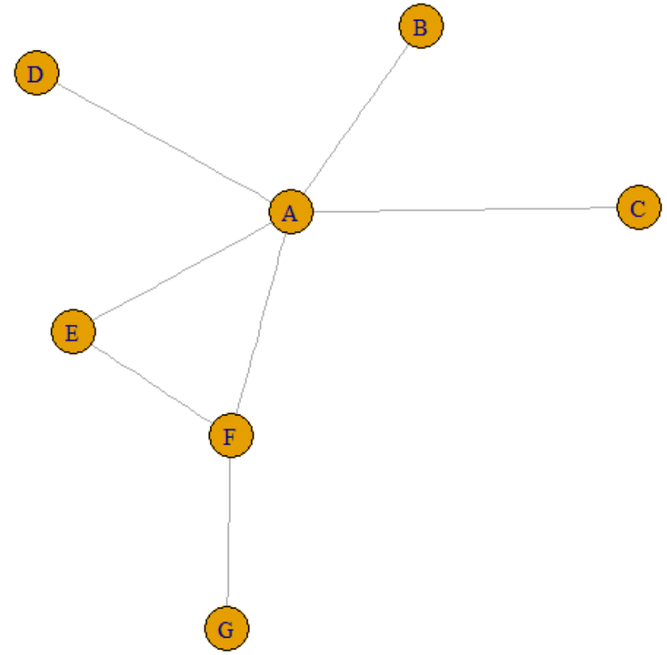
vertex_attr(g)

```
$name
[1] "A" "B" "C" "D" "E" "F" "G"

$age
[1] 20 25 21 23 24 23 22
```

edge_attr(g)

```
$frequency
[1] 2 1 1 1 3 2 4
```

```
plot(g)
```




```
is.directed(g)
```

```
[1] TRUE
```

```
is.weighted(g)
```

```
[1] FALSE
```

Exploring the network

```
# explore the set of nodes and print the number of nodes
V(g)
vcount(g)

# explore the set of ties and print the number of ties
E(g)
ecount(g)
# add the name attribute "Madrid network" to the network and print it
g$name <- "Madrid network"
g$name
# add node attribute id and print the node `id` attribute
V(g)$id <- 1:vcount(g)

# print the tie `weight` attribute
E(g)$weight
```

Is there an edge between A & E?

```
g['A','E']
```

```
[1] 1
```

Show all edges to or from A:

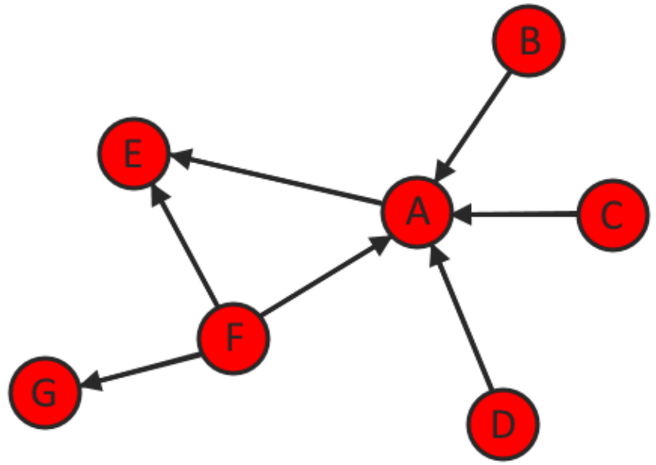
```
incident(g,'A', mode=c("all"))
```

```
+ 5/7 edges (vertex names):
[1] A->E B->A C->A D->A F->A
```

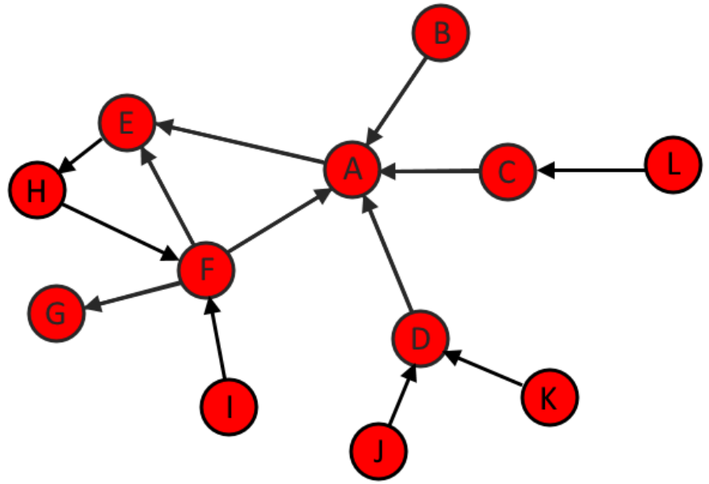
Find the starting vertex of all edges:

```
head_of(g, E(g))
```

```
+ 7/7 vertices, named:
[1] A B C D F F F
```



Identifying neighbors



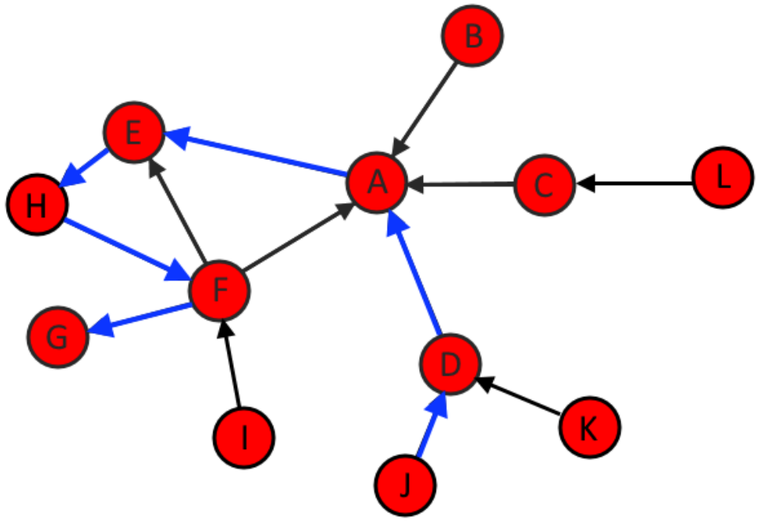

```
neighbors(g, "F", mode = c("all"))
```

```
+ 5/12 vertices, named:
[1] A E G H I
```

```
x <- neighbors(
  g, "F", mode = c("all")
)

y <- neighbors(
  g, "D", mode = c("all")
)

intersection(x,y)
```

```
A
```

Paths



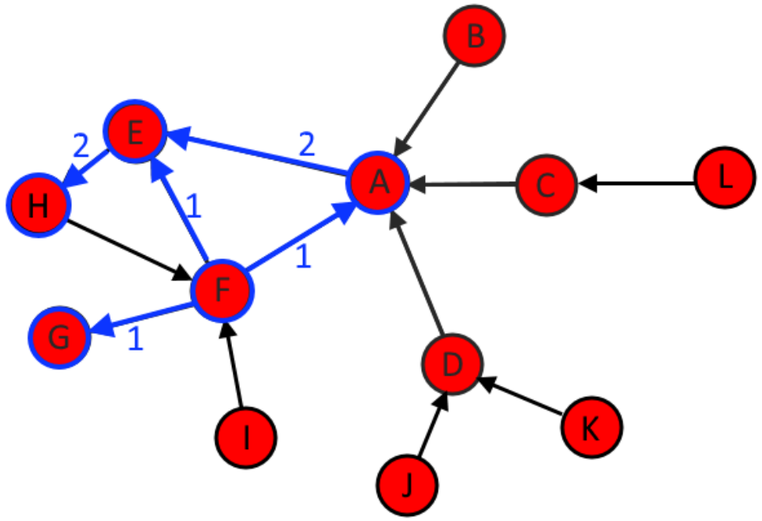

```
farthest_vertices(g)
```

```
$vertices
+ 2/12 vertices, named:
[1] J G

$distance
[1] 6
```

```
get_diameter(g)
```

```
+ 7/12 vertices, named:
[1] J D A E H F G
```

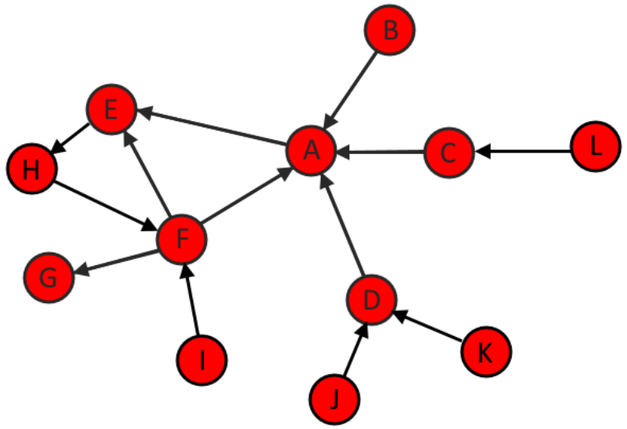
Identifying vertices reachable in N steps




```
ego(g, 2, 'F', mode=c('out'))
```

```
+ 5/12 vertices, named:
[1] F A E G H
```

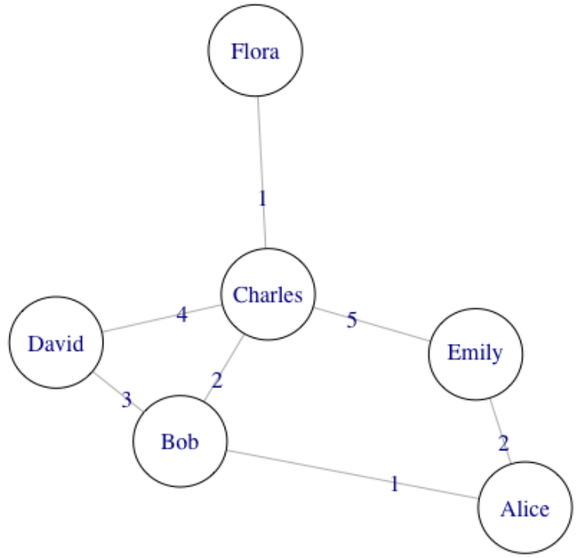
Out-degree and in-degree



	out-degree	in-degree
A	1	4
B	1	0
C	1	1
D	1	2
E	1	2
F	3	2
G	0	1
H	1	1
I	0	1
J	1	0
K	1	0

```
degree(g, mode = c("out"))
```

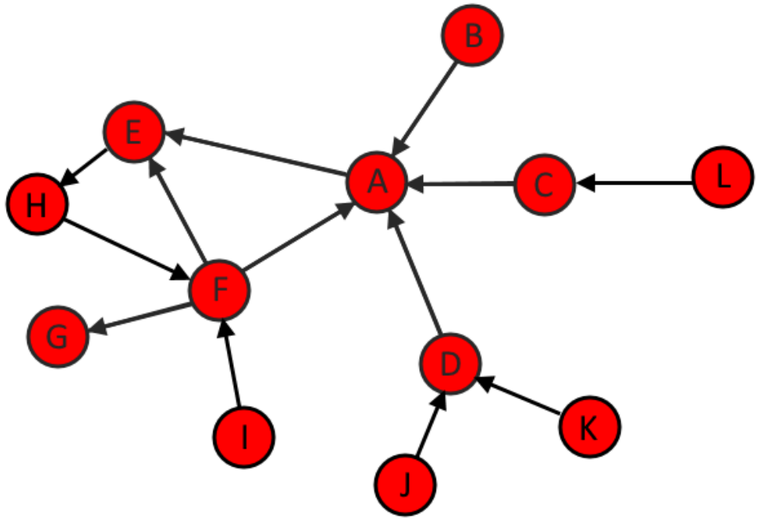
```
A B C D E F G H I J K L
1 1 1 1 1 3 0 1 1 1 1 1
```




```
# compute node strengths
strength(g)
```

```
Charles   Alice
   12       3
```

Betweenness



I to H:

```
I -> F -> E -> H
I -> F -> A -> E -> H
```

K to E:

```
K -> D -> A -> E
```

B to G:

```
B -> A -> E -> H -> F -> G
```

```
betweenness(g, directed = TRUE)
```

```
 A  B  C  D  E  F  G  H  I  J  K  L
24  0  5 10 23 16  0 17  0  0  0  0
```

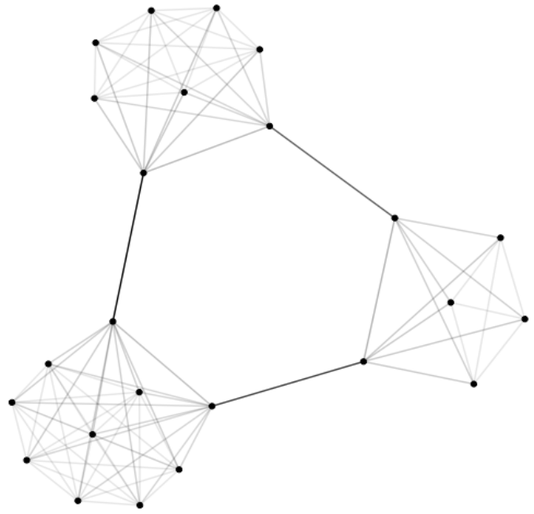
```
betweenness(g, directed = TRUE,
            normalized = TRUE)
```

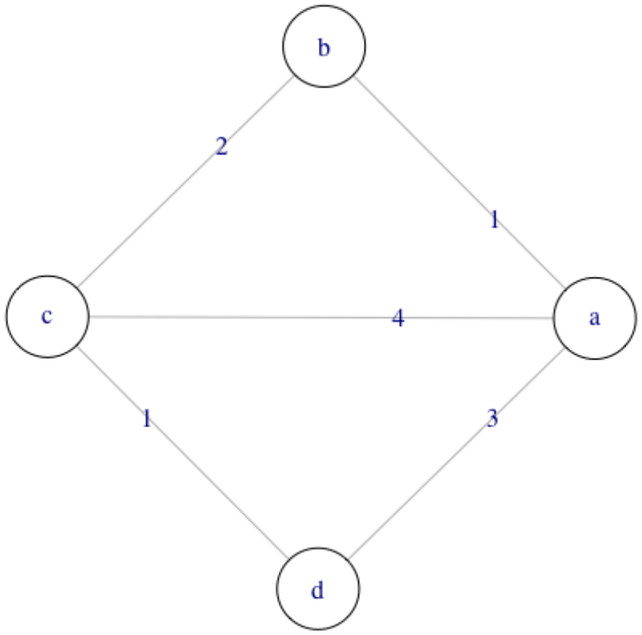
```
   A    B    C    D    E    F
0.22 0.00 0.05 0.09 0.21 0.15
   G    H    I    J    K    L
0.00 0.15 0.00 0.00 0.00 0.00
```

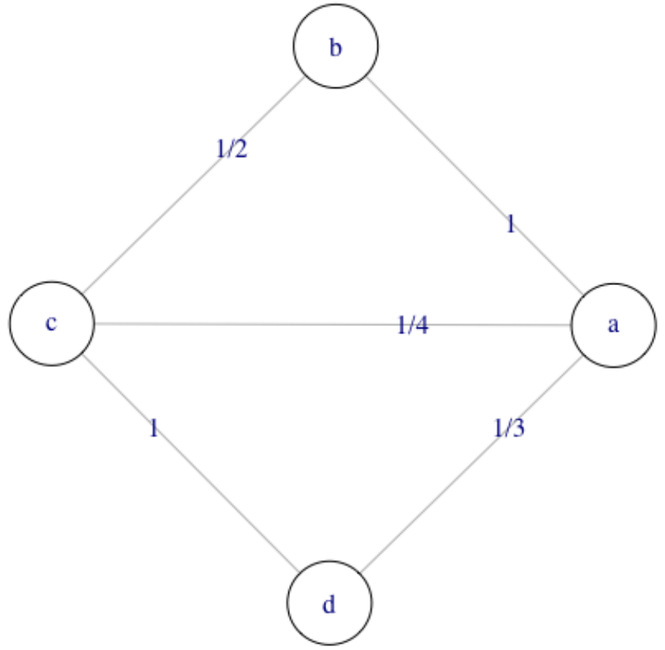
- `closeness()` : a measure that quantifies how close a node is to all other nodes in the network in terms of shortest path distance.

Computing betweenness

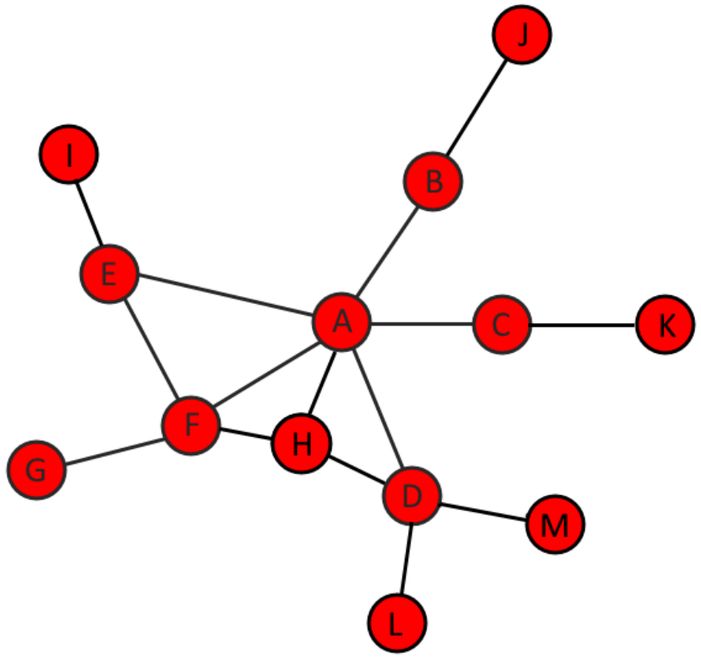
```
# compute distance weights for ties
dist_weight = 1 / E(g)$weight
# compute weighted betweenness on ties
edge_betweenness(g, weights = dist_weight)
```







Eigenvector centrality



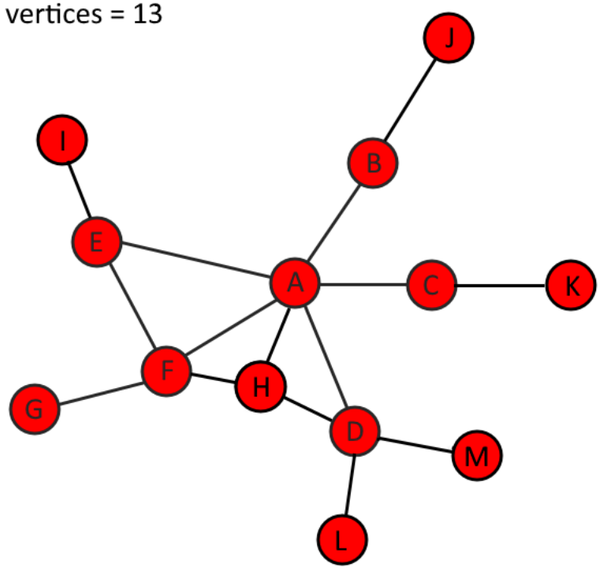

```
eigen_centrality(g)$vector
```

```
   A    B    C    D    E    F    G
1.00 0.33 0.33 0.63 0.58 0.76 0.23

   H    I    J    K    L    M
0.71 0.17 0.10 0.10 0.19 0.19
```

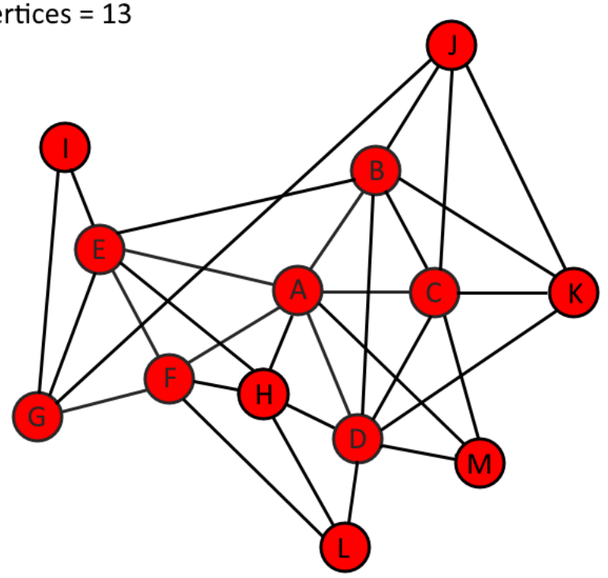
Eigenvector centrality is a measure of how well connected a vertex is. Vertices with the highest eigenvector centrality are those that are connected to many others but especially to other vertices who themselves are highly connected to others.

Density

density = 0.19
edges = 15
vertices = 13



density = 0.38
edges = 30
vertices = 13

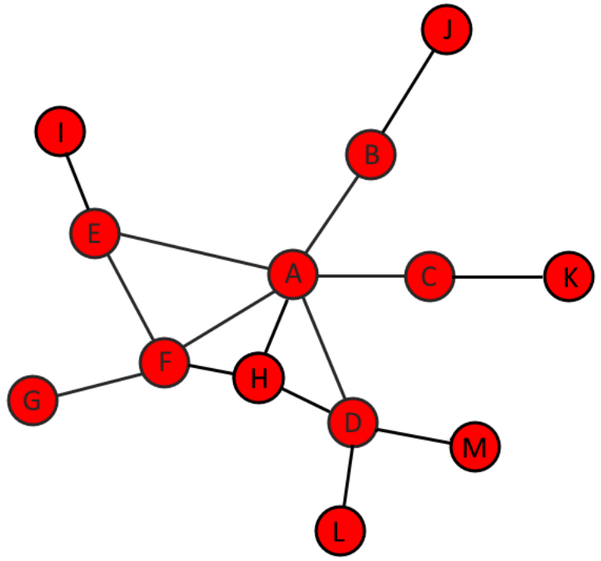


Is equivalent to the proportion of edges that actually do exist in a network out of all those that potentially could exist between every pair of vertices.

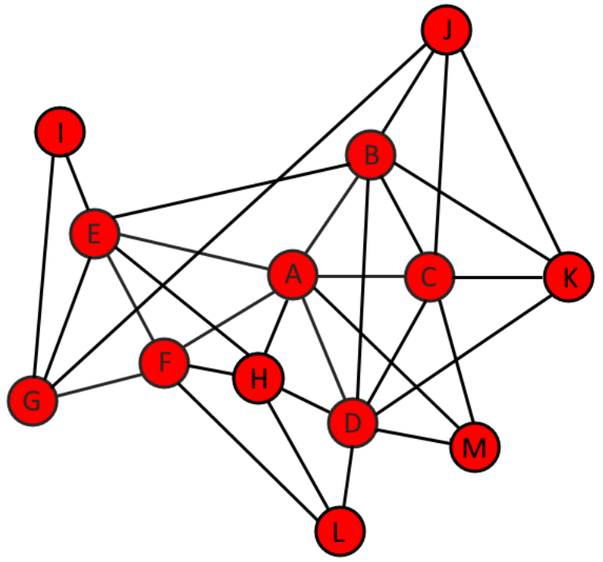
```
edge_density(g)
```

Average path length

average path length = 2.47



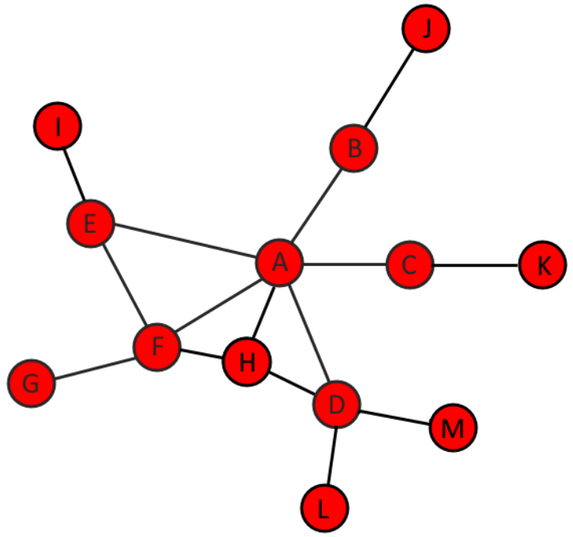
average path length = 1.81

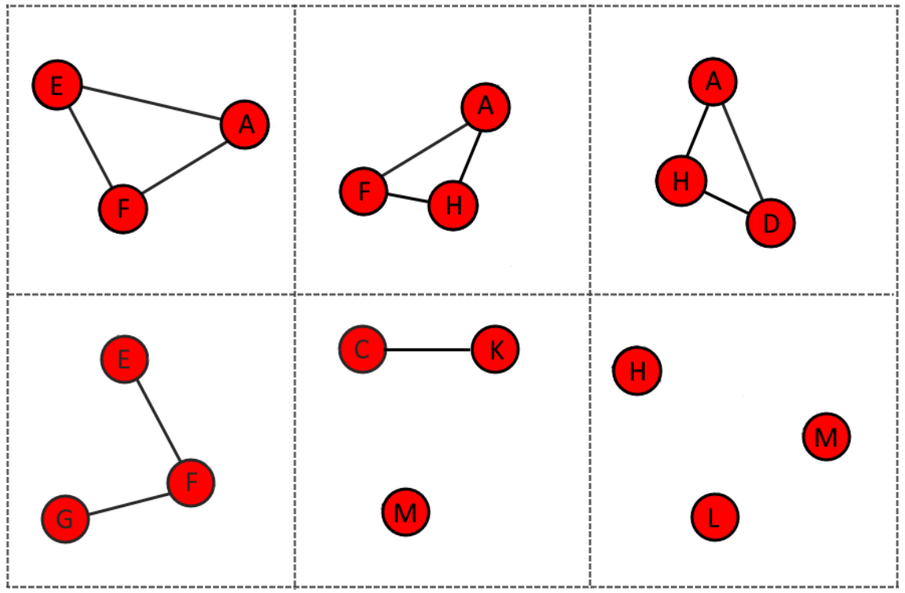


the mean of the lengths of the shortest paths between all pairs of vertices in the network.

```
mean_distance(g, directed = FALSE)
```

Transitivity





`triangles(g)` Returns all closed triangules in the graph

```
# Show all triangles in the network.
matrix(triangles(g), nrow = 3)
```

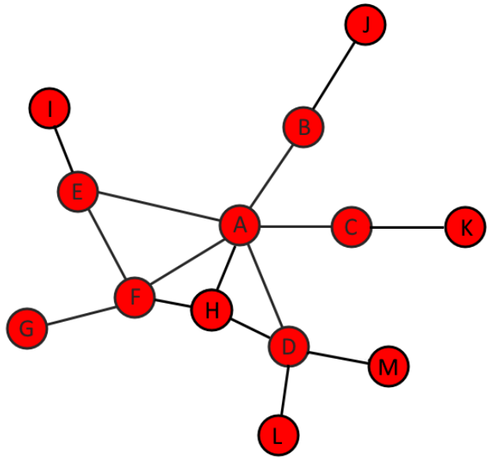
Global transitivity

```
transitivity(g)
```

```
[1] 0.26
```

Measures the probability that the adjacent vertices of a given vertex are connected

Local transitivity




```
transitivity(g,
             vids = 'A',
             type = "local")
```

```
0.2
```

```
count_triangles(g, vids = 'A')
```

```
3
```

```
count_triangles(g, vids = 'F')
```

```
2
```

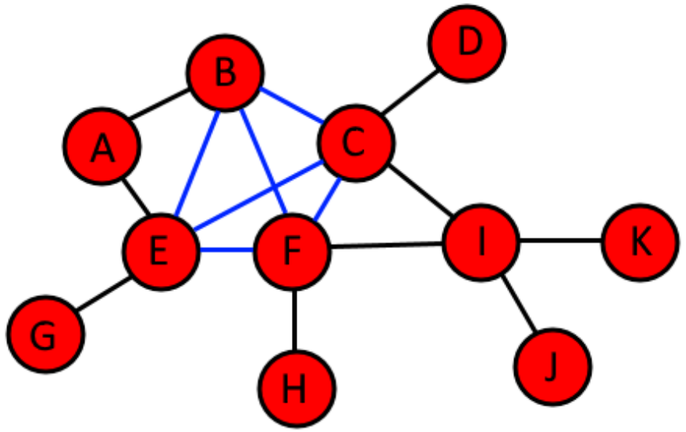
```
transitivity(g,
             vids = 'F',
             type = "local")
```

```
0.33
```

Identifying cliques

```
largest_cliques(g)
```

```
+ 4/11 vertices, named:
[1] C F B E
```

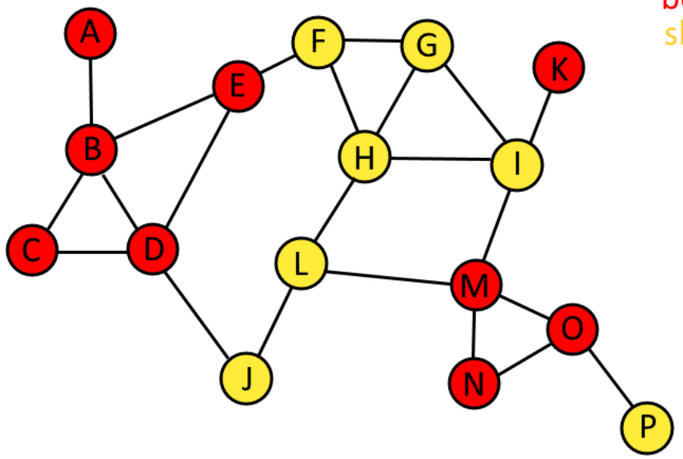



```
max_cliques(g)
```

```
...
[[6]]
+ 3/11 vertices, named:
[1] A B E

[[7]]
+ 3/11 vertices, named:
[1] I C F

[[8]]
+ 4/11 vertices, named:
[1] E B F C
```

In a clique, every vertex is connected to every other vertex.

Assortativity



bold
shy

```
assortativity(g, values)
```

```
0.45
```

bold -> 1 and shy ->2

* 0 indicates no overall pattern of preferential attachment.

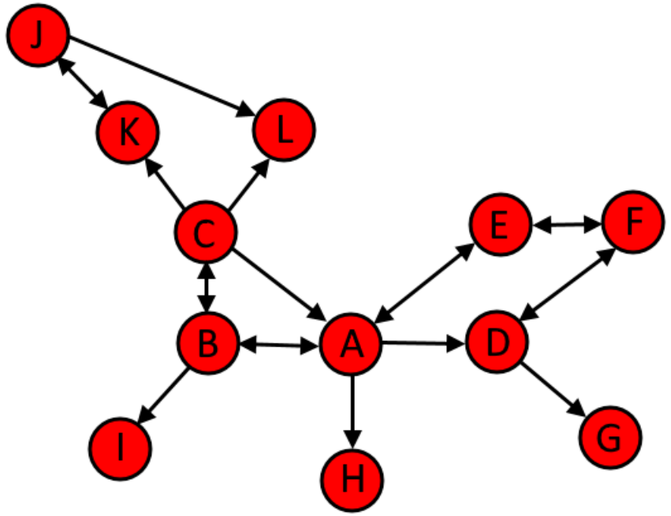
* +1 would indicate individuals only attach to similar individuals

* -1 would indicate that individuals actively avoid similar individuals.

```
assortativity.degree(
  g,
  directed = FALSE
)
```

```
-0.31
```

In this example, we have a negative value for the assortativity degree indicating that highly connected individuals do not connect preferentially to other highly connected individuals.

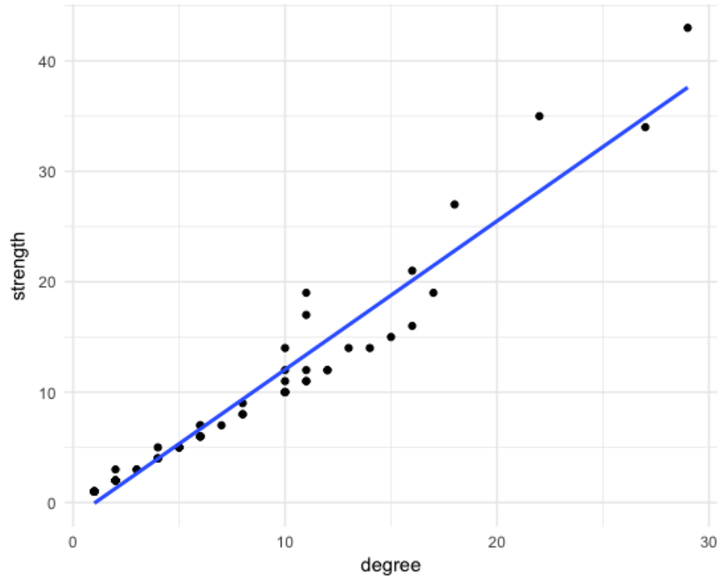



```
reciprocity(g)
```

```
0.6
```

Visualizing correlation

```
# scatterplot of degree and strength
ggplot(data = nodes, mapping = aes(x = degree, y = strength)) +
    geom_point() +
    geom_smooth(method = "lm", se = FALSE)
```



Computing correlation

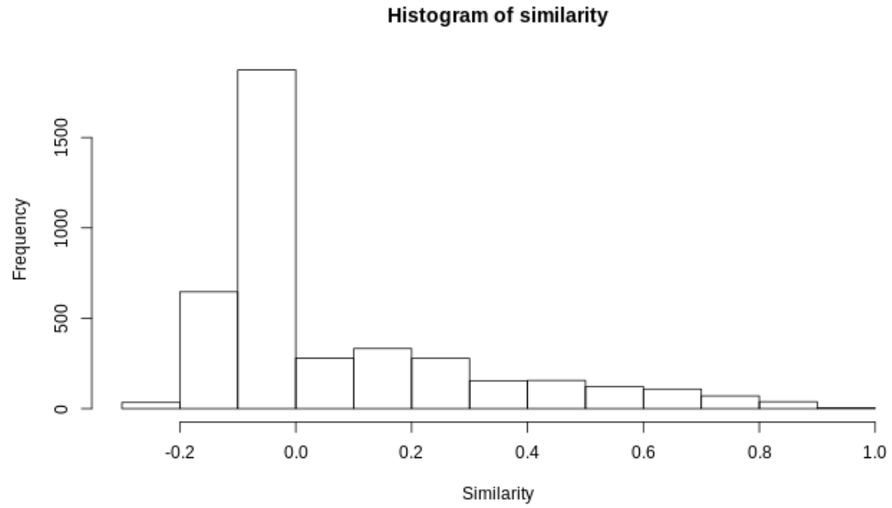
- Positive values indicate positive correlation
- Negative values indicate negative correlation
- Null values indicate no correlation

```
# Pearson correlation coefficient
cor(nodes$degree, nodes$strength)
```

```
0.9708946
```

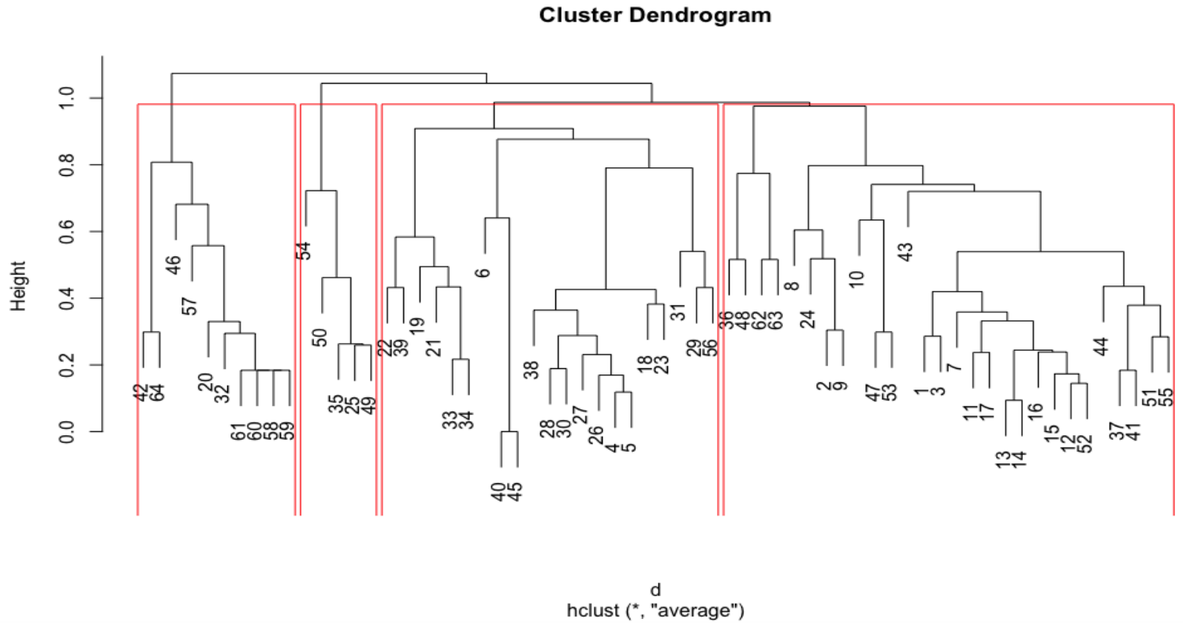
```
# graph to matrix
A <- as_adjacency_matrix(g)
```

```
# Compute the Pearson correlation matrix of A
S <- cor(A)

# Set the diagonal of S to 0
diag(S) <- 0

# Flatten S to be a vector
flat_S <- as.vector(S)

# Plot a histogram of similarities
hist(flat_S, xlab = "Similarity",
     main = "Histogram of similarity")
```



Hierarchical clustering in R

```
# distance matrix from similarity matrix
D <- 1-S    diag(S) = 0
# distance object from distance matrix
d <- as.dist(D)
# average-linkage clustering method
cc <- hclust(d, method = "average")
# cut dendrogram at 4 clusters
cutree(cc, k = 4)
```




```
[1] 1 1 1 2 2 2 1 1 1 1 1 1 1 1 1 1 2 2 3 2 2 2 1 4 2 2 2
[29] 2 2 2 3 2 2 4 1 1 2 2 2 1 3 1 1 2 3 1 1 4 4 1 1 1 4 1 2
[57] 3 3 3 3 3 1 1 3
```

The similarity measure

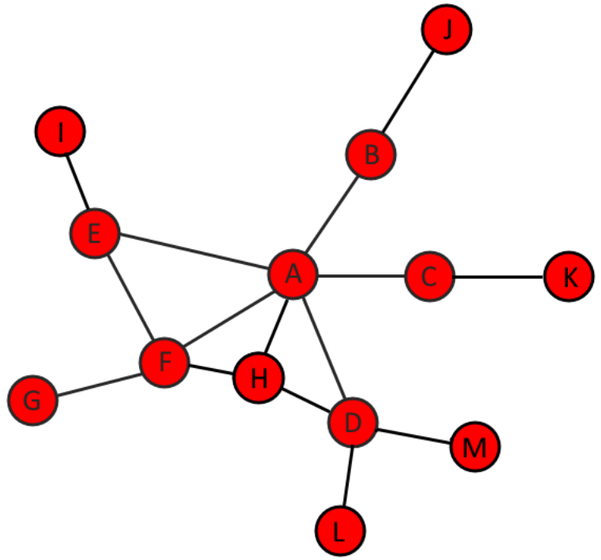
- **Single-linkage**: the similarity between two groups is the maximum of the similarities between nodes of different groups.
- **Complete-linkage**: the similarity between two groups is the minimum of the similarities between nodes of different groups.
- **Average-linkage**: the similarity between two groups is the average of the similarities between nodes of different groups.

The clustering algorithm

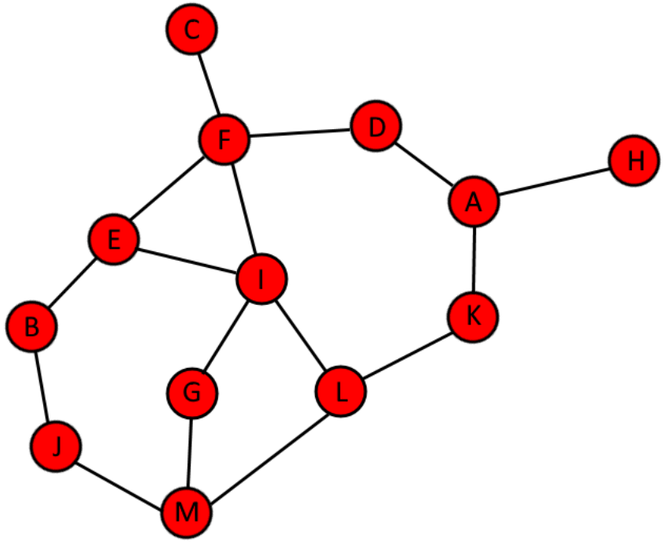
1. Evaluate the similarity measures for all node pairs.
2. Assign each node to a group of its own.
3. Find the pair of groups with the highest similarity and join them together into a single group.
4. Calculate the similarity between the new composite group and all others.
5. Repeat steps 3 and 4 until all nodes have been joined into a single group.

Random graphs

density = 0.19
vertices = 13



density = 0.21
vertices = 13




```
erdos.renyi.game(n = gorder(g), p.or.m = edge_density(g), type = "gnp")
```

Number of vertices

Density or Number of edges

type = "gnp "

type = "gnm"

Random graphs & randomization tests

1. Generate 1000 random graphs based on the original network - e.g. with the same number of vertices and approximate density.
2. Calculate the **average path length** of the original network.
3. Calculate the average path length of the 1000 random networks.
4. Determine how many random networks have an average path length greater or less than the original network's average path length.

Generate 1000 random graphs:

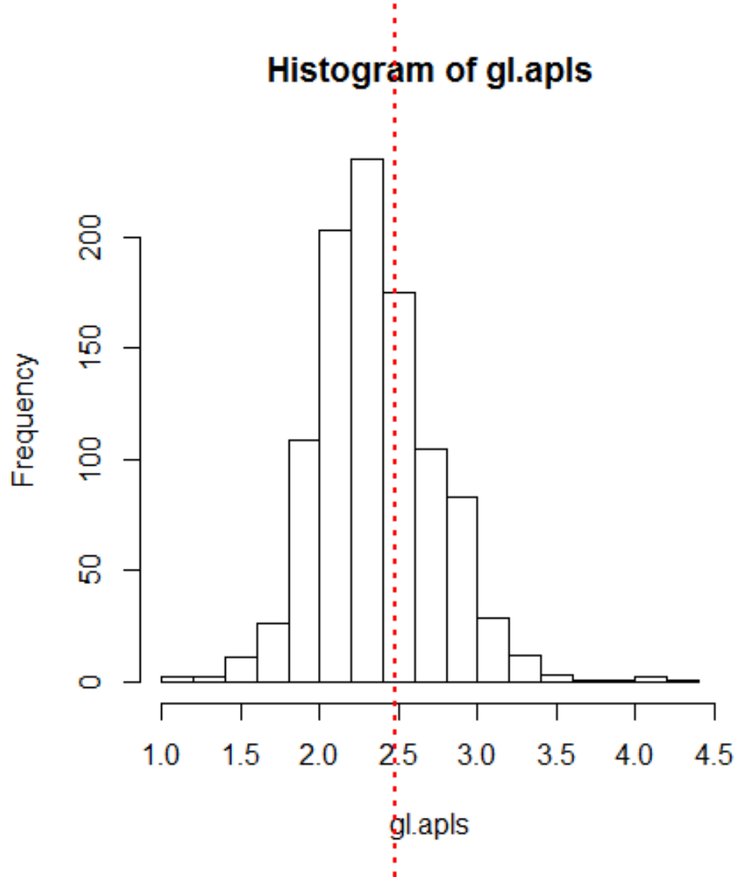
```
gl <- vector('list',1000)

for(i in 1:1000){
    gl[[i]] <- erdos.renyi.game(
                    n = gorder(g),
                    p.or.m = edge_density(g),
                    type = "gnp"
                     )
}
```

Calculate average path length of 1000 random graphs:

```
gl.apls <- unlist(
  lapply(gl, mean_distance, directed = FALSE)
)
```

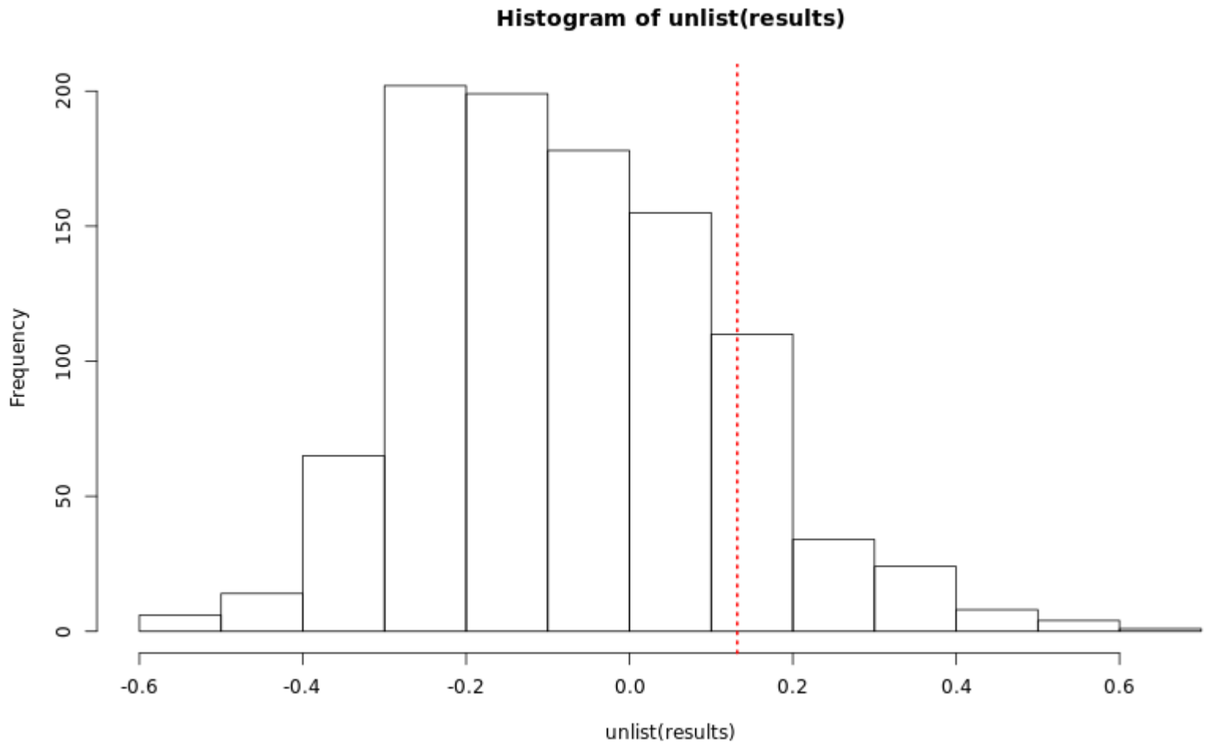
Comparing to the original network

```
hist(gl.apls, breaks = 20)

abline(
  v = mean_distance(
    g, directed=FALSE
    ),
      col = "red",
      lty = 3,
      lwd = 2
)
```

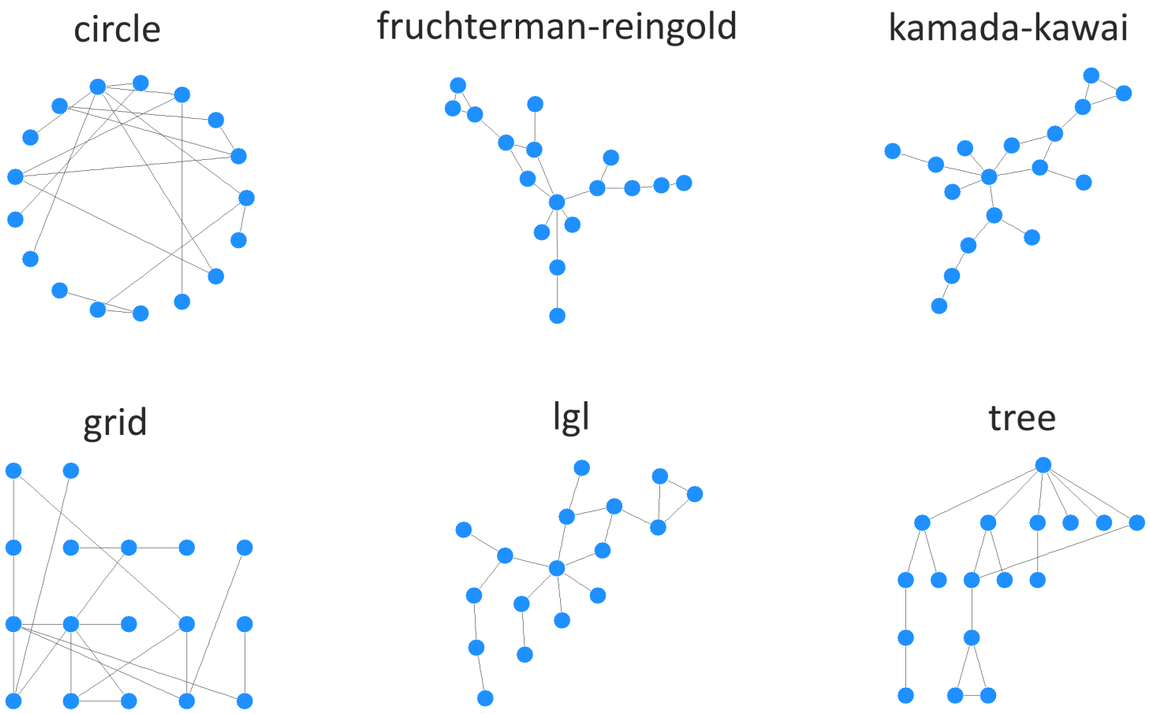


Or we can sample the groups

```r
# Calculate the observed assortativity
observed.assortativity <- assortativity(g1, values)

# Calculate the assortativity of the network
# randomizing the gender attribute 1000 times
results <- vector('list', 1000)

for(i in 1:1000){
  results[[i]] <- assortativity(g1, sample(values))
}

# Plot the distribution of assortativity values
# and add a red vertical line at the original
# observed value
hist(unlist(results))
abline(v = observed.assortativity,
       col = "red",
       lty = 3,
       lwd=2)
```



igraph layouts



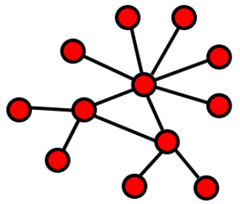

```
plot(g, layout = layout.fruchterman.reingold(g))
```

ls("package:igraph", pattern = "^layout_.")

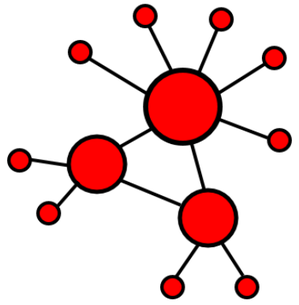
layout_as_bipartite
layout_as_star
layout_as_tree
layout_components
layout_in_circle
layout_nicely
layout_on_grid
layout_on_sphere
layout_randomly
layout_with_dh
layout_with_drl
layout_with_fr
layout_with_gem
layout_with_graphopt
layout_with_kk
layout_with_lgl
layout_with_mds
layout_with_sugiyama

Styling vertices and edges

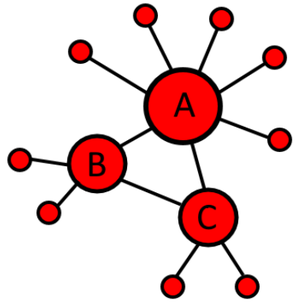
default



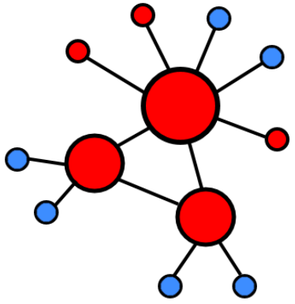
size



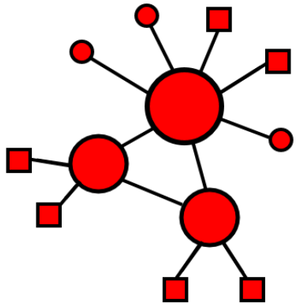
labels



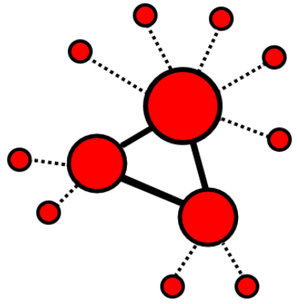
color



shape



edges



NODES

vertex.color	Node color
vertex.frame.color	Node border color
vertex.shape	One of “none”, “circle”, “square”, “csquare”, “rectangle” “crectangle”, “vrectangle”, “pie”, “raster”, or “sphere”
vertex.size	Size of the node (default is 15)
vertex.size2	The second size of the node (e.g. for a rectangle)
vertex.label	Character vector used to label the nodes NA
vertex.label.family	Font family of the label (e.g.“Times”, “Helvetica”)
vertex.label.font	Font: 1 plain, 2 bold, 3, italic, 4 bold italic, 5 symbol
vertex.label.cex	Font size (multiplication factor, device-dependent)
vertex.label.dist	Distance between the label and the vertex
vertex.label.degree	The position of the label in relation to the vertex, where 0 right, “pi” is left, “pi/2” is below, and “-pi/2” is above

EDGES

edge.color	Edge color
edge.width	Edge width, defaults to 1
edge.arrow.size	Arrow size, defaults to 1
edge.arrow.width	Arrow width, defaults to 1
edge.lty	Line type, could be 0 or “blank”, 1 or “solid”, 2 or “dashed”, 3 or “dotted”, 4 or “dotdash”, 5 or “longdash”, 6 or “twodash”
edge.label	Character vector used to label edges
edge.label.family	Font family of the label (e.g.“Times”, “Helvetica”)
edge.label.font	Font: 1 plain, 2 bold, 3, italic, 4 bold italic, 5 symbol
edge.label.cex	Font size for edge labels
edge.curved	Edge curvature, range 0-1 (FALSE sets it to 0, TRUE to 0.5)
arrow.mode	Vector specifying whether edges should have arrows, possible values: 0 no arrow, 1 back, 2 forward, 3 both

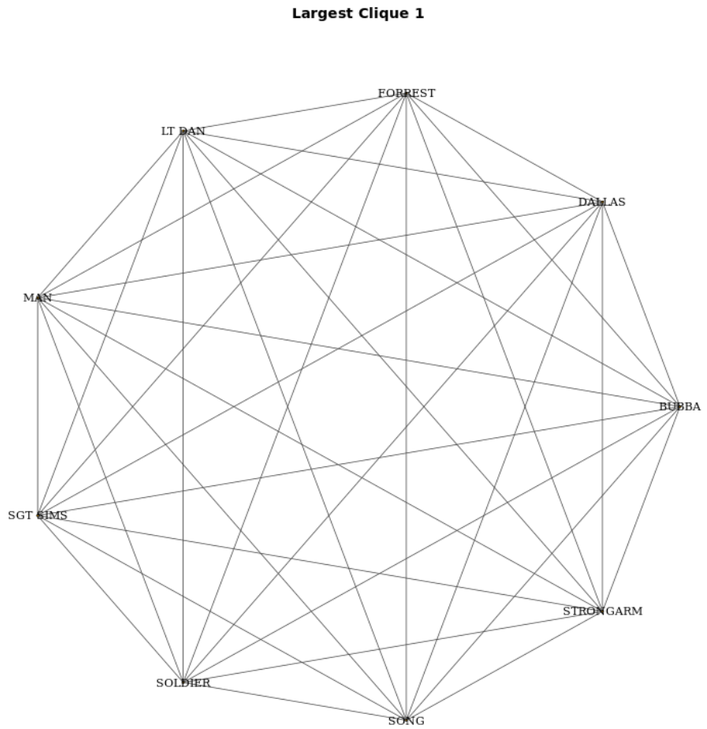
OTHER

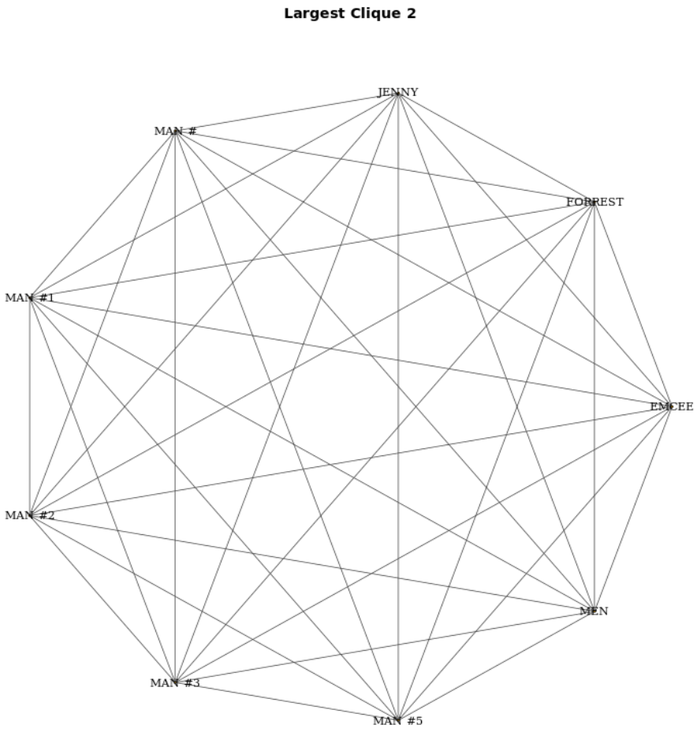
margin	Empty space margins around the plot, vector with length 4
frame	if TRUE, the plot will be framed
main	If set, adds a title to the plot
sub	If set, adds a subtitle to the plot

Source: https://kateto.net/netscix2016.html

Side-by-side Plot Example

```
# Plot the two largest cliques side-by-side

par(mfrow=c(1,2)) # To plot two plots side-by-side

plot(gs1,
     vertex.label.color = "black",
     vertex.label.cex = 0.9,
     vertex.size = 0,
     edge.color = 'gray28',
     main = "Largest Clique 1",
     layout = layout.circle(gs1)
)

plot(gs2,
     vertex.label.color = "black",
     vertex.label.cex = 0.9,
     vertex.size = 0,
     edge.color = 'gray28',
     main = "Largest Clique 2",
     layout = layout.circle(gs2)
)
```





```
x <- fastgreedy.community(g)
length(x)
```

```
[1] 3
```

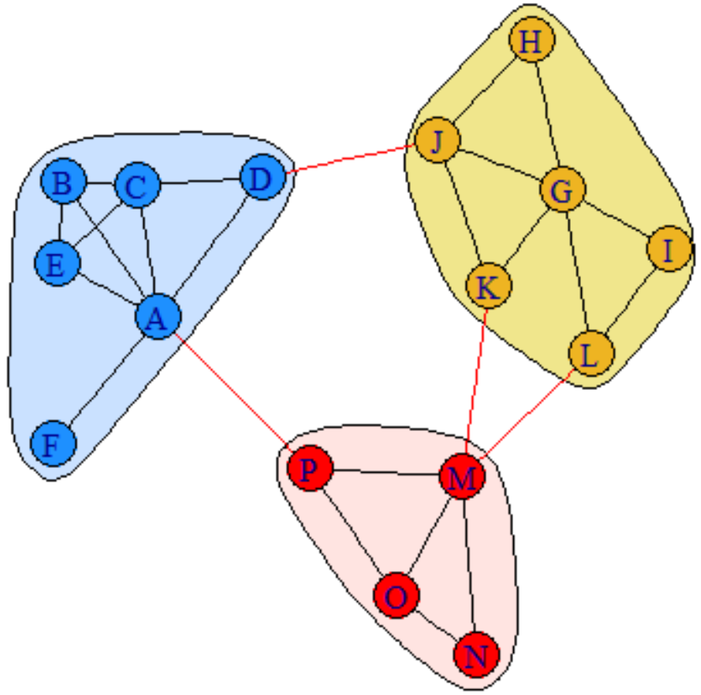
```
sizes(x)
```

```
Community sizes
1 2 3
6 6 4
```

```
membership(x)
```

```
A B C D E F J G H I K L M N O P
1 1 1 1 1 1 2 2 2 2 2 2 3 3 3 3
```

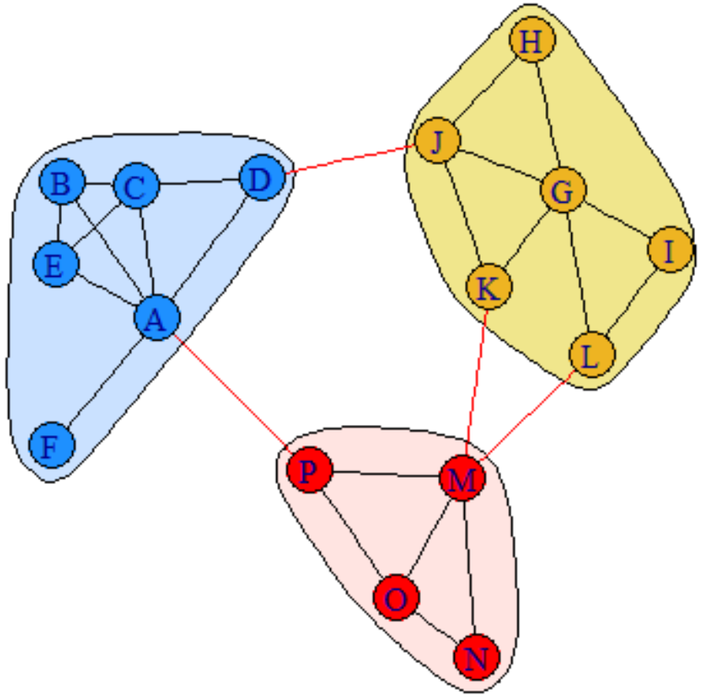
```
plot(x, g)
```



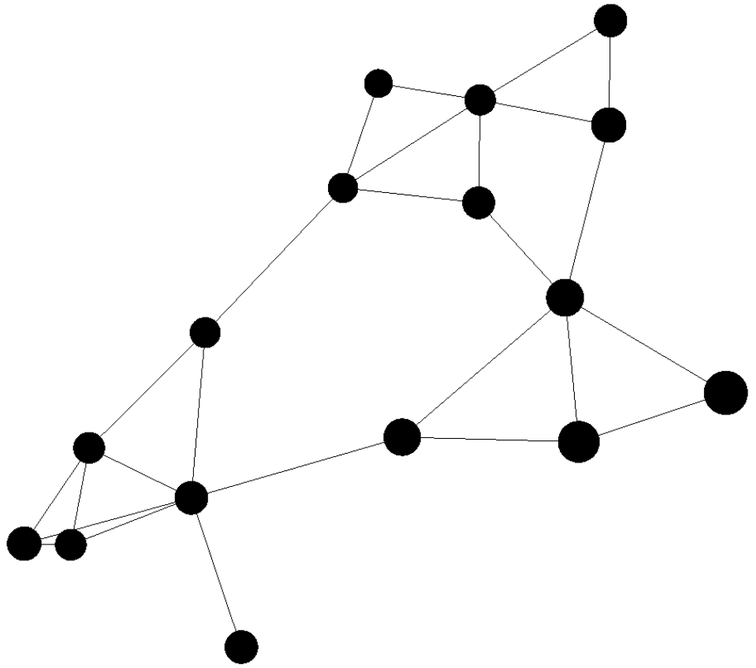
R network visualization packages

- igraph
- statnet
- ggnet
- ggnetwork
- ggraph
- visNetwork
- networkD3
- sigma
- rgexf (igraph to Gephi)
- **threejs**

Creating a threejs visualization

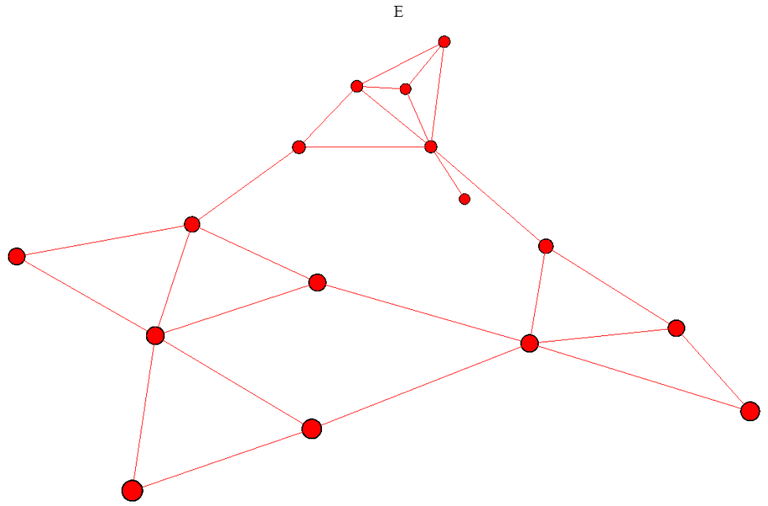



```
library(threejs)
graphjs(g)
```



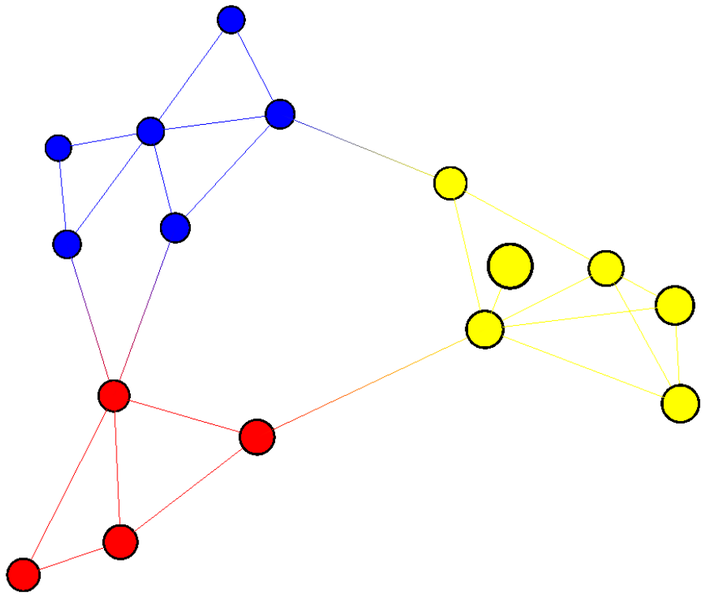
Adding attributes

```
g <- set_vertex_attr(
  g,
  "label",
  value = V(g)$name
  )

g <- set_vertex_attr(
  g,
  "color",
  value = "mistyrose"
  )

graphjs(g, vertex.size = 1)
```



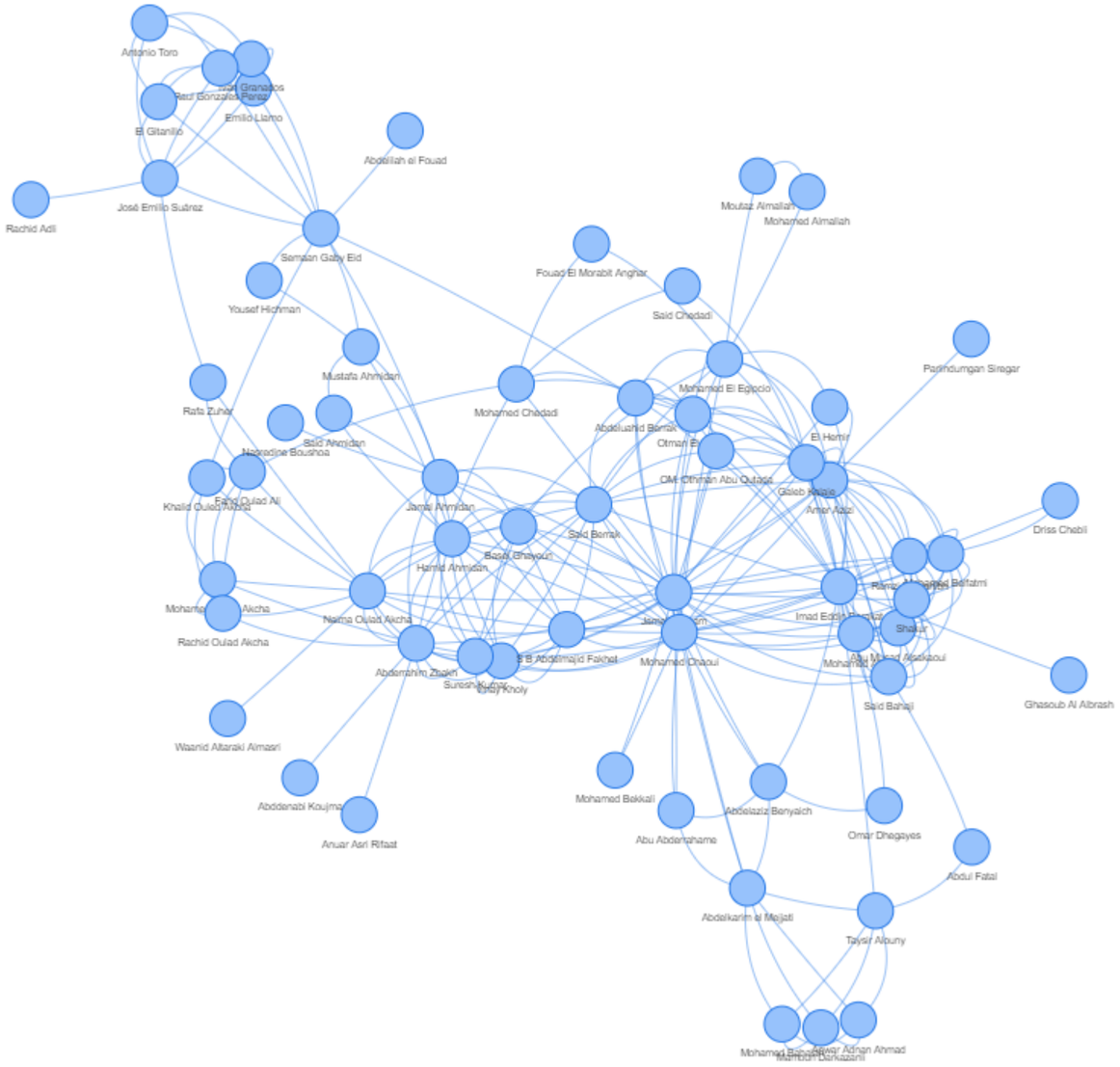
Coloring communities

```
x = edge.betweenness.community(g)
i <-  membership(x)

g <- set_vertex_attr(
  g,
  "color",
  value = c(
    "yellow", "blue", "red"
    )[i]
  )

graphjs(g)
```



visNetwork

```
# From previous step
data <- toVisNetworkData(g)

# Visualize the network
visNetwork(nodes = data$nodes,
           edges = data$edges,
           width = 800, height = 800)
```




```
head(data$nodes)
```

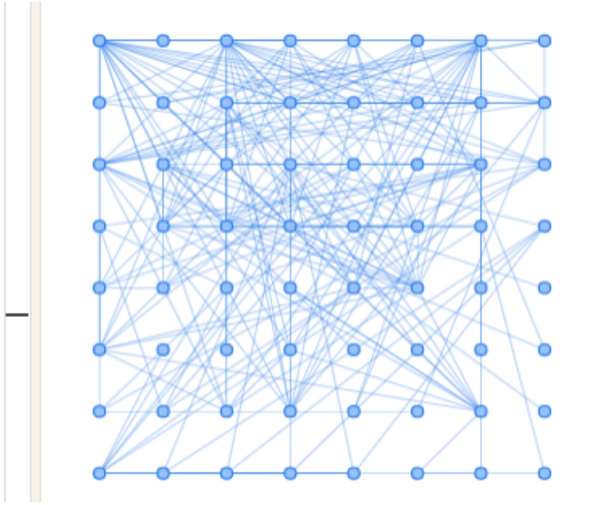
	id	degree	strength	cluster	label
Jamal Zougam	Jamal Zougam	29	43	1	Jamal Zougam
Mohamed Bekkali	Mohamed Bekkali	2	2	1	Mohamed Bekkali
Mohamed Chaoui	Mohamed Chaoui	27	34	1	Mohamed Chaoui
Vinay Kholy	Vinay Kholy	10	10	2	Vinay Kholy
Suresh Kumar	Suresh Kumar	10	10	2	Suresh Kumar
Mohamed Chedadi	Mohamed Chedadi	7	7	2	Mohamed Chedadi

```
head(data$edges)
```

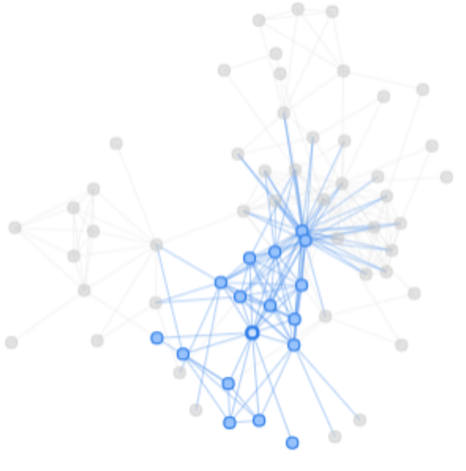
	from	to	weight	betweenness
1	Jamal Zougam	Mohamed Bekkali	1	47.41667
2	Jamal Zougam	Mohamed Chaoui	3	16.00000
3	Jamal Zougam	Vinay Kholy	1	27.08333
4	Jamal Zougam	Suresh Kumar	1	27.08333
5	Jamal Zougam	Mohamed Chedadi	1	47.66190
6	Jamal Zougam	Imad Eddin Barakat	4	268.00000

visNetwork

```
# See a list of possible layouts
ls("package:igraph", pattern = "^layout_.")

# Update the plot
visNetwork(nodes = data$nodes, edges = data$edges,
           width = 300, height = 300) %>%
  # Change the layout to be on a grid
  visIgraphLayout(layout = "layout_on_grid")
```

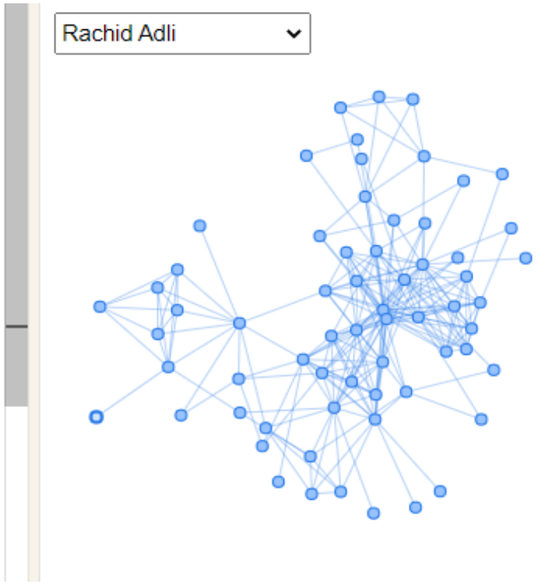


```
# Add to the plot
visNetwork(nodes = data$nodes, edges = data$edges,
           width = 300, height = 300) %>%
  # Choose an operator
  visIgraphLayout(layout = "layout_with_kk") %>%
  # Change the options to highlight
  # the nearest nodes and ties
  visOptions(highlightNearest = TRUE)
```

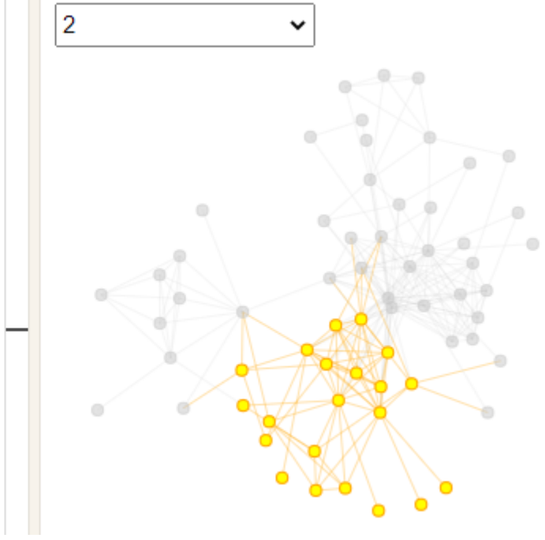


visNetwork

```
# Update the plot
visNetwork(nodes = data$nodes, edges = data$edges,
           width = 300, height = 300) %>%
  visIgraphLayout(layout = "layout_with_kk") %>%
  # Change the options to allow selection
  # of nodes by ID
  visOptions(nodesIdSelection = TRUE)
```




```
# Copy cluster node attribute to color node attribute
V(g)$color <- V(g)$cluster

# Convert g to vis network data
data <- toVisNetworkData(g)

# Update the plot
visNetwork(nodes = data$nodes, edges = data$edges,
           width = 300, height = 300) %>%
  visIgraphLayout(layout = "layout_with_kk") %>%
  # Change options to select by group
  visOptions(selectedBy = "group")
```



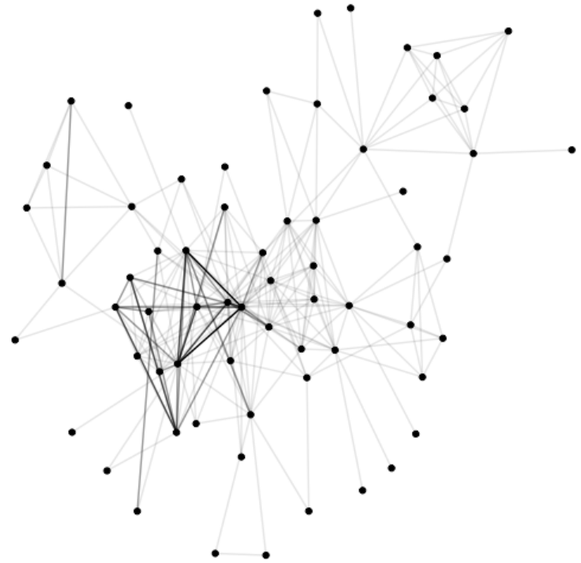
ggraph()

```
library (igraph)
library(dplyr)
library(ggplot2)
library(ggraph)
```

- Geometries for nodes have names starting `geom_node_` . For example, `geom_node_point()` draws each node as a point. `geom_node_text()` draws a text label on each node.
- Geometries for ties have names starting `geom_edge_` . For example, `geom_edge_link()` draws edges as a straight line between nodes.

For your convenience, `ggraph` is already loaded, the *graph theme* is set with the function `set_graph_style()` , and the network `g` is at your disposal.

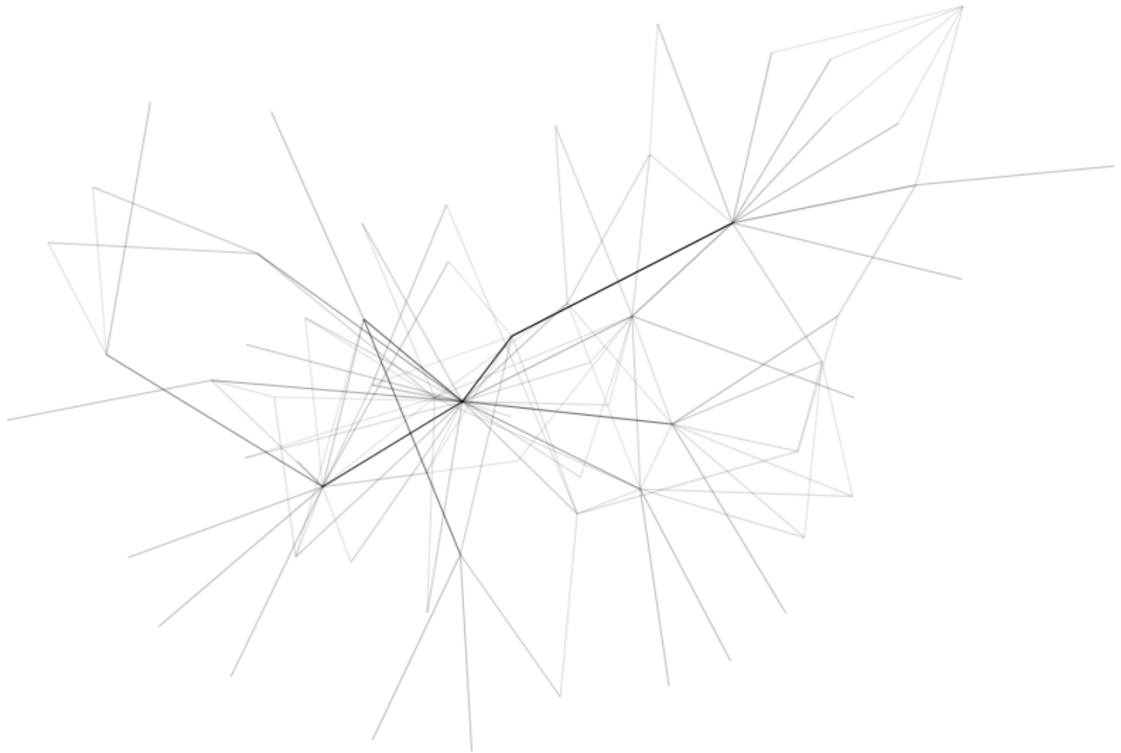
```
# visualize the network
ggraph(g, layout = "with_kk") +
    geom_edge_link(aes(alpha = weight)) +
    geom_node_point()
```



```
> ggraph:::igraphlayouts
 [1] "as_bipartite"  "as_star"       "as_tree"       "in_circle"
 [5] "nicely"        "with_dh"       "with_drl"      "with_gem"
 [9] "with_graphopt" "on_grid"       "with_mds"      "with_sugiyama"
[13] "on_sphere"     "randomly"      "with_fr"       "with_kk"
[17] "with_lgl"
```

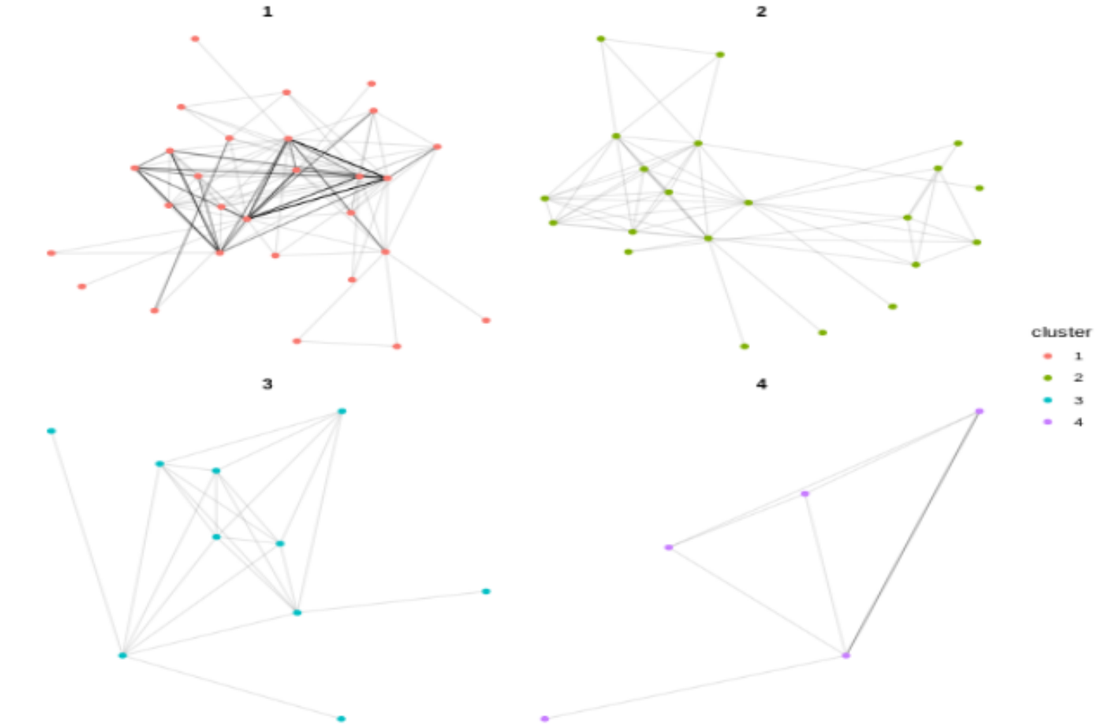
Applying filters to the network

```
# Calculate the median betweenness
median_betweenness = median(E(g)$betweenness)

ggraph(g, layout = "with_kk") +
  # Filter ties for betweenness greater than the median
  geom_edge_link(aes(alpha = betweenness,
                     filter = betweenness > median_betweenness)) +
  theme(legend.position="none")
```

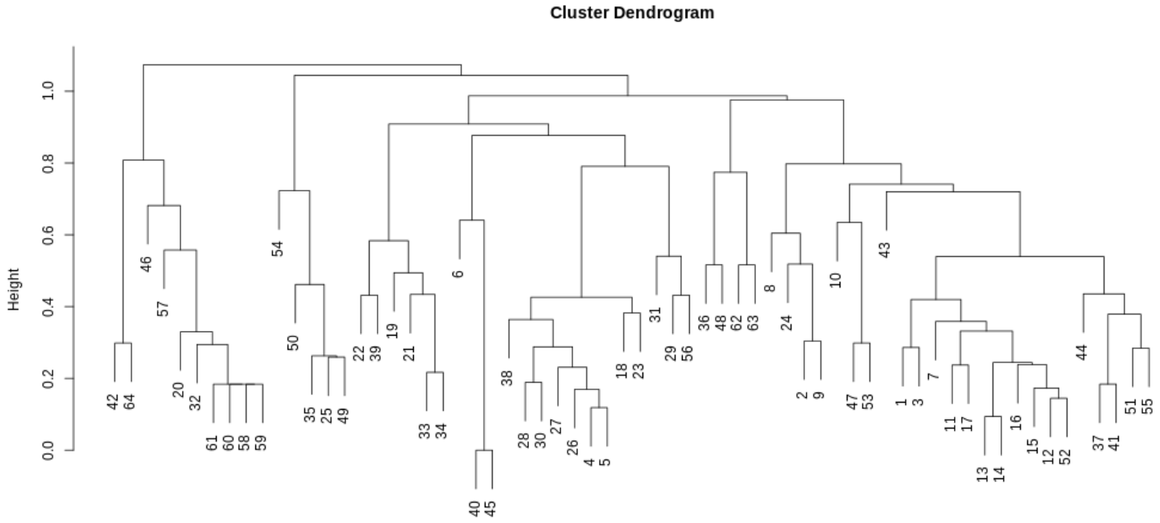


Plotting clusters

```
# From previous step
V(g)$cluster <- nodes$cluster

# Update the plot
ggraph(g, layout = "with_kk") +
  geom_edge_link(aes(alpha = weight), show.legend=FALSE) +
  geom_node_point(aes(color = factor(cluster))) +
  labs(color = "cluster") +
  # Facet the nodes by cluster, with a free scale
  facet_nodes(facets = ~cluster,
              scales = "free")
```



plot(cc)



Motivation: social networks and predictive analytics

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Bart Baesens, Ph.D.

Professor of Data Science, KU Leuven and University of Southampton

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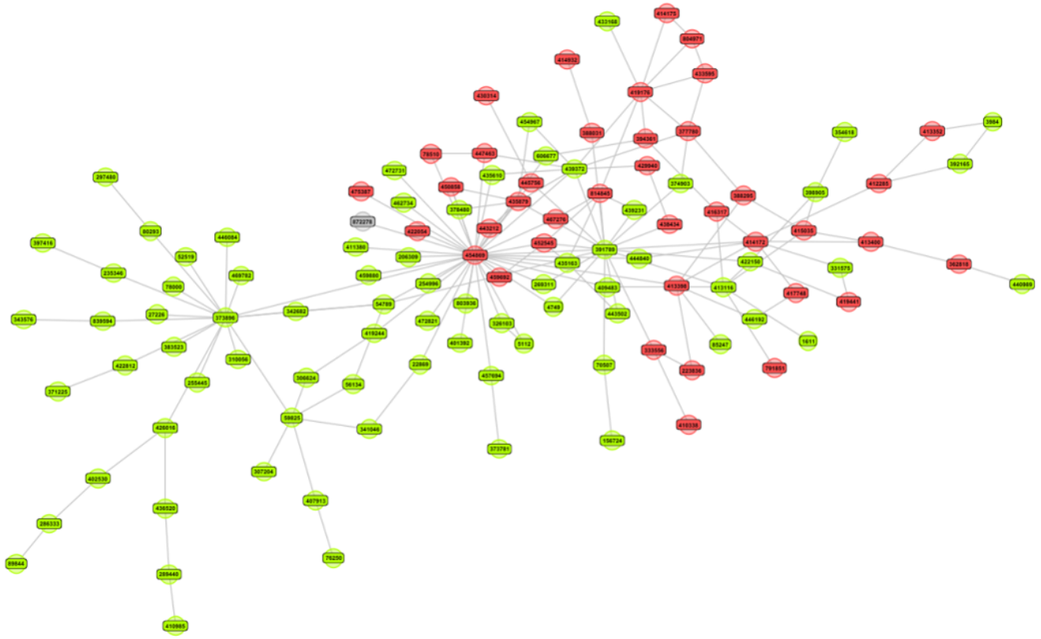
Applications

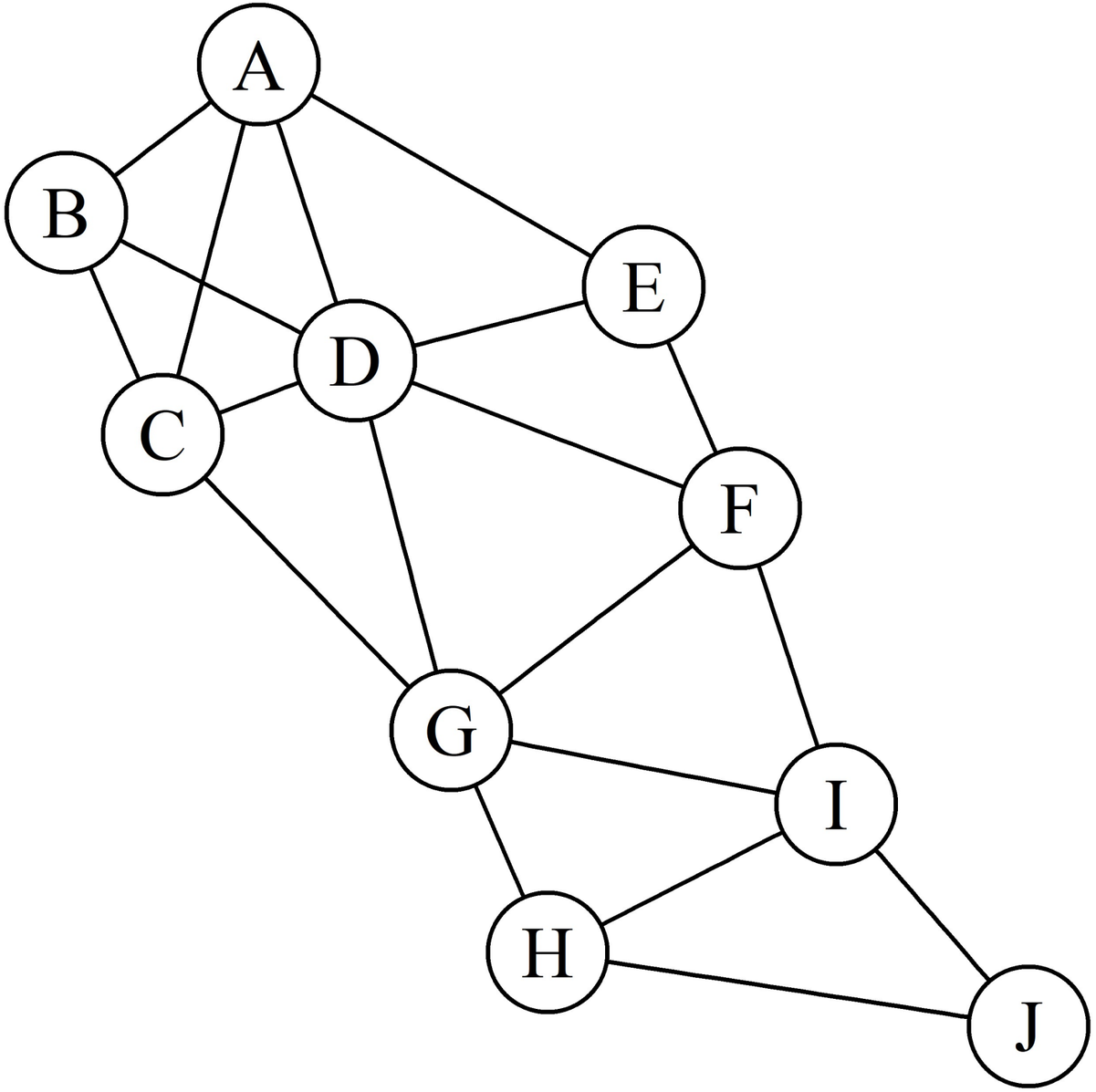
- Age
- Gender
- Fraud



- Churn
  - Customer defection
  - Companies predict who is most likely to churn using
    1. Machine learning techniques
    2. Social networks

Overview

- Labeled social networks
  - Construct and label networks
  - Network learning
- Homophily
  - Measure relational dependency
  - Heterophilicity and dyadicity
- Network featurization
  - Compute node features
- Predictive modeling with networks
  - Turn a network into a flat dataset
  - Predict churn among customers


A
B
C
D
E
F
G
H
I
J

Collaboration Network

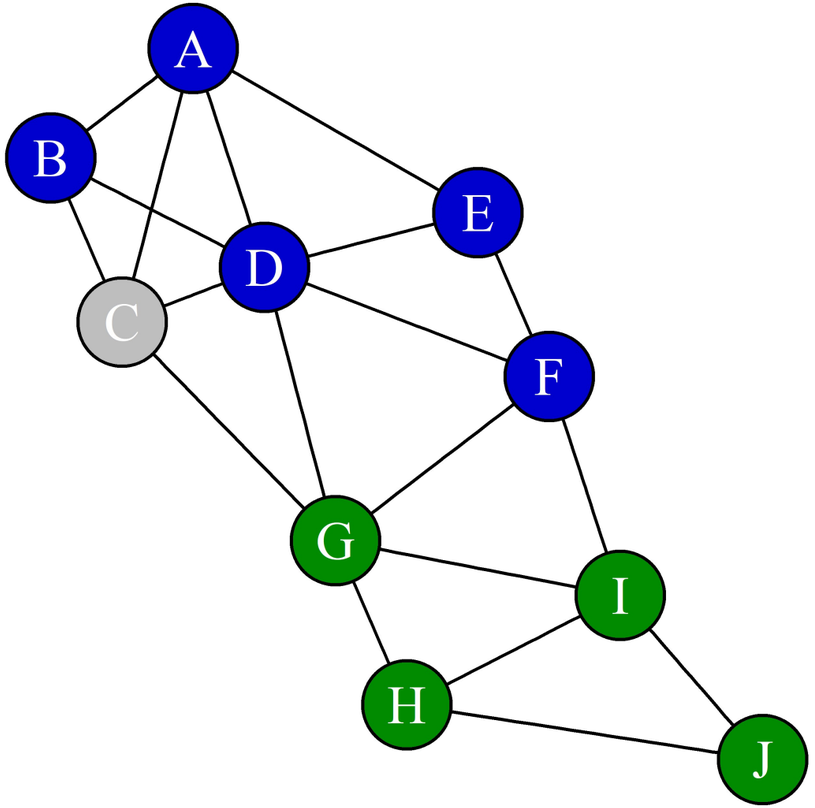
```
library(igraph);
DataScienceNetwork <- data.frame(
  from = c('A', 'A', 'A', 'A', 'B', 'B', 'C', 'C', 'D', 'D', 'D', 'E',
           'F', 'F', 'G', 'G', 'H', 'H', 'I'),
  to = c('B','C','D','E','C','D','D', 'G','E', 'F','G','F','G','I',
           'I','H','I','J','J'))
g <- graph_from_data_frame(DataScienceNetwork, directed = FALSE)
```

```
pos <- cbind(c(2, 1, 1.5, 2.5, 4, 4. 5, 3, 3.5, 5, 6),
             c(10.5, 9.5, 8, 8.5, 9, 7.5, 6, 4.5, 5.5, 4))
plot.igraph(g, edge.label = NA, edge.color = 'black', layout = pos,
            vertex.label = V(g)$name, vertex.color = 'white',
            vertex.label.color = 'black', vertex.size = 25)
```

Collaboration Network

```
V(g)$technology <-
  c('R','R','?','R','R',
    'R','P','P','P','P')
V(g)$color <- V(g)$technology
```

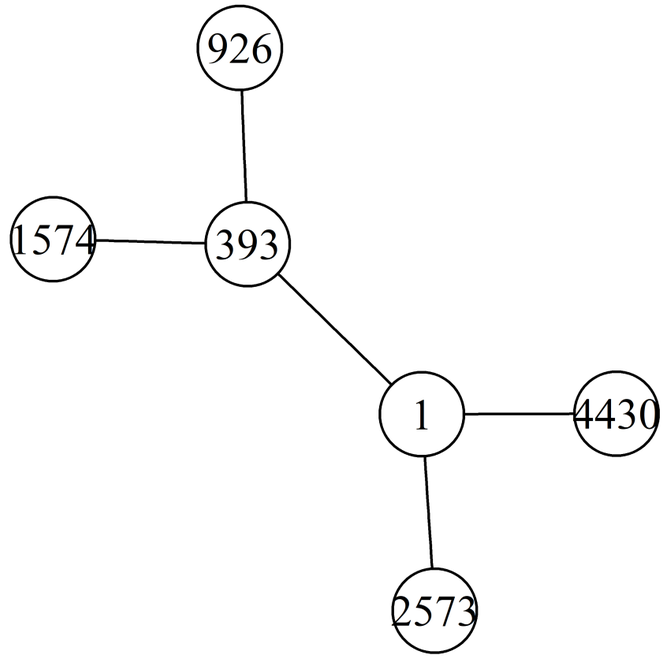
```
V(g)$color <- gsub('R',"blue3", V(g)$color)
V(g)$color <- gsub('P',"green4", V(g)$color)
V(g)$color <- gsub('?',"gray", V(g)$color)
```



Churn Network

```
edgeList
```

```
  from    to
1    1   393
2    1  2573
3    1  4430
4  393   926
5  393  1574
```



Let's practice!

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Labeled networks and network learning

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

María Óskarsdóttir, Ph.D.
Post-doctoral researcher

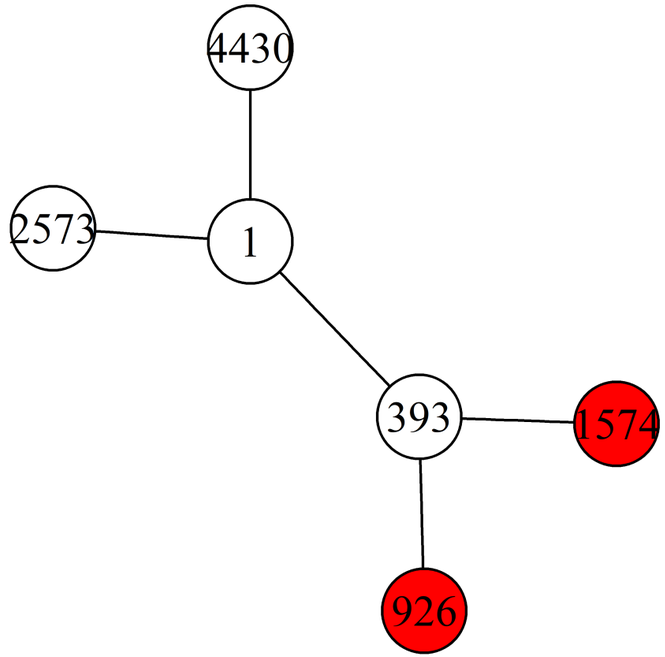
datacamp

```
customers
```

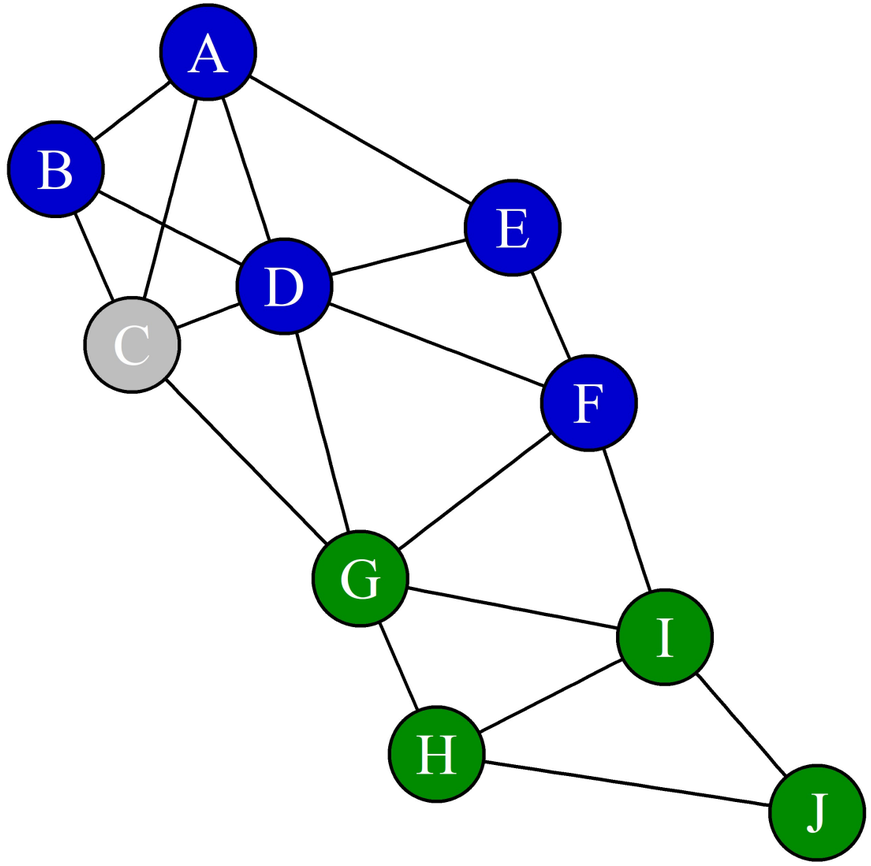
```
    id churn
1    1     0
2  393     0
3 2573     0
4 4430     0
5  926     1
6 1574     1
```

```
edgeList
```

```
  from    to
1    1   393
2    1  2573
3    1  4430
4  393   926
5  393  1574
```

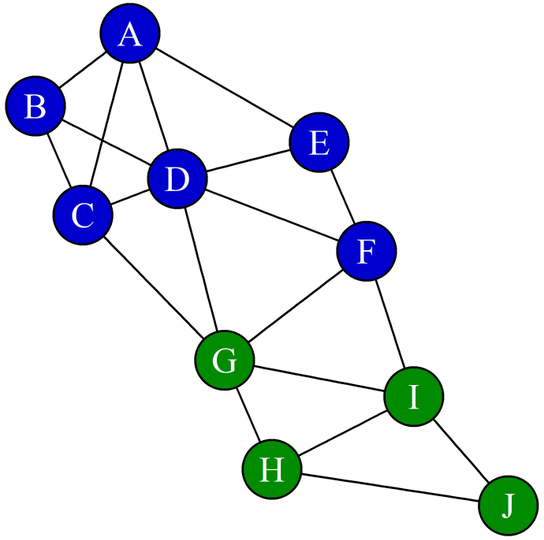


The Relational Neighbor Classifier



- Neighbors of **C**ecelia
  - A,B,D,G
- Neighbors of **C**ecelia that prefer R
  - A, B, D (75%)
- Neighbors of **C**ecelia that prefer Python
  - G (25%)
- **C**ecelia has a higher probability to prefer R

The Relational Neighbor Classifier




```
rNeighbors <- c(4,3,3,5,3,2,3,0,1,0)
pNeighbors <- c(0,0,1,1,0,2,2,3,3,2)
rRelationalNeighbor <- rNeighbors / (rNeighbors + pNeighbors)
rRelationalNeighbor
```

```
1.00 1.00 0.75 0.86 1.00 0.50 0.60 0.00 0.00 0.00
```

Let's practice!

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Challenges of network-based inference

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

María Óskarsdóttir, Ph.D.
Post-doctoral researcher

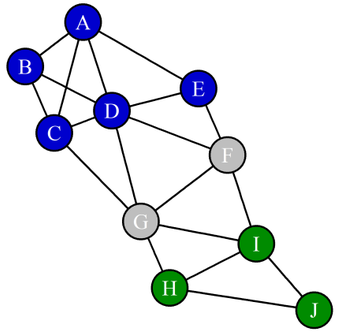
datacamp

First challenge

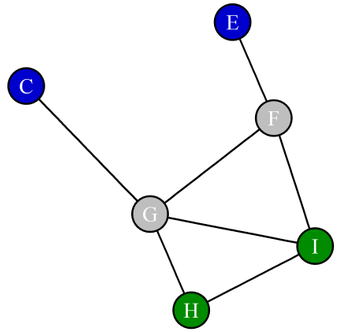
Splitting the data!

```
set.seed(1001)
sampleVertices <- sample(1:10, 6, replace=FALSE)
plot(induced_subgraph(g, V(g)[sampleVertices]))
plot(induced_subgraph(g, V(g)[-sampleVertices]))
```

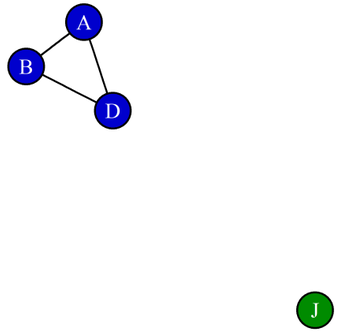
Full network



Training set

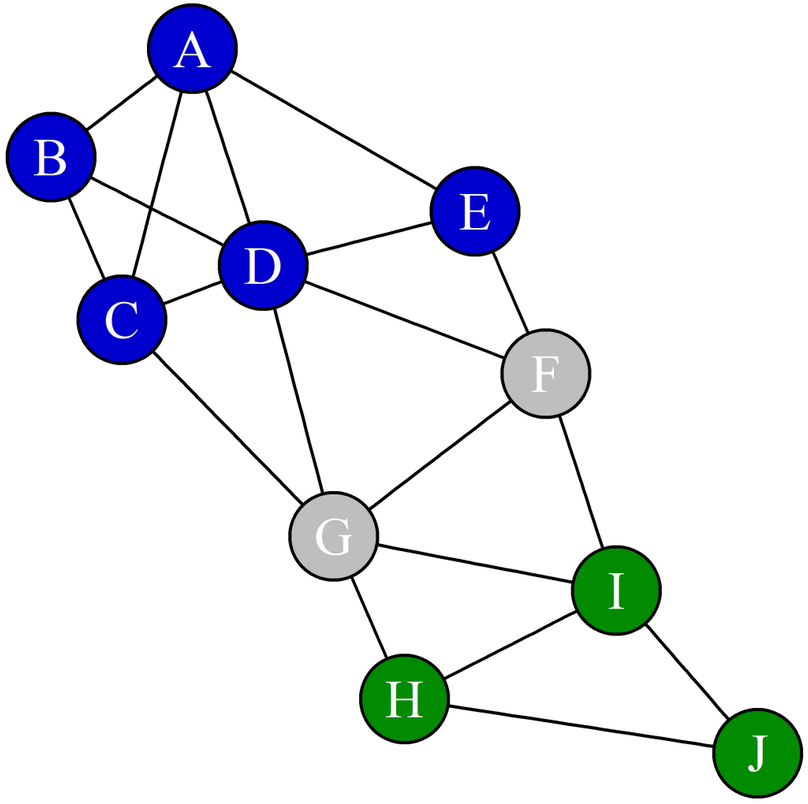


Test set



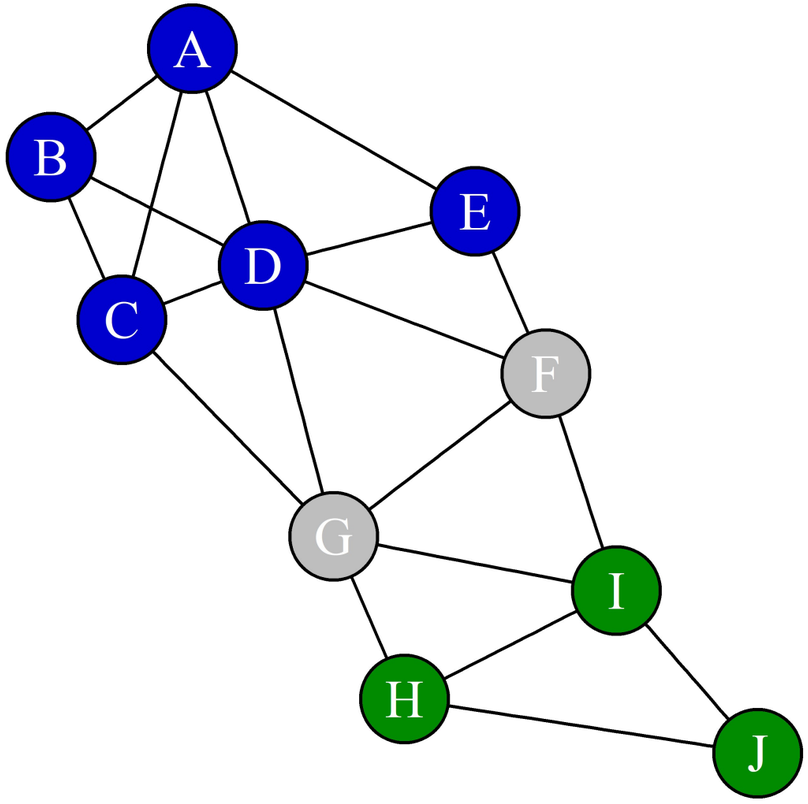
Second challenge

The observations in the dataset are not independent and identically distributed (iid)

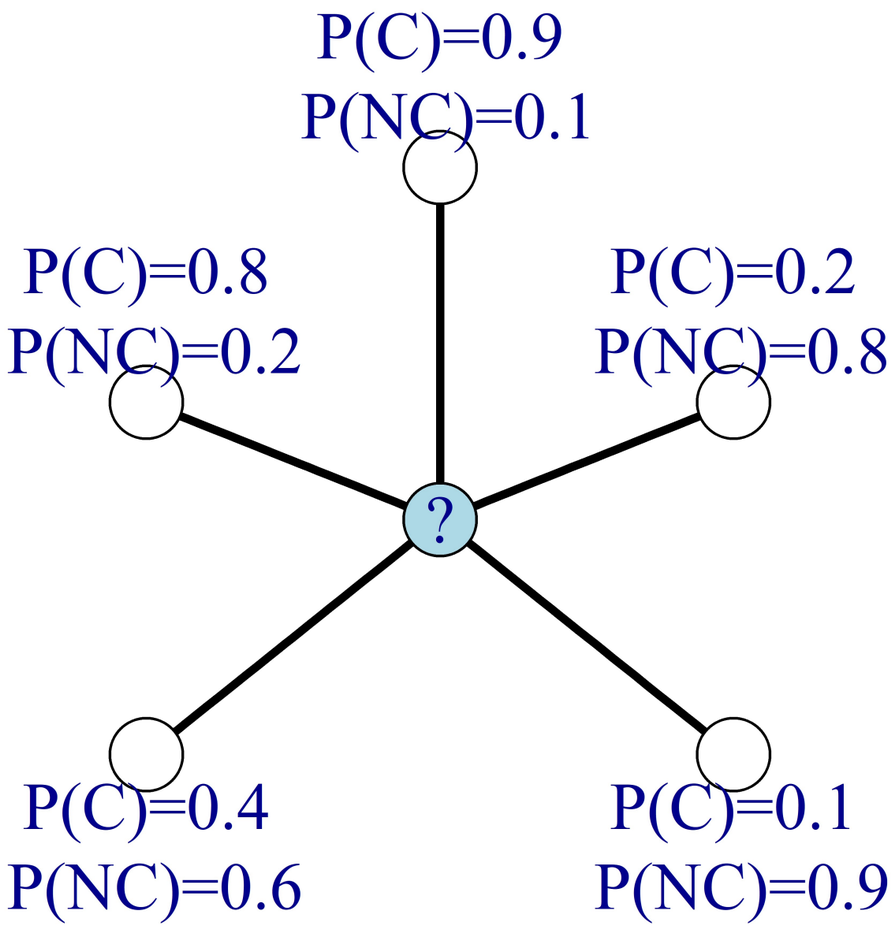


Third challenge

Collective Inference!



Probabilistic relational neighbor classifier




```
# probability churn (C)
(0.9 + 0.2 + 0.1 + 0.4 + 0.8) / 5
```

```
0.48
```

```
# probability non-churn (NC)
(0.1 + 0.8 + 0.9 + 0.6 + 0.2) / 5
```

```
0.52
```

Let's practice!

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Homophily

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Bart Baesens, Ph.D.

Professor of Data Science, KU Leuven
and University of Southampton

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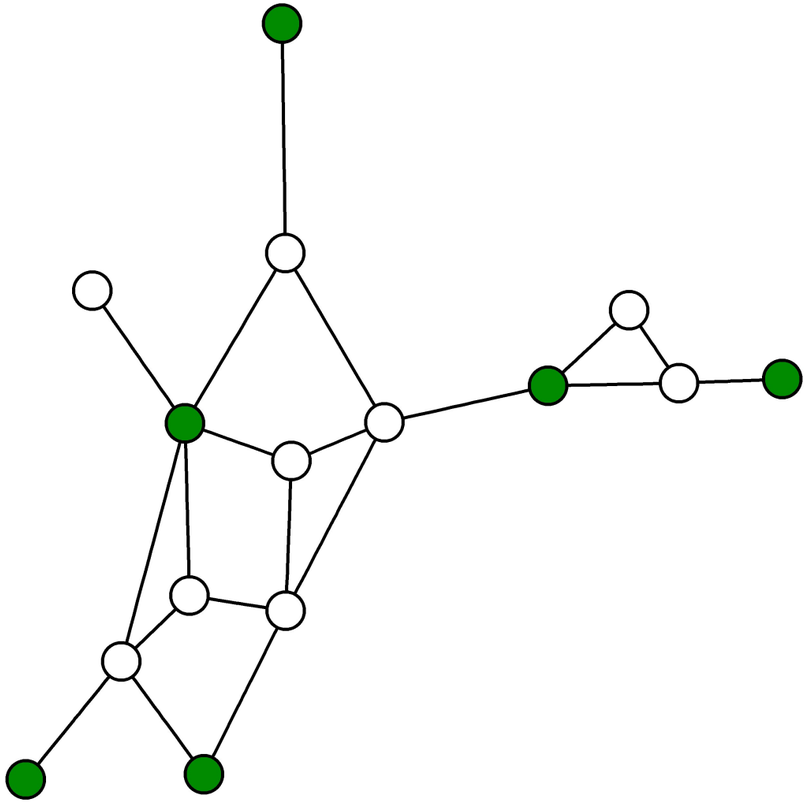
Homophily explained

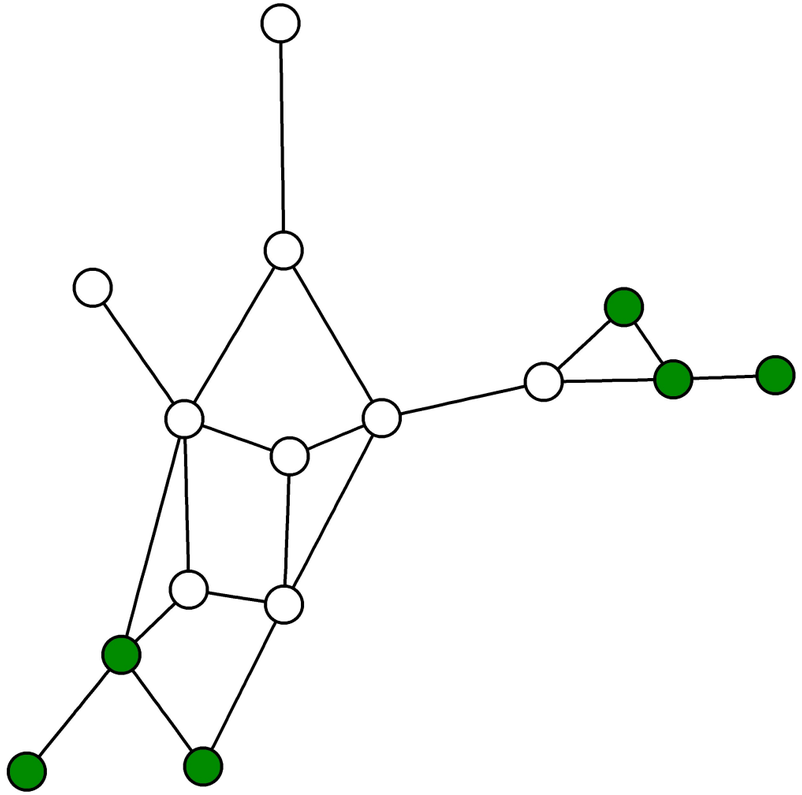
> Birds of a feather flock together

- Share common property, hobbies, interest, origin, etc.
- Depends on:
  - Connectedness between nodes with **same** label
  - Connectedness between nodes with **opposite** labels

Homophilic Networks



- Not Homophilic



- Homophilic

```
names <- c('A','B','C','D','E','F','G','H','I','J')
tech <- c(rep('R',6),rep('P',4))
DataScientists <- data.frame(name=names,technology=tech)
DataScienceNetwork <- data.frame(
 from=c('A','A','A','A','B','B','C','C','D','D',
        'D','E','F','F','G','G','H','H','I'),
 to=c('B','C','D','E','C','D','D','G','E','F',
        'G','F','G','I','I','H','I','J','J'),
 label=c(rep('rr',7),'rp','rr','rr','rp','rr','rp','rp',rep('pp',5)))

g <- graph_from_data_frame(DataScienceNetwork,directed = FALSE)
```

Add the technology as a node attribute

```
V(g)$label <- as.character(DataScientists$technology)
V(g)$color <- V(g)$label
V(g)$color <- gsub('R',"blue3",V(g)$color))
V(g)$color <- gsub('P',"green4",V(g)$color)
```

Types of edges

Code to color the edges

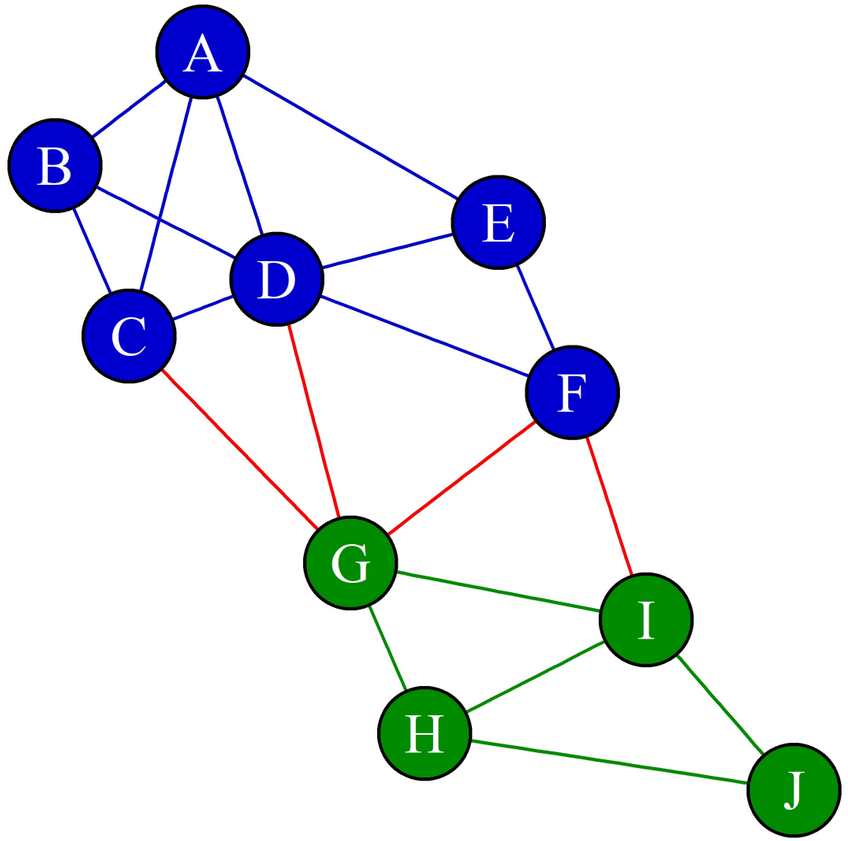
```
E(g)$color<-E(g)$label
E(g)$color=gsub('rp','red',E(g)$color)
E(g)$color=gsub('rr','blue3',E(g)$color)
E(g)$color=gsub('pp','green4',E(g)$color)
```

Code to visualize the network

```
pos<-cbind(c(2,1,1.5,2.5,4,4.5,3,3.5,5,6),
c(10.5,9.5,8,8.5,9,7.5,6,4.5,5.5,4))

plot(g,edge.label=NA,vertex.label.color='white',
layout=pos, vertex.size = 25)
```

Counting edge types



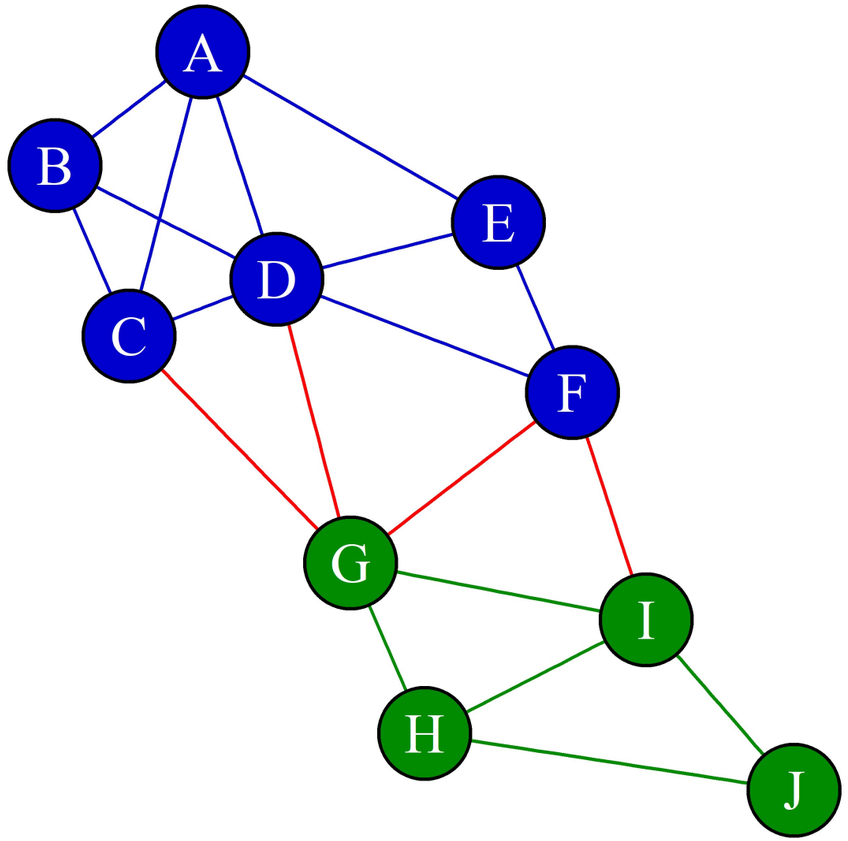

```
# R edges
edge_rr<-sum(E(g)$label=='rr')

# Python edges
edge_pp<-sum(E(g)$label=='pp')

# cross label edges
edge_rp<-sum(E(g)$label=='rp')
```

- `edge_rr=` 10
- `edge_pp=` 5
- `edge_rp=` 4

Network connectance



$$p = \frac{2 \cdot edges}{nodes(nodes-1)}$$

```
p <- 2*edges/nodes*(nodes-1)
```

- `p = 0.42`
- Number of edges in a fully connected network: $\binom{nodes}{2} = \frac{nodes(nodes-1)}{2}$

Let's practice!

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Dyadicity

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

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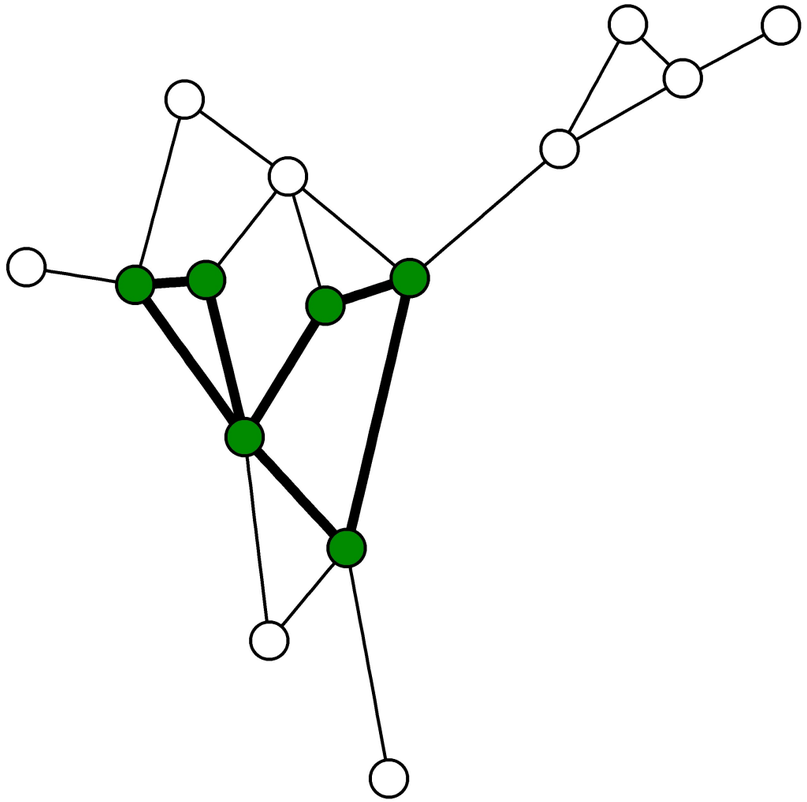
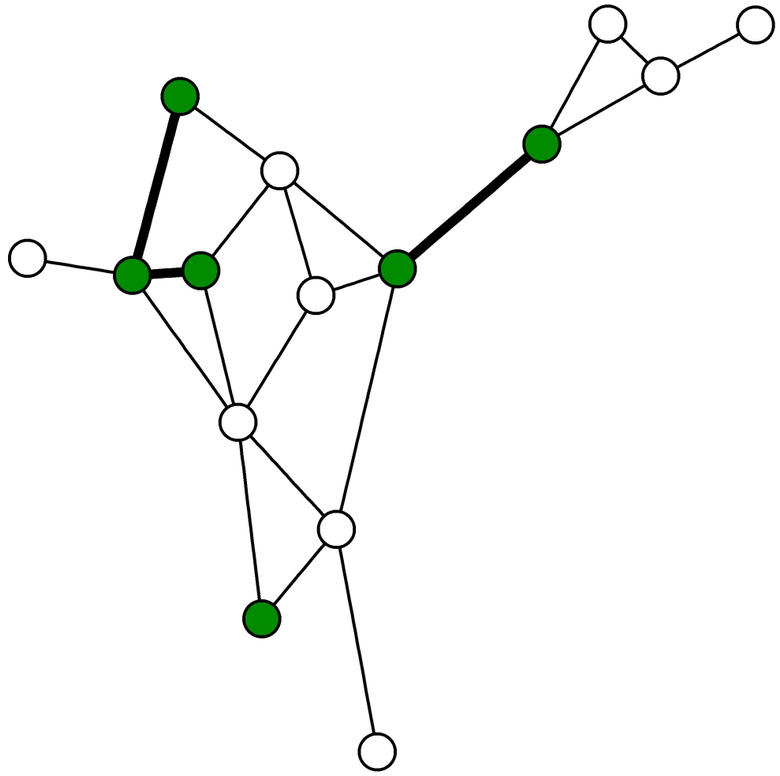
Dyadicity



7 edges between green nodes



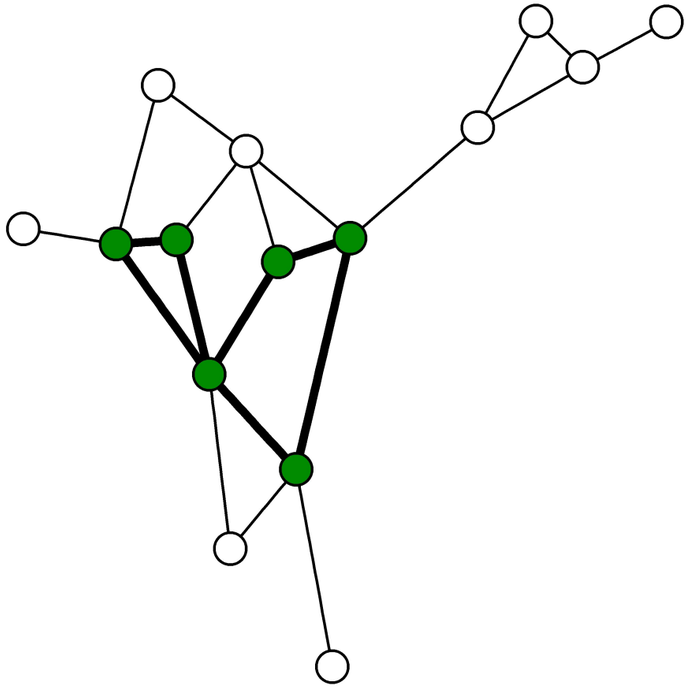
3 edges between green nodes

Dyadicity

Connectedness between nodes with the **same** label compared to what is expected in a random configuration of the network

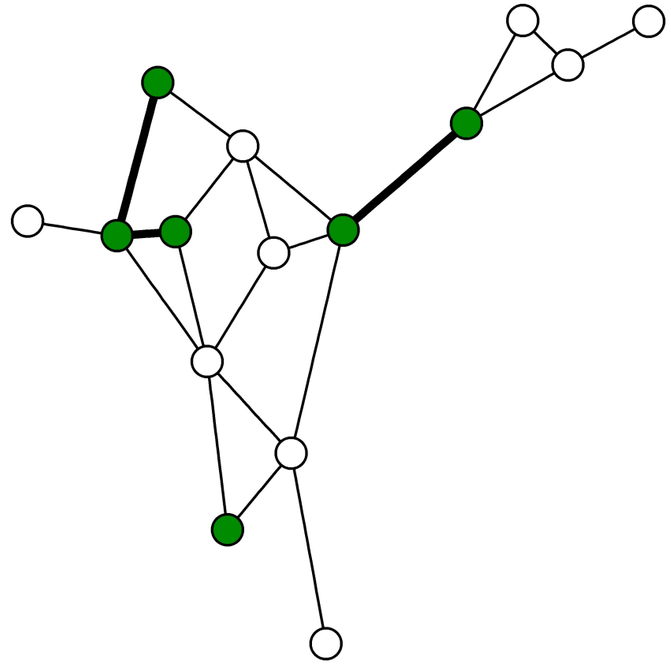
- Expected number of same label edges: $\binom{n_g}{2} \cdot p = \frac{n_g(n_g-1)}{2} \cdot p$
- Example:
  - Network with 9 white nodes, 6 green nodes, 21 edges, and connectance $p = 0.2$
  - Expected number of edges connecting two green nodes is 3 ($= \frac{6 \cdot 5 \cdot p}{2}$)
- Dyadicity equals the actual number of same label edges divided by the expected number of same label edge
  - $D = \frac{\text{number of same label edges}}{\text{expected number of same label edges}}$

Dyadicity



7 edges between green nodes

- $D = 7/3 = 2.33$



3 edges between green nodes

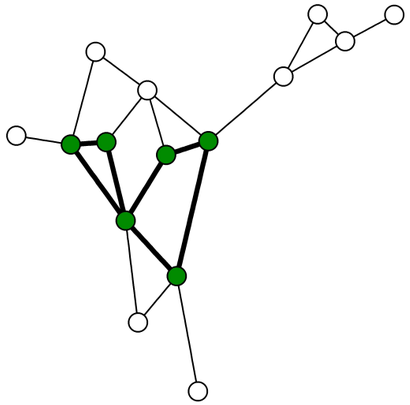
- $D = 3/3 = 1$

Types of Dyadicity

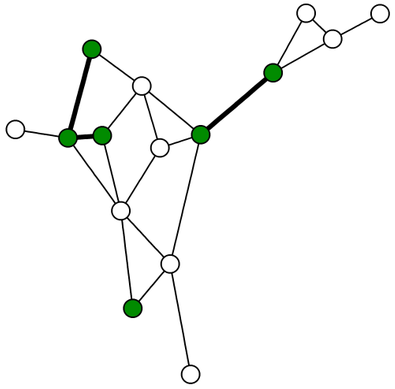
Three scenarios

1. $D > 1 \Rightarrow$ Dyadic
2. $D \simeq 1 \Rightarrow$ Random
3. $D < 1 \Rightarrow$ Anti-Dyadic

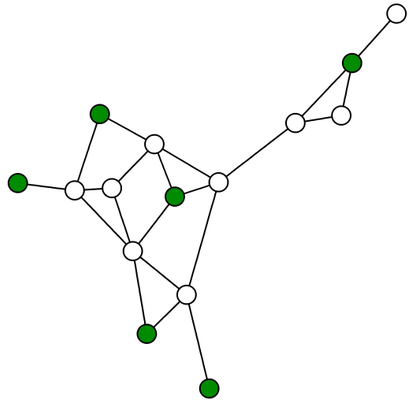
$D = 2.33$



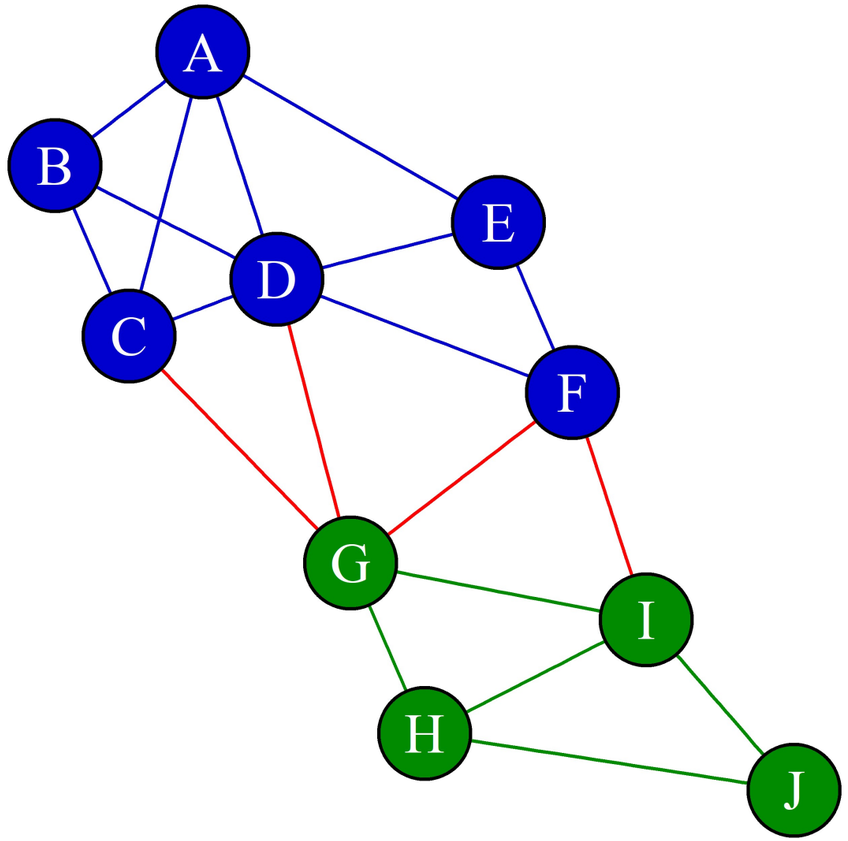
$D = 1$



$D = 0$



Dyadicity in the Network of Data Scientists




```
p <- 2 * 19 / (10 * 9)
expectedREdges <- 6 * 5 / 2 * p
expectedPEdges <- 4 * 3 / 2 * p
dyadicityR <- rEdges / expectedREdges
dyadicityP <- pEdges / expectedPEdges
dyadicityR
```

```
1.578947
```

```
dyadicityP
```

```
1.973684
```

Let's practice!

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Heterophilicity

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

María Óskarsdóttir, Ph.D.
Post-doctoral researcher

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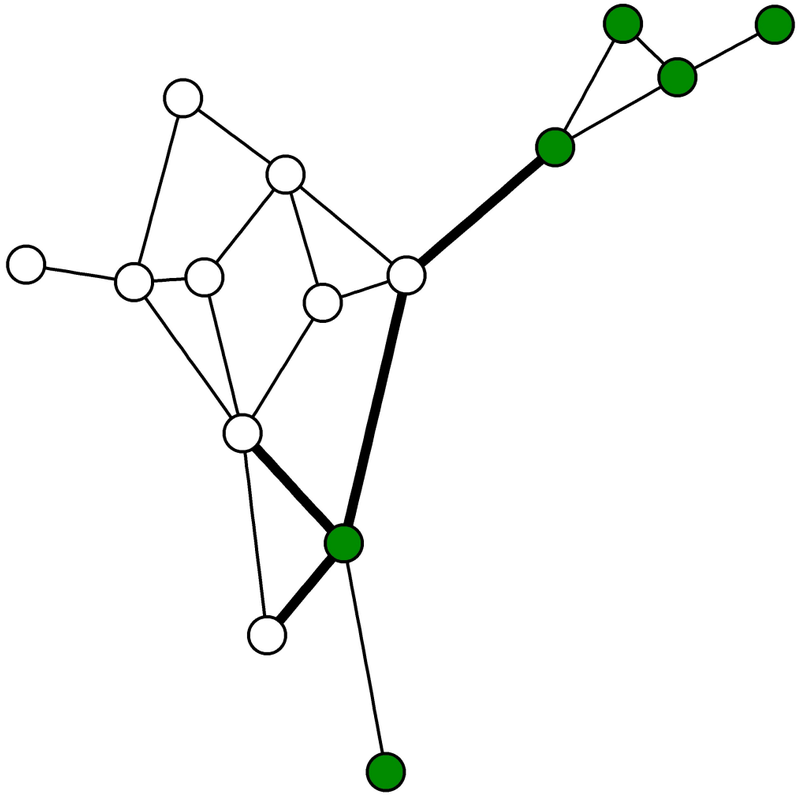
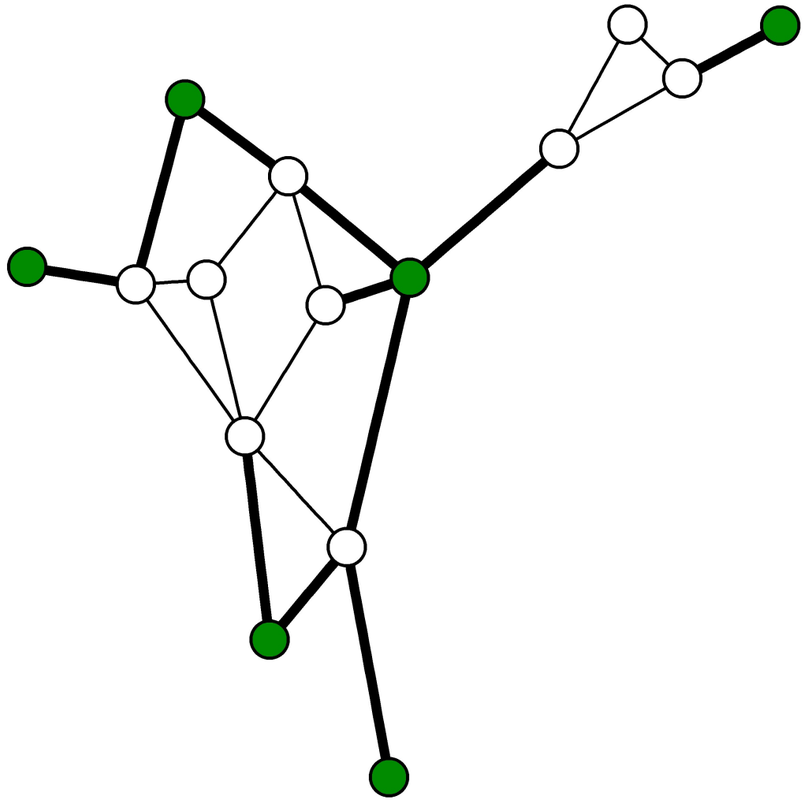
Heterophilicity



4 cross label edges



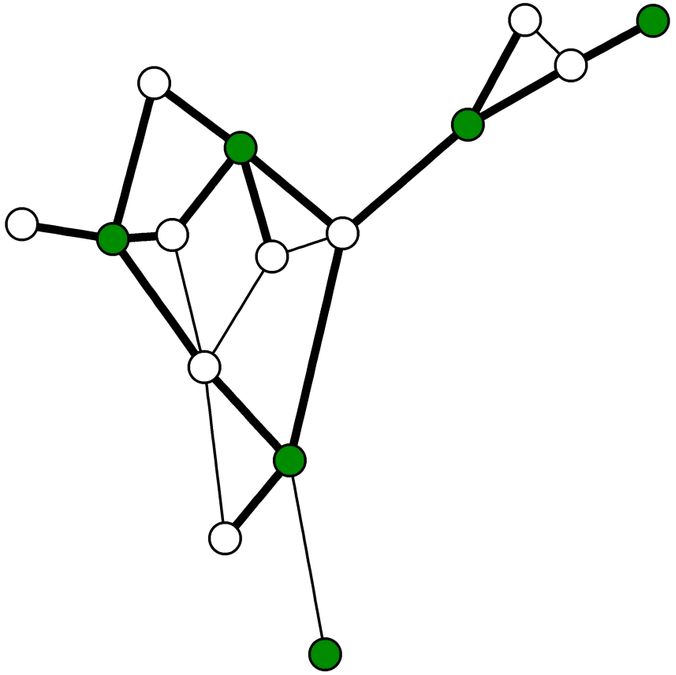
11 cross label edges

Heterophilicity

Connectedness between nodes with **different** labels compared to what is expected for a random configuration of the network

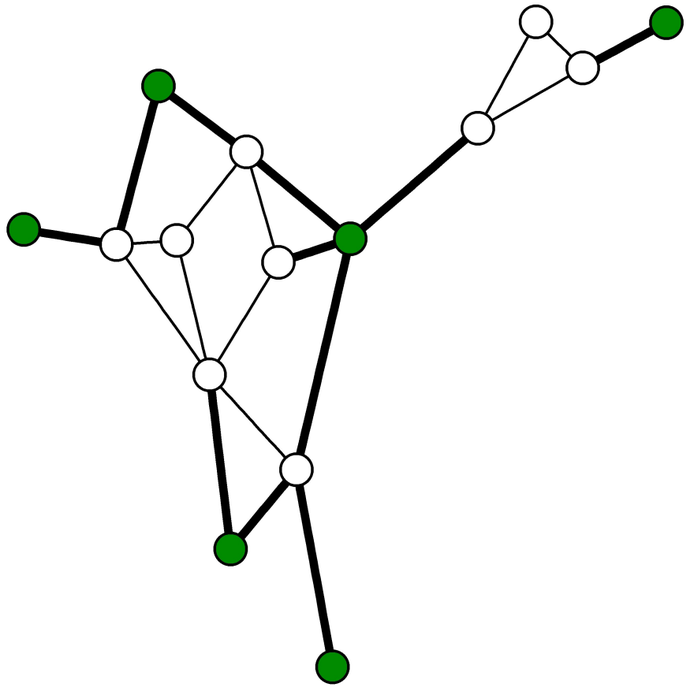
- Expected number of cross label edges $= n_w n_g p$
- Example:
  - Network with 9 white nodes, 6 green nodes, 21 edges, and connectance $p = 0.2$
  - Expected number of cross label edges is 11 $(= 9 \cdot 6 \cdot p)$
- Heterophilicty equals the actual number of cross label edges divided by the expected number of cross label edges
  - $H = \frac{\text{number of cross label edges}}{\text{expected number of cross label edges}}$

Heterophilicity



15 cross label edges

- $H = 15/11 = 1.39$



11 cross label edges

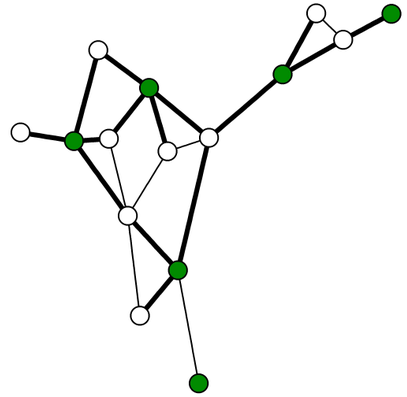
- $H = 11/11 = 1.02$

Types of Heterophilicity

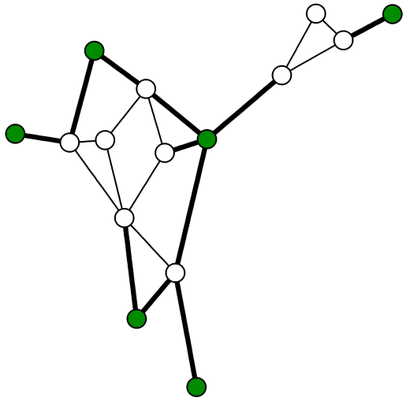
Three scenarios

1. $H > 1 \Rightarrow$ Heterophilic
2. $H \simeq 1 \Rightarrow$ Random
3. $H < 1 \Rightarrow$ Heterophobic

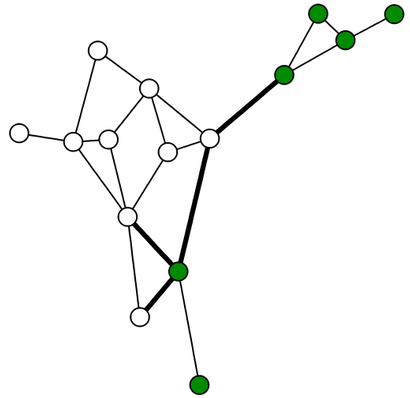
$H = 1.39$



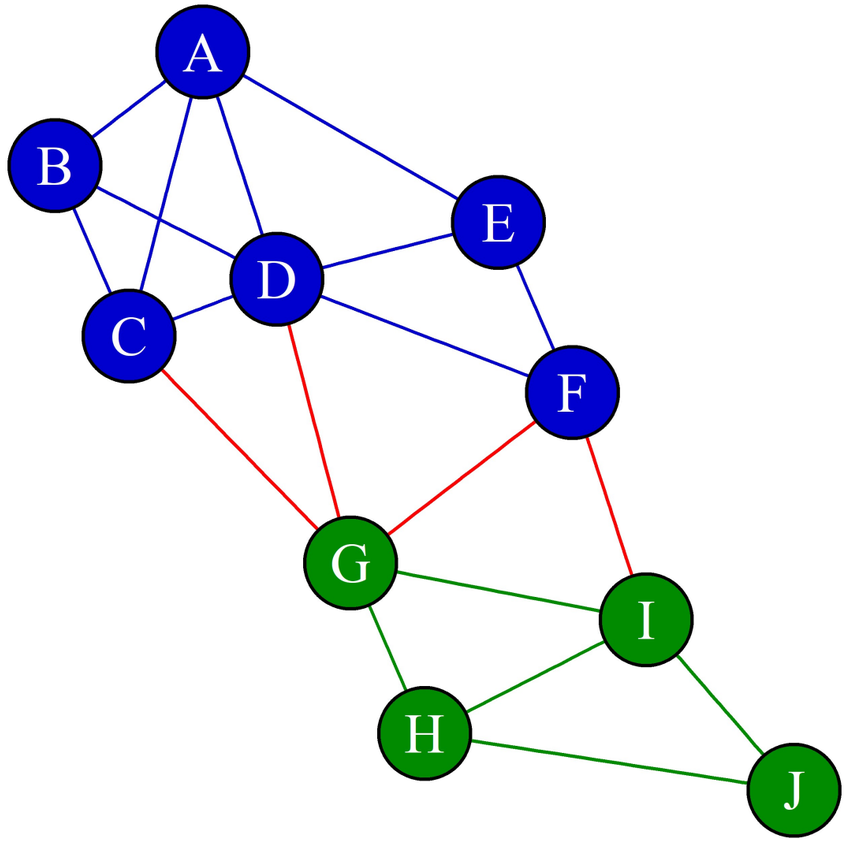
$H = 1.02$



$H = 0.37$



Heterophilicity in the network of data scientists




```
p<-2*19/(10*9)
m_rp<-6*4*p


H_rp<-edge_rp/m_rp
```

```
H_rp
```

```
0.3947368
```

Let's practice!

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Summary of homophily

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

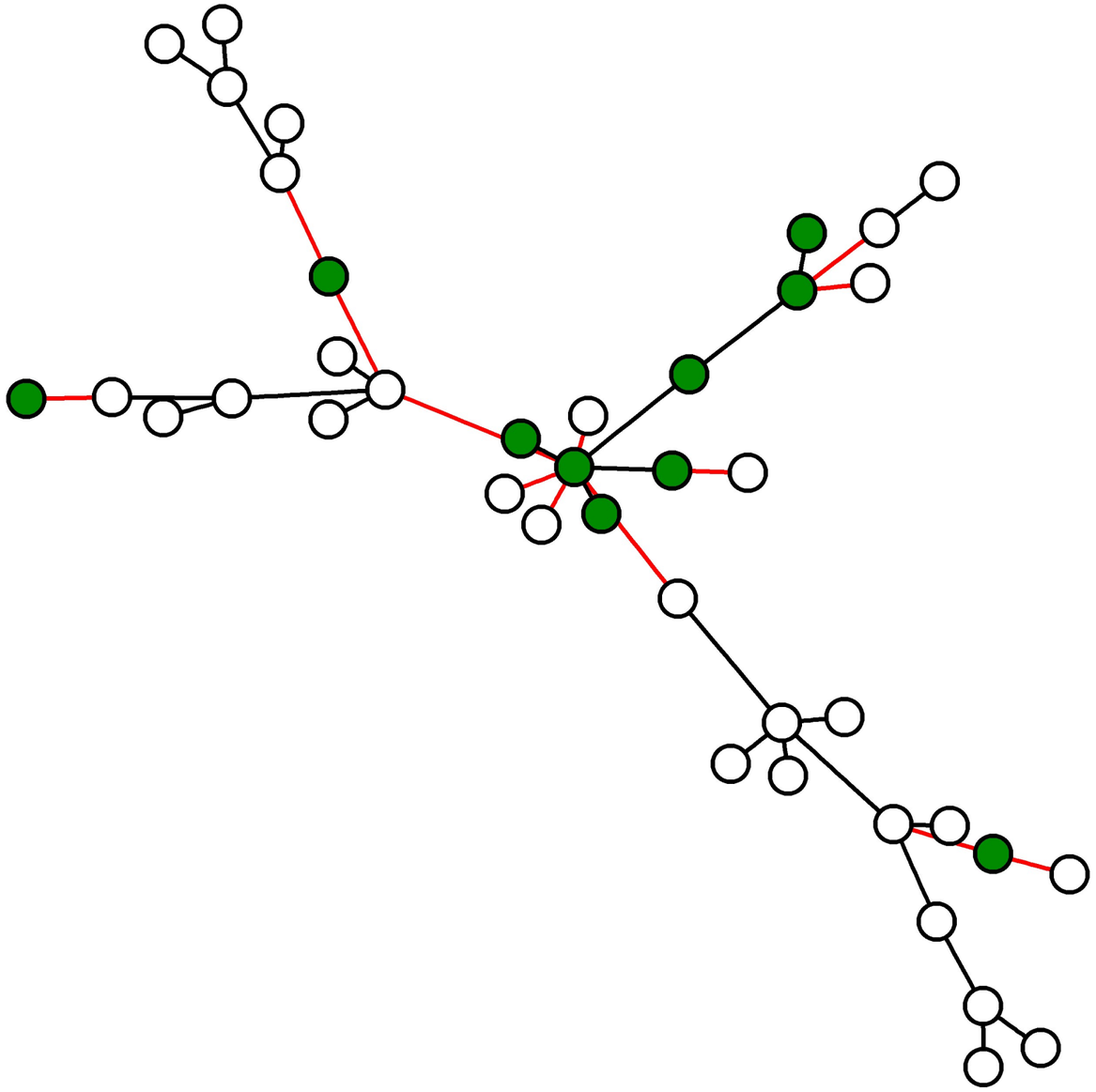
María Óskarsdóttir, Ph.D.
Postdoctoral researcher

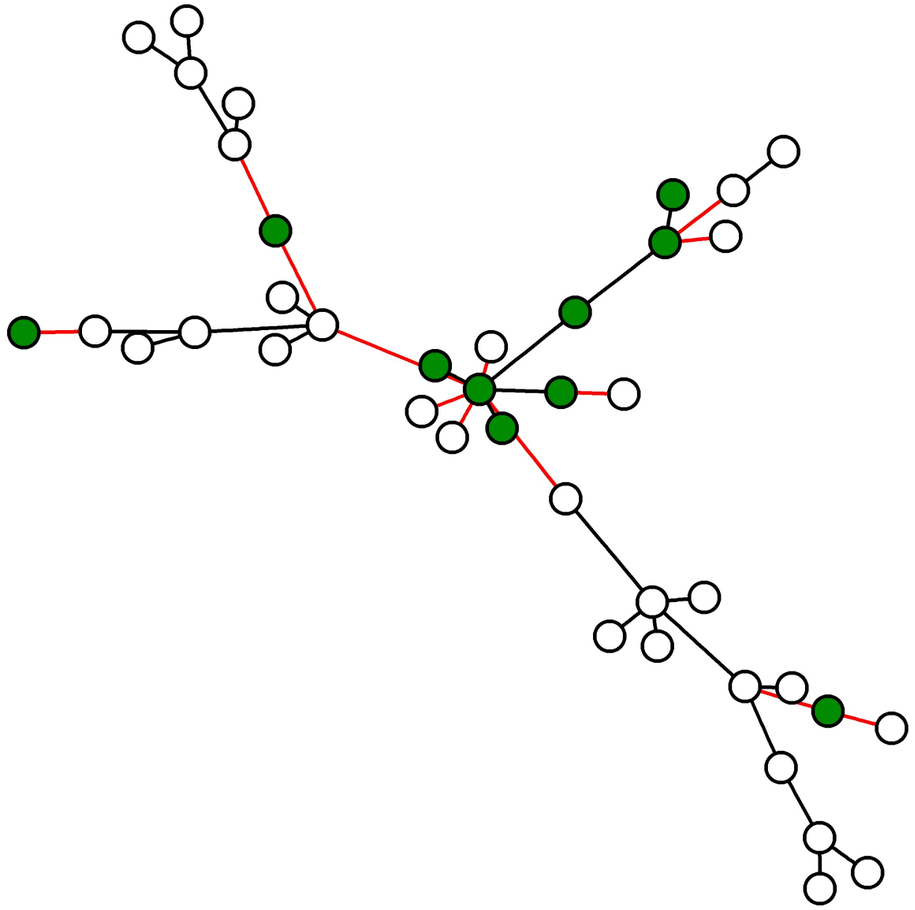
Can I do predictive analytics with my network?

> Are the relationships between nodes important?

> Are the labels randomly spread through the network or is there some structure?

> **Is the network homophilic?**





```
N <- 40
E <- 39
n_green <- 10
n_white <- 30
e_green <- 6
e_mixed <- 13
p <- 2 * E / N / (N-1)
m_green <- n_green * (n_green-1)/2 * p
m_mixed <- n_green * n_white * p
# Dyadicity
e_green / m_green
```

```
2.666667
```

```
# Heterophilicity
e_mixed / m_mixed
```

```
0.8666667
```

⇒ Homophilic

Let's practice!

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Basic Network features

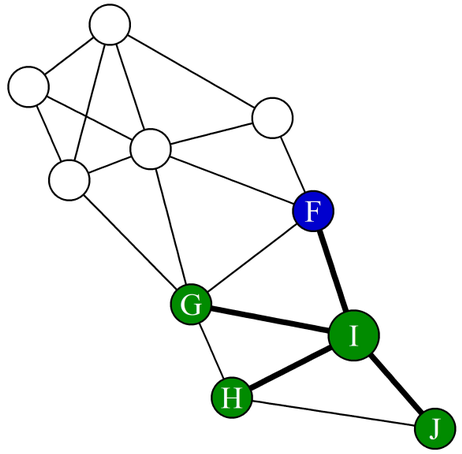
PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Bart Baesens, Ph.D.

Professor of Data Science, KU Leuven and University of Southampton

datacamp

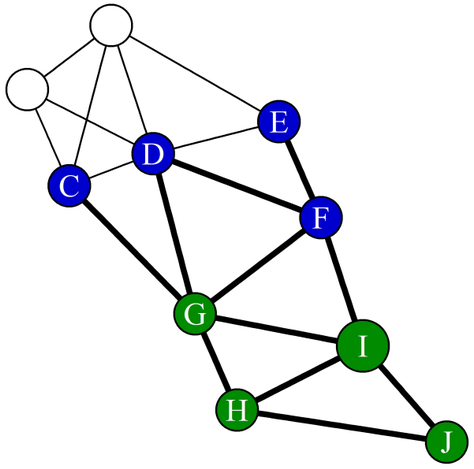
Neighborhood features



- First order degree
  - Number of connected nodes

```
degree(g)
```

```
A B C D E F G H I J
4 3 4 6 3 4 5 3 4 2
```

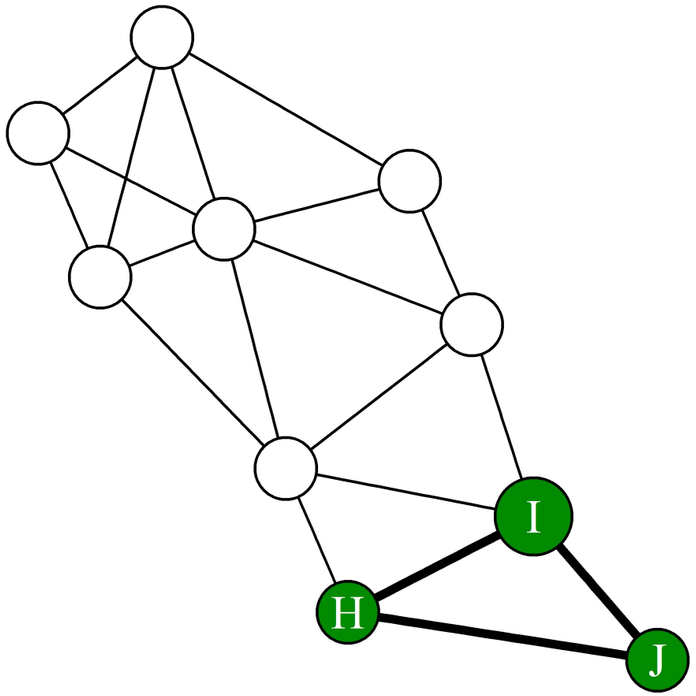


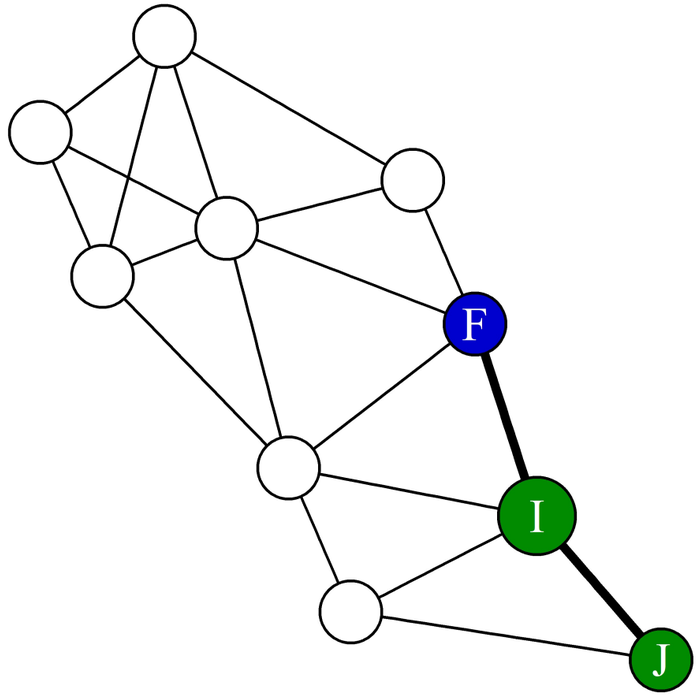
- Second order degree
  - Number of connected nodes that are two or less edges away

```
neighborhood.size(g, order = 2)
```

```
7  7  9  9  8 10 10  7  8  5
```

Neighborhood features - triangles



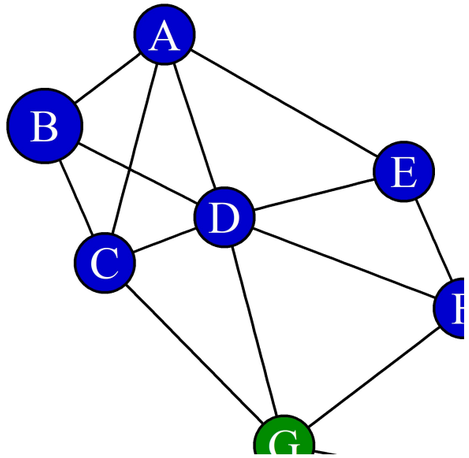



```
count_triangles(g)
```

```
4 3 4 7 2 3 4 2 3 1
```

Centrality features

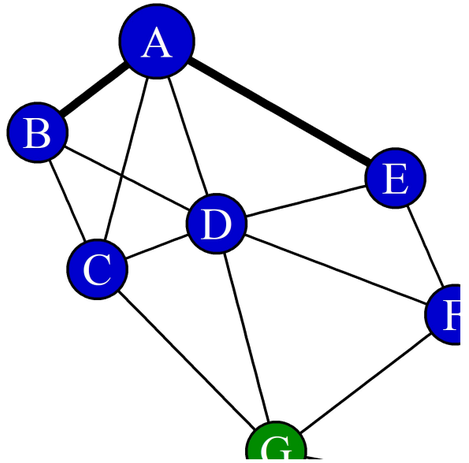
- Betweenness




```
betweenness(g)
```

```
   A    B    C    D    E    F     G     H    I    J
1.00 0.00 3.32 8.10 0.92 5.37 11.47 2.07 5.77 0.00
```

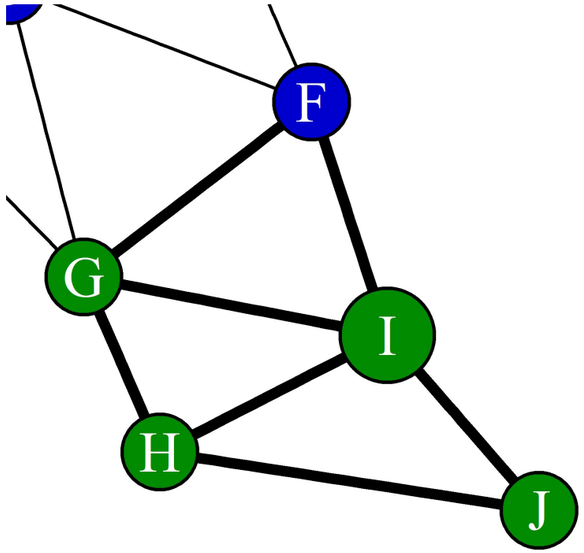
- Closeness

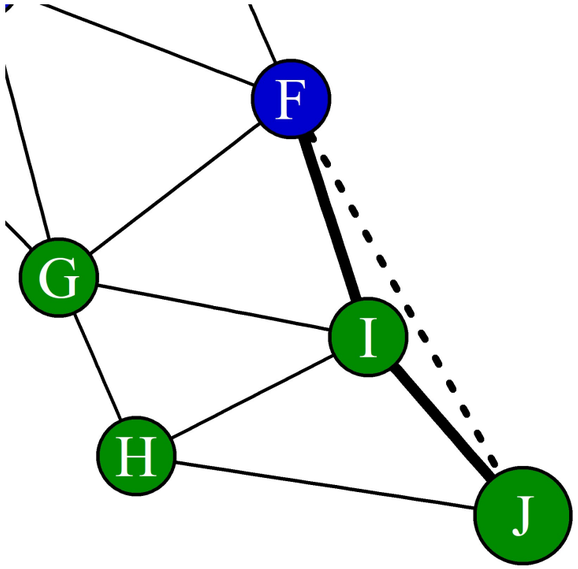



```
closeness(g)
```

```
   A    B    C    D    E    F    G    H    I    J
0.06 0.05 0.07 0.08 0.06 0.07 0.08 0.06 0.06 0.04
```

Transitivity






```
transitivity(g,type = 'local')
```

```
0.67 1.00 0.67 0.47 0.67 0.50 0.40 0.67 0.50 1.00
```

Let's practice!

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Link Based Features

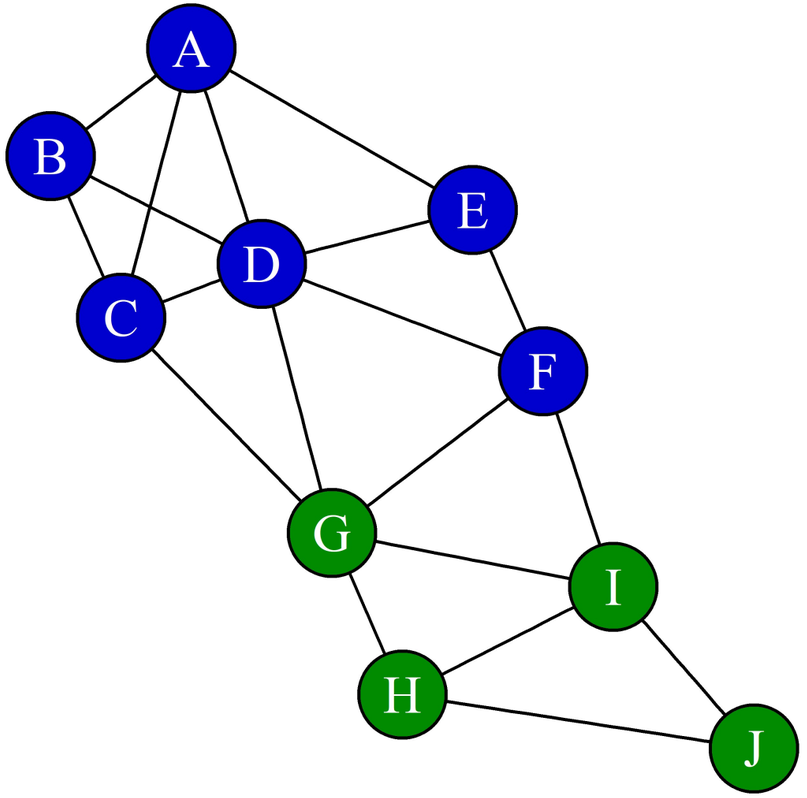
PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

María Óskarsdóttir, Ph.D.
Post-doctoral researcher

datacamp

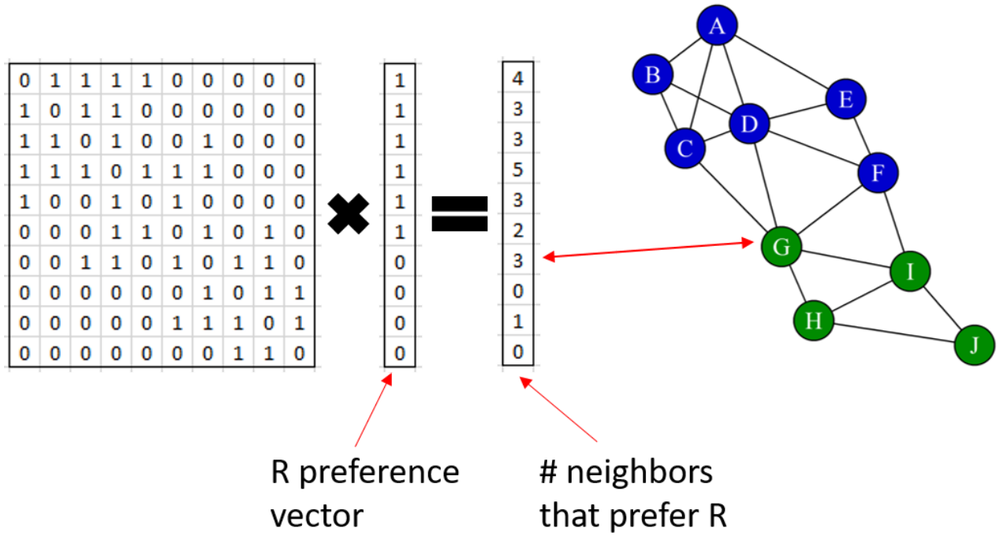
Adjacency matrices

	A	B	C	D	E	F	G	H	I	J
A	0	1	1	1	1	0	0	0	0	0
B	1	0	1	1	0	0	0	0	0	0
C	1	1	0	1	0	0	1	0	0	0
D	1	1	1	0	1	1	1	0	0	0
E	1	0	0	1	0	1	0	0	0	0
F	0	0	0	1	1	0	1	0	1	0
G	0	0	1	1	0	1	0	1	1	0
H	0	0	0	0	0	0	1	0	1	1
I	0	0	0	0	0	1	1	1	0	1
J	0	0	0	0	0	0	0	1	1	0




```
A <- get.adjacency(g)
```

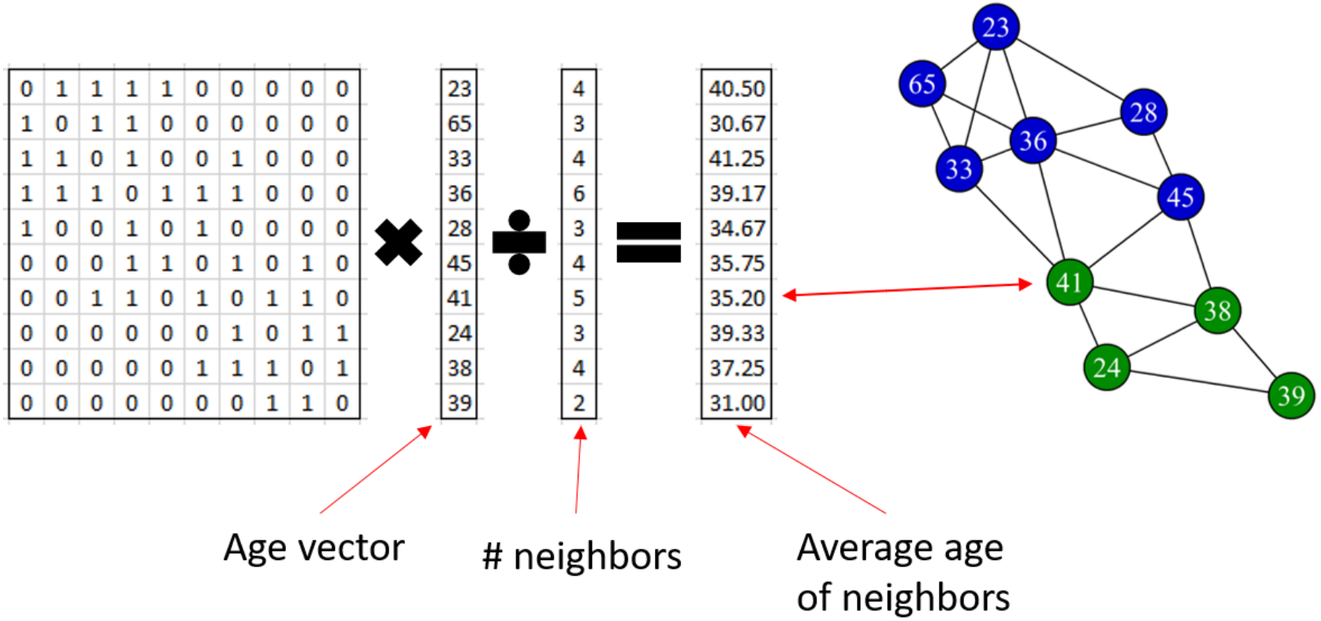
Link based features




```
preference <- c(1,1,1,1,1,1,0,0,0,0)
rNeighbors <- A %*% preference
as.vector(rNeighbors)
```

```
4 3 3 5 3 2 3 0 1 0
```

Neighborhood features




```
age <- c(23,65,33,36,28,45,41,24,38,39)
degree <- degree(g)
averageAge <- A %*% age / degree
```

Let's practice!

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

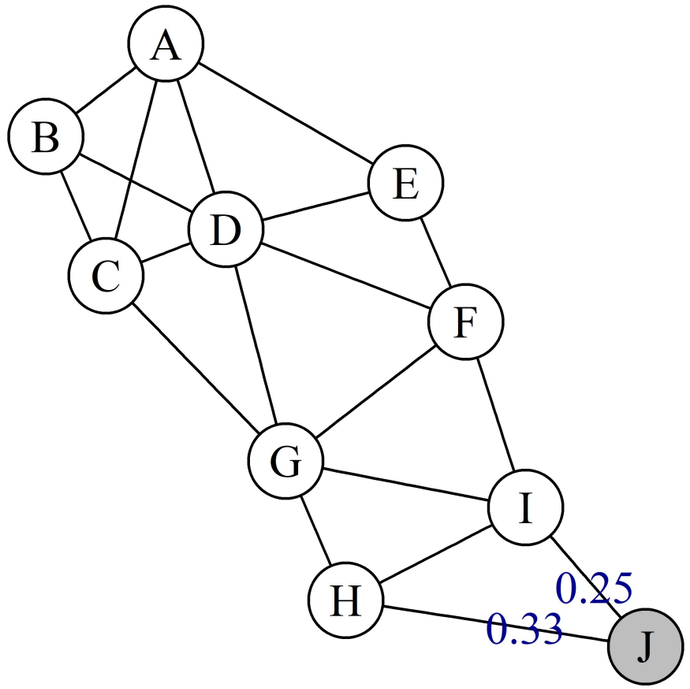
PageRank

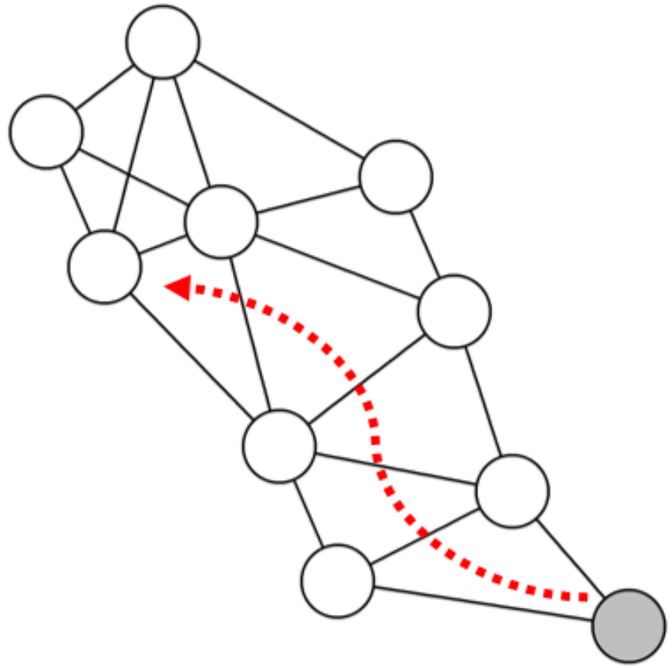
PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

María Óskarsdóttir, Ph.D.
Post-doctoral researcher

datacamp

The PageRank algorithm





$$\text{PageRank}_J = \alpha \cdot (\tfrac{1}{3} \cdot \text{PageRank}_H + \tfrac{1}{4} \cdot \text{PageRank}_I) + (1 - \alpha) \cdot e_J$$

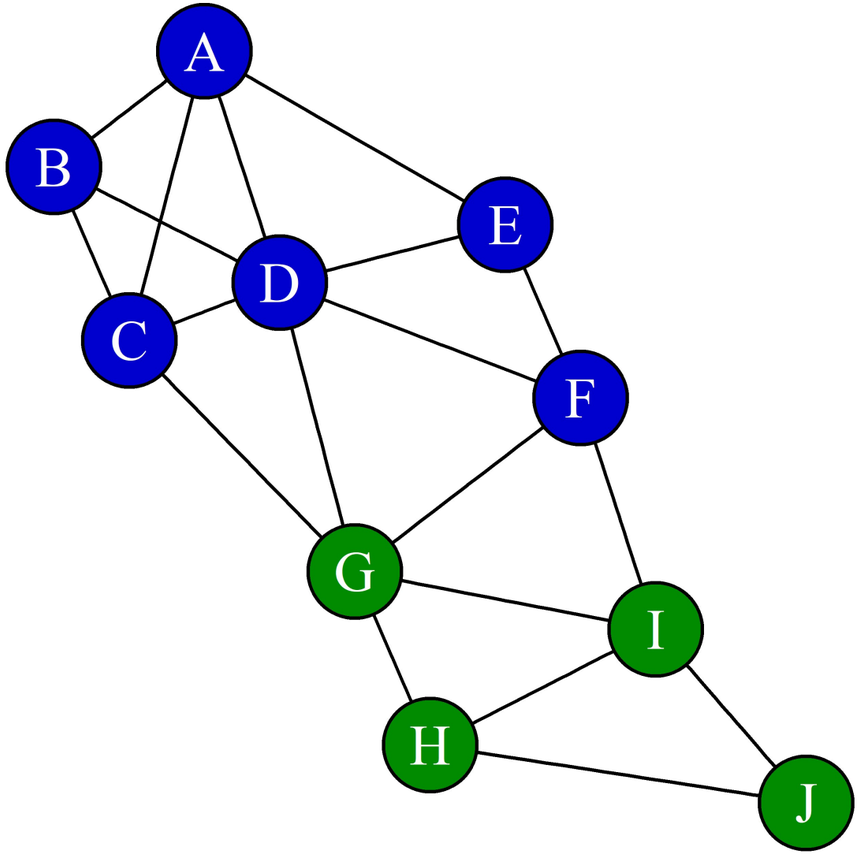
The PageRank algorithm

$$\vec{PR} = \alpha \cdot A \cdot \vec{PR} + (1 - \alpha) \cdot \vec{e}$$

```
page.rank(g)
```

```
$vector
         A          B          C          D          E          F          G
0.10238312 0.07917232 0.10164910 0.14693274 0.07953551 0.10335821 0.12732387
         H          I          J
0.08675903 0.10994175 0.06294435

$value
[1] 1

$options
NULL
```

Personalized PageRank




```
page.rank(g,
 personalized = c(1,0,0,0,0,0,0,0,0,0))
```

```
$vector
         A          B          C          D          E
0.25528911 0.10363533 0.12156935 0.16625582 0.09366836
         F          G          H          I          J
0.07466596 0.08473039 0.03285162 0.04785657 0.01947748

$value
[1] 1

$options
NULL
```

Let's practice!

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Extract a dataset

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

María Óskarsdóttir, Ph.D.
Post-doctoral researcher

datacamp

```
V(g)$degree<-degree(g)
V(g)$triangles<-count_triangles(g)
V(g)$betweeness<-betweenness(g,normalized=TRUE)
V(g)$transitivity<-transitivity(g,type='local',isolates='zero')
A <- get.adjacency(g)
preference <- c(1,1,1,1,1,1,0,0,0,0)
age <- c(23,65,33,36,28,45,41,24,38,39)
V(g)$rNeighbors <- as.vector(A%*%preference)
V(g)$averageAge <- as.vector(A%*%age/V(g)$degree)
V(g)$pageRank<-page.rank(g)$vector
V(g)$personalizePageRank<-page.rank(g,
  personalized = c(1,0,0,0,0,0,0,0,0,0))$vector
g
```

```
IGRAPH UN-- 10 19 --
 attr: name (v/c), degree (v/n), triangles (v/n), transitivity
| (v/n), rNeighbors (v/n), averageAge (v/n), pageRank (v/n),
| pPageRank (v/n), label (e/c)
 edges (vertex names):
 A--B A--C A--D A--E B--C B--D C--D C--G D--E D--F D--G E--F F--G F--I G--I G--H H--I H--J I--J
```

```
IGRAPH UN-- 10 19 --
 attr: name (v/c), degree (v/n), triangles (v/n), transitivity
| (v/n), rNeighbors (v/n), averageAge (v/n), pageRank (v/n),
| pPageRank (v/n), label (e/c)
 edges (vertex names):
 [1] A--B A--C A--D A--E B--C B--D C--D C--G D--E D--F D--G E--F F--G F--I G--I G--H H--I H--J I--J
```

```
as_data_frame(g,what='vertices')
```

```
  name degree triangles transitivity rNeighbors averageAge   pageRank  pPageRank
A    A      4         4    0.6666667          4   40.50000 0.10238312 0.25528911
B    B      3         3    1.0000000          3   30.66667 0.07917232 0.10363533
C    C      4         4    0.6666667          3   41.25000 0.10164910 0.12156935
D    D      6         7    0.4666667          5   39.16667 0.14693274 0.16625582
E    E      3         2    0.6666667          3   34.66667 0.07953551 0.09366836
F    F      4         3    0.5000000          2   35.75000 0.10335821 0.07466596
G    G      5         4    0.4000000          3   35.20000 0.12732387 0.08473039
H    H      3         2    0.6666667          0   39.33333 0.08675903 0.03285162
I    I      4         3    0.5000000          1   37.25000 0.10994175 0.04785657
J    J      2         1    1.0000000          0   31.00000 0.06294435 0.01947748
```

Preprocessing - missing values

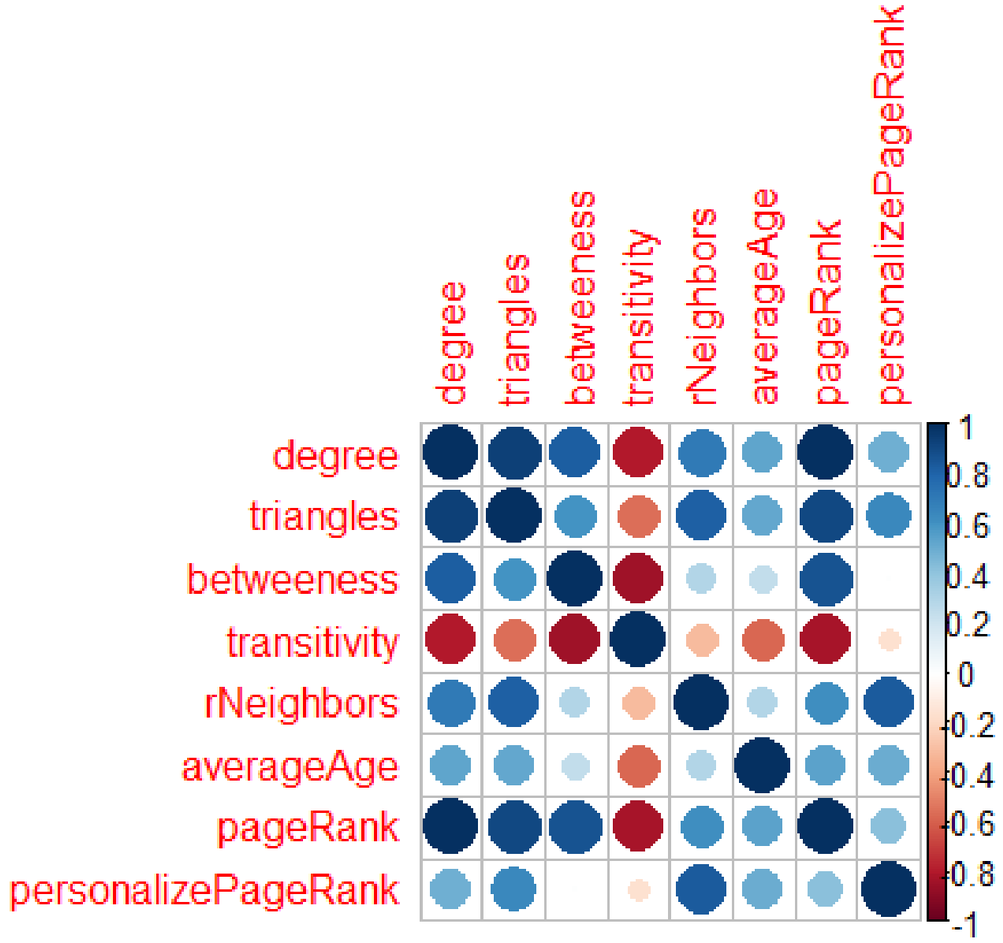
name	degree	triangles	transitivity	rNeighbors	averageAge	pageRank	pPageRank
A	4	4	0.6666667	4	40.50000	0.10238312	0.25528911
B	3	3	1.0000000	3	30.66667	0.07917232	0.10363533
C	NA	4	0.6666667	3	41.25000	0.10164910	0.12156935
D	6	7	0.4666667	5	39.16667	0.14693274	0.16625582
E	3	2	0.6666667	3	34.66667	0.07953551	0.09366836
F	4	3	0.5000000	2	35.75000	0.10335821	0.07466596
G	5	4	0.4000000	3	35.20000	0.12732387	0.08473039
H	3	2	0.6666667	0	39.33333	0.08675903	0.03285162
I	NA	3	0.5000000	1	37.25000	0.10994175	0.04785657
J	2	1	1.0000000	0	31.00000	0.06294435	0.01947748

```
sum(is.na(dataset$degree))
```

```
2
```

Preprocessing - correlated variables

```
library(corrplot)

M <- cor(dataset[,-1])

corrplot(M, method = 'circle')
```



Let's practice!

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

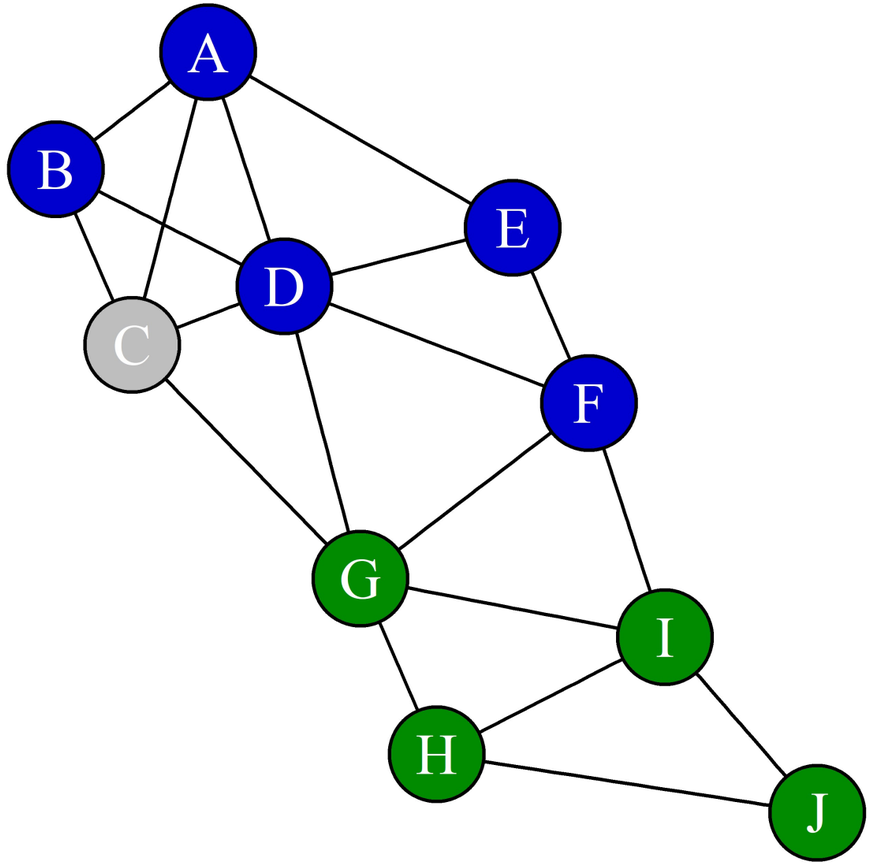
Building a predictive model

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

María Óskarsdóttir, Ph.D.
Post-doctoral researcher

datacamp

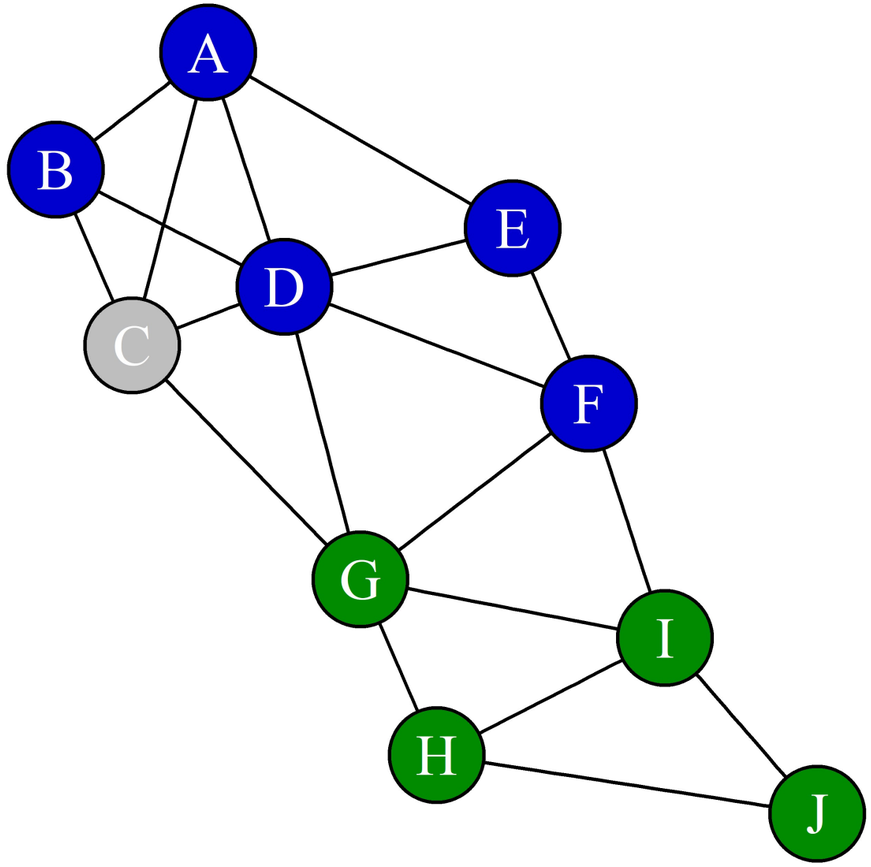
Predictive modeling




```
dataset$preference<-c(rep('R',2),'?',
rep('R',3),rep('P',4))
dataset[,c(1,9)]
```

```
  name preference
A    A          R
B    B          R
C    C          ?
D    D          R
E    E          R
F    F          R
G    G          P
H    H          P
I    I          P
J    J          P
```

Predictive modeling

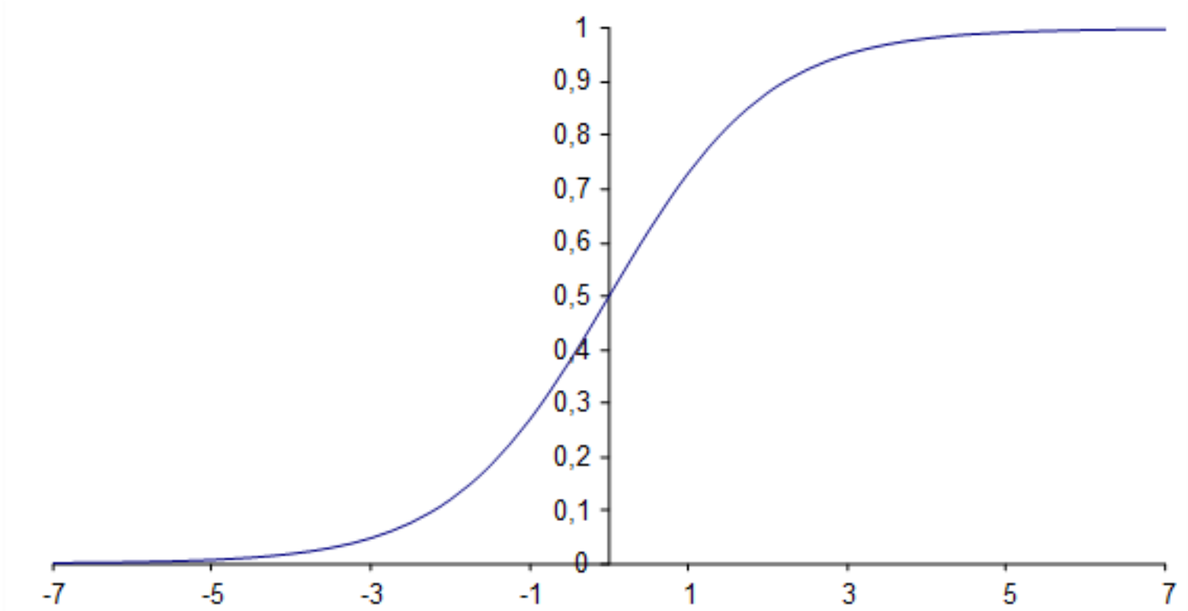



```
dataset$R<-c(1,1,'?',1,1,1,0,0,0,0)
dataset[,c(1,9,10)]
```

```
  name preference R
A    A          R 1
B    B          R 1
C    C          ? ?
D    D          R 1
E    E          R 1
F    F          R 1
G    G          P 0
H    H          P 0
I    I          P 0
J    J          P 0
```

```
training_set<-dataset[-3,-9]
test_set<-dataset[3,-9]
```

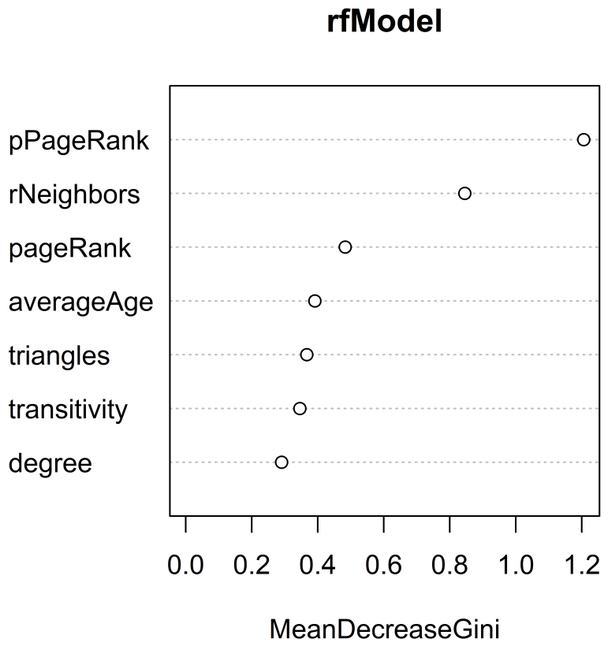
Logistic regression




```
glm(R~degree+pageRank, dataset=training_set,family='binomial')
glm(R~., dataset=training_set,family='binomial')
```

Random forests

```
library(randomForest)
rfModel<-randomForest(R~., dataset=training_set)
varImpPlot(rfModel)
```



Let's practice!

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Evaluating model performance

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

María Óskarsdóttir, Ph.D.
Post-doctoral researcher

datacamp

Making predictions

```
library(pROC)
```

- Logistic regression

```
logPredictions <- predict(logModel, newdata = test_set, type = "response")
```

- Random forest

```
rfPredictions<- predict(rfModel, newdata = test_set, type='prob')
rfPredictions
attr(,"class")
```

```
      0     1
C 0.136 0.864
"matrix" "votes"
```

AUC

- Probability that a randomly chosen churner gets a higher score than a randomly chosen non-churner
- Displays the trade-off between the model's sensitivity and specificity
- A number between:
  - **0.5**: random model
  - **1**: perfect model

```
library(pROC)
auc(test_set$label, logPredictions)
```

Top decile lift

- How much better is the prediction model at identifying churners, compared to a random sample of customers
- Computes the proportion of actual churners amongst the 10% of customers with the highest predicted churn probability
- Lift value greater than 1 means that the model is better than a random model
- If, in the top 10% of the highest scores there are **60%** churners and in the whole population there are **10%** churners, then the lift is $60/10 = 6$

```
library(lift)
TopDecileLift(test_set$label, predictions, plot=TRUE)
```

Let's practice!

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Summary and final thoughts

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Bart Baesens, Ph.D.

Professor of Data Science, KU Leuven and University of Southampton

datacamp

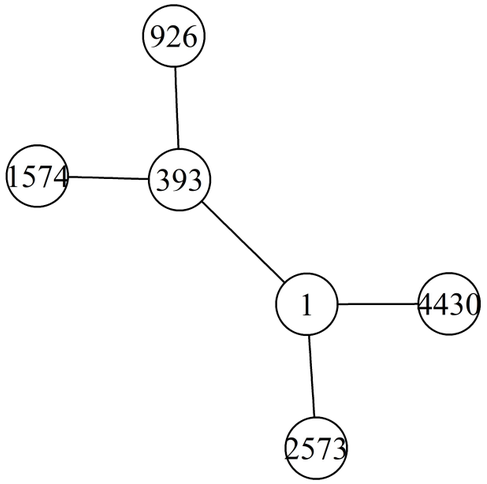
Labeled networks

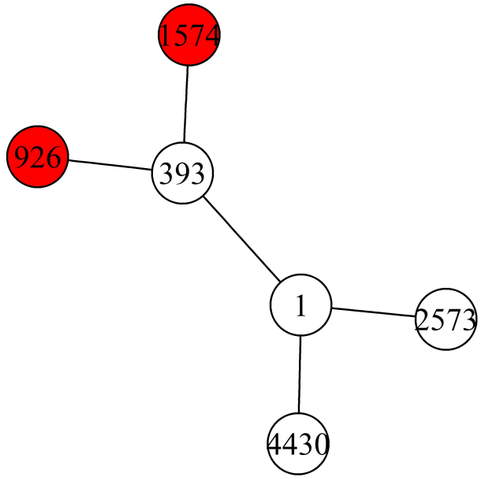
`edgeList`

```
  from    to
1    1   393
2    1  2573
3    1  4430
4  393   926
5  393  1574
```

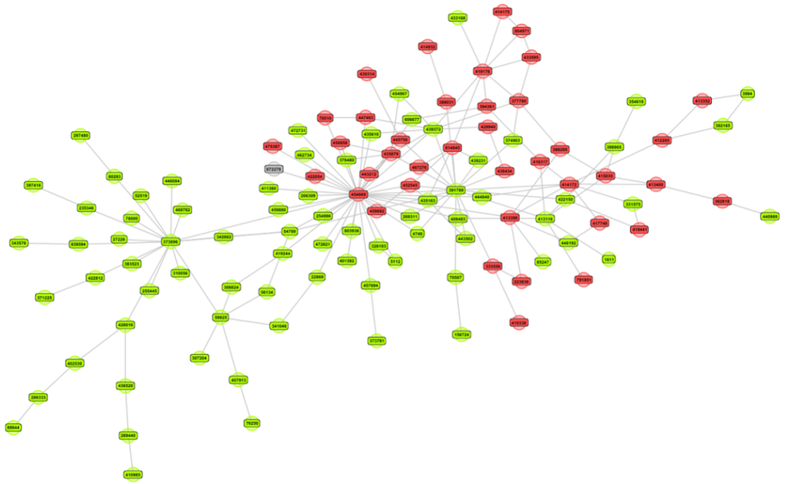
`customers`

```
    id churn
1    1     0
2  393     0
3 2573     0
4 4430     0
5  926     1
6 1574     1
```





Homophily



> Birds of a feather flock together

Dyadicity: connectedness between nodes with same label

Heterophilicty: connectedness between nodes with opposite labels

Network Featurization

```
g
IGRAPH UN-- 10 19 --
 attr: name (v/c), label (e/c)
 edges (vertex names):
 A--B A--C A--D A--E B--C B--D C--D C--G D--E D--F D--G E--F F--G F--I G--I G--H H--I H--J I--J
```

```
V(g)$degree<-degree(g)
```

```
g
IGRAPH UN-- 10 19 --
 attr: name (v/c), degree (v/n), triangles (v/n), transitivity
| (v/n), rNeighbors (v/n), averageAge (v/n), pageRank (v/n),
| pPageRank (v/n), label (e/c)
 edges (vertex names):
 A--B A--C A--D A--E B--C B--D C--D C--G D--E D--F D--G E--F F--G F--I G--I G--H H--I H--J I--J
```

1. Extract dataframe:

```
dataset <- as_data_frame(g, what='vertices')
```

2. Preprocess data set:
   - Missing values, outliers, correlated variables, and normalization
3. Build model:

```
glm(R~., dataset=training_set, family='binomial')
```

4. Make predictions:

```
logPredictions <- predict(logModel, newdata=test_set, type="response")
```

5. Measure performance:

```
auc(test_set$label, logPredictions)
TopDecileLift(test_set$label, predictions, plot=TRUE)
```

Congratulations!

PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Exploring your data set

CASE STUDIES: NETWORK ANALYSIS IN R

Edmund Hart
Instructor

datacamp

```
library(igraph)
library(dplyr)
amzn_raw <- read.csv("datasets/amazon_purchase_no_book.csv")
head(amzn_raw)
```

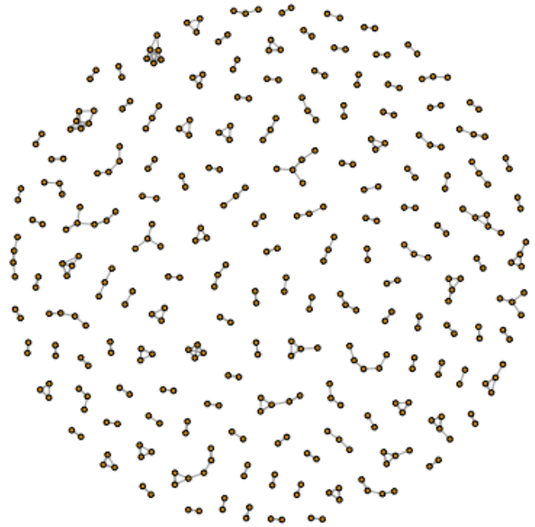
```
    from to                     title.from group.from categories.from salesrank.from
1 1   44 42   The NBA's 100 Greatest Plays        DVD           33124              5
2 2  179 71 Africa Screams/Jack & The Bean        DVD           53825             21

  totalreviews.from totalreviews.1.from
1                13                  13
2                13                  13

                                    title.to group.to
1                                     Pixote      DVD
2 Jonny Quest - Bandit in Adventures Best Friend    Video

  categories.to salesrank.to totalreviews.to totalreviews.1.to       date
1         19685           15              24                24 2003-03-02
2         21571            5               2                 2 2003-03-02
```

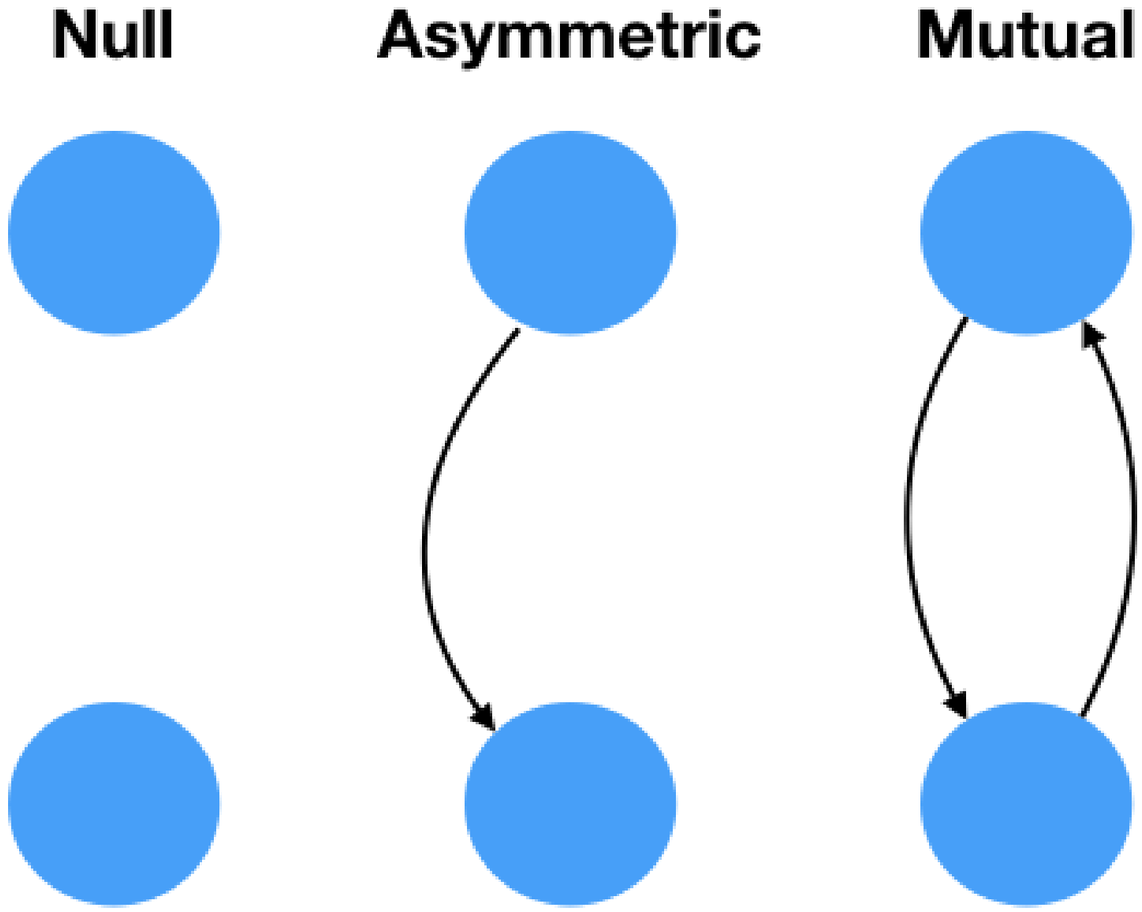
Creating the graph

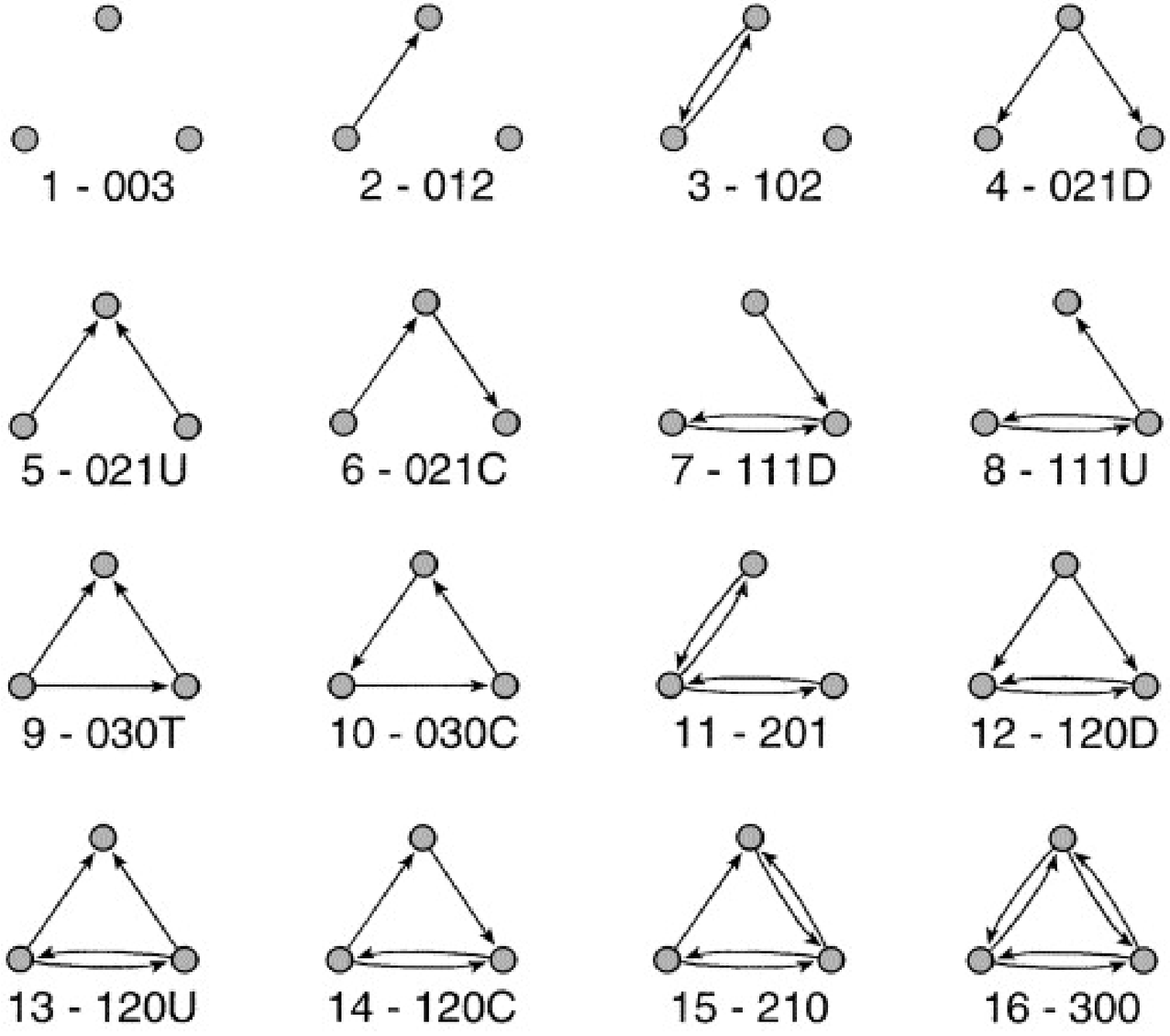
```
amzn_g <- amzn_raw %>%
  filter(date == "2003-03-02") %>%
  select(from, to) %>%
  graph_from_data_frame(directed = TRUE)
gorder(amzn_g)
gsize(amzn_g)
```

Visualize the graph

```
sg <- induced_subgraph(amzn_g, 1:500)
sg <- delete.vertices(sg, degree(sg) == 0)
plot(sg, vertex.label = NA, edge.arrow.width = 0,
  edge.arrow.size = 0, margin = 0, vertex.size = 2)
```




Null
Asymmetric
Mutual


1 - 003
2 - 012
3 - 102
4 - 021D
5 - 021U
6 - 021C
7 - 111D
8 - 111U
9 - 030T
10 - 030C
11 - 201
12 - 120D
13 - 120U
14 - 120C
15 - 210
16 - 300

Let's practice

CASE STUDIES: NETWORK ANALYSIS IN R

Exploring temporal structure

CASE STUDIES: NETWORK ANALYSIS IN R

Edmund Hart
Instructor

datacamp

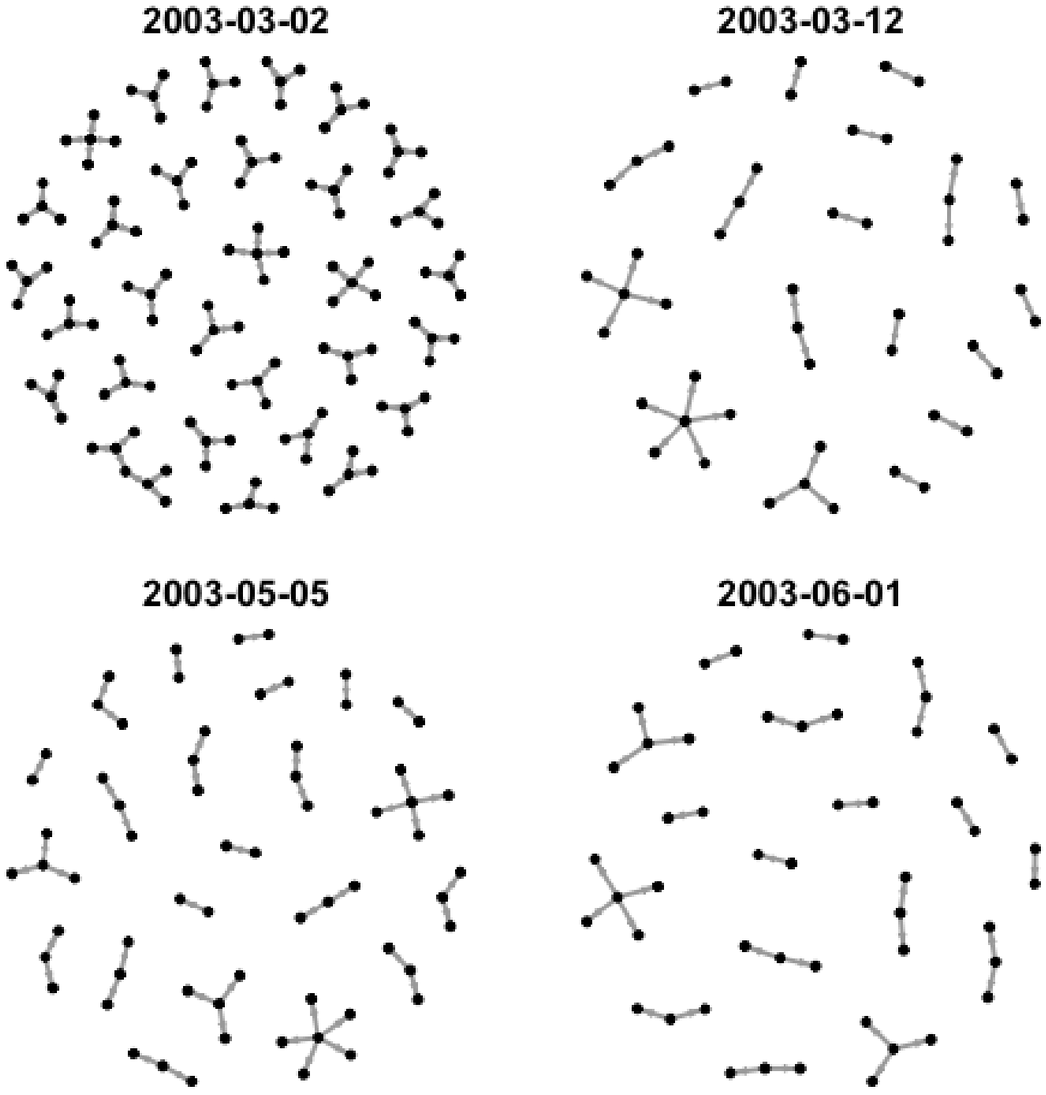
Are important products always important?

```
# Get unique Dates
d <- sort(unique(amzn_raw$date))
# Create graph from first date
amzn_g <- graph_from_data_frame(
  amzn_raw %>%
  filter(date == d[1]) %>%
  select(from, to), directed = TRUE
)
```

Are important products always important?

```
# Find products that are "important"
high_out_degree <- degree(amzn_g, mode = "out") > 2

low_in_degree <- degree(amzn_g, mode = "in") < 1

important_nodes <- high_out_degree & low_in_degree

imp_prod <- V(amzn_g)[importnant_nodes]

# Store as a data frame to later join on
tmp_df <- data.frame(imp_prod = as.numeric(names(imp_prod)))
```

```
## Create list to hold output
time_graph <- list()
## Create a 2x2 layout for plots and increase margins
par(mfrow = c(2, 2), mar = c(1.1, 1.1, 1.1, 1.1))
## Loop over the data to build
for(i in 1:length(d)){
  ## Create a data frame at each time stamp
  ip_df <- amzn_raw %>%
    filter(date == d[i]) %>%
    right_join(tmp_df, by = c("from" = "imp_prod")) %>%
    na.omit()
  ## Create an igraph object from that data frame
  time_graph[[i]] <- ip_df %>%
    select(from, to) %>%
    graph_from_data_frame(directed = TRUE)
  ## See what important vertices look like by date
  plot(time_graph[[i]], main = d[i])   }
```


2003-03-02
2003-03-12
2003-05-05
2003-06-01

Let's practice!

CASE STUDIES: NETWORK ANALYSIS IN R

Building a graph from raw data

CASE STUDIES: NETWORK ANALYSIS IN R

Edmund Hart
Instructor

datacamp

Exploring the data

- Data is several days of all the tweets mentioning #rstats
- Key attributes for building a graph are:
  - screen name
  - raw text of the tweet

Anatomy of a tweet

1. *ReecheshJC*: "Hey #rstats, how do I do fct_lump but where I lump based on count values in a column?"
2. *kom_256*: "RT @elenagbg: Retweeted R-Ladies Madrid (@RLadiesMAD):\n\nEn el #OCSummit17... Fast Talks sobre #rstats organizado por... **https://t.co/CKY5aG..."**

```
library(igraph)
library(stringr)
raw_tweets <- read.csv("datasets/rstatstweets.csv",
  stringsAsFactors = FALSE)
```

Data sample, single row

```
user_name:    Karen Millidine
screen_name:    KJMillidine
tweet_tex:t    RT @Rbloggers: RStudio v1.1 Released
https://t.co/kCMHc689nY #rstats #DataScience
favorites:    0
retweets:    96
location:    None
expanded_url:    https://wp.me/pMm6L-ExV
in_reply_to_tweet_id:    NA
in_reply_to_user_id:    NA
dt:    10/10/17
```

Building the graph

```
## Get all the screen names
all_sn <- unique(raw_tweets$screen_name)

## Create graph
retweet_graph <- graph.empty()

## Add screen names as vertices
retweet_graph <- retweet_graph + vertices(all_sn)
```

Building the graph

```
## Extract name and add edges
for(i in 1:dim(raw_tweets)[1]){
  # Extract retweet name
  rt_name <- find_rt(raw_tweets$tweet_text[i])
  # If there is a name add an edge
   if(!is.null(rt_name)){
      # Check to make sure the vertex exists, if not, add it
      if(!rt_name %in% all_sn){
        retweet_graph <- retweet_graph + vertices(rt_name)
      }
     # add the edge
     retweet_graph <- retweet_graph +
       edges(c(raw_tweets$screen_name[i], rt_name))
   }
}
```

Cleaning the graph

```
## Size the number of degree 0 vertices
sum(degree(retweet_graph) == 0)

## Trim and simplify
retweet_graph <- simplify(retweet_graph)
retweet_graph <- delete.vertices(retweet_graph,
  degree(retweet_graph) == 0)
```

Let's practice!

CASE STUDIES: NETWORK ANALYSIS IN R

Building a mentions graph

CASE STUDIES: NETWORK ANALYSIS IN R

Edmund Hart
Instructor

datacamp

Recall tweet anatomy

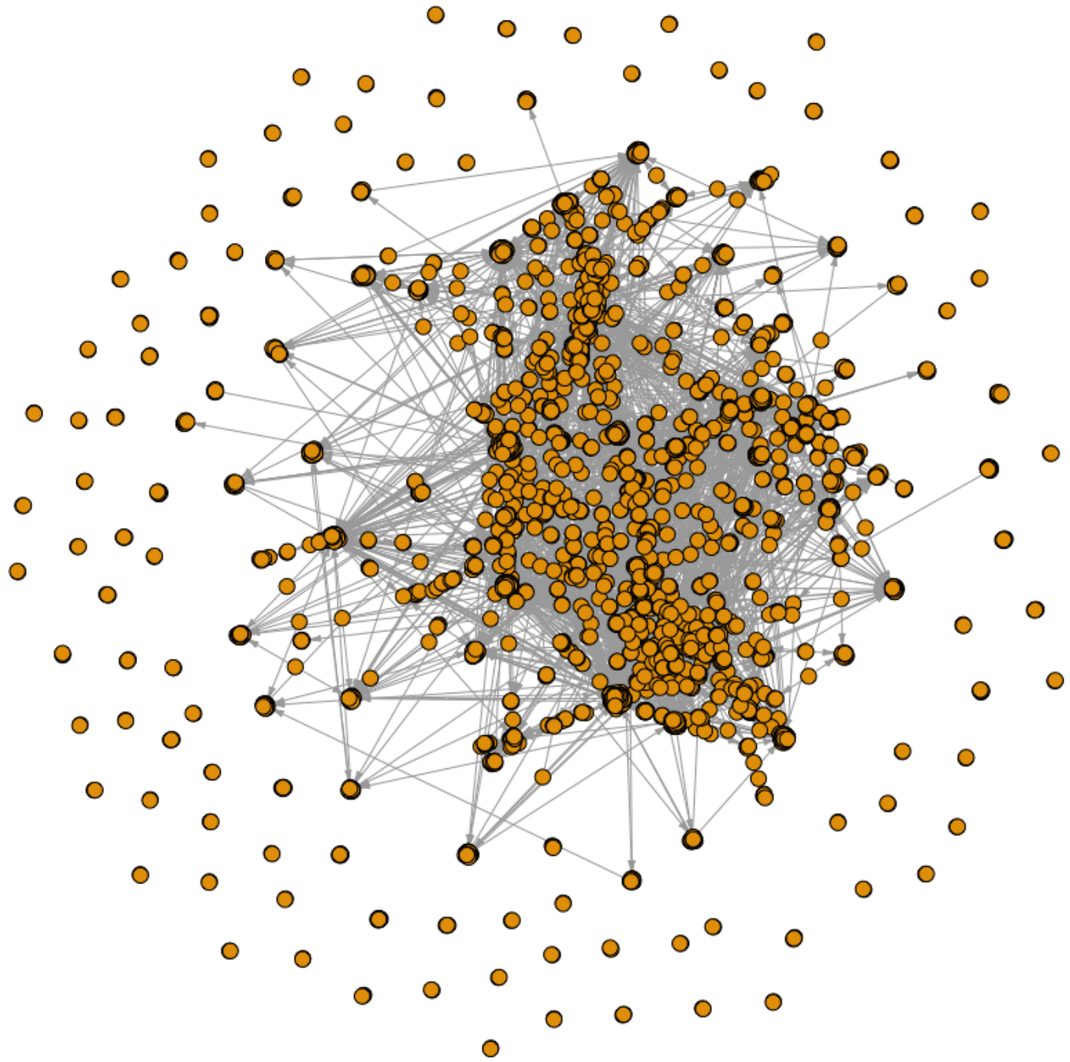
AlexisAchim: "@LAStools @Lees_Sandbox @jhollist
@LeahAWasser LidR is also available directly on CRAN #rstats"

timelyportfolio: "just might have a demo of @emeeks new
#reactjs/#d3js semiotic in #rstats in the works"

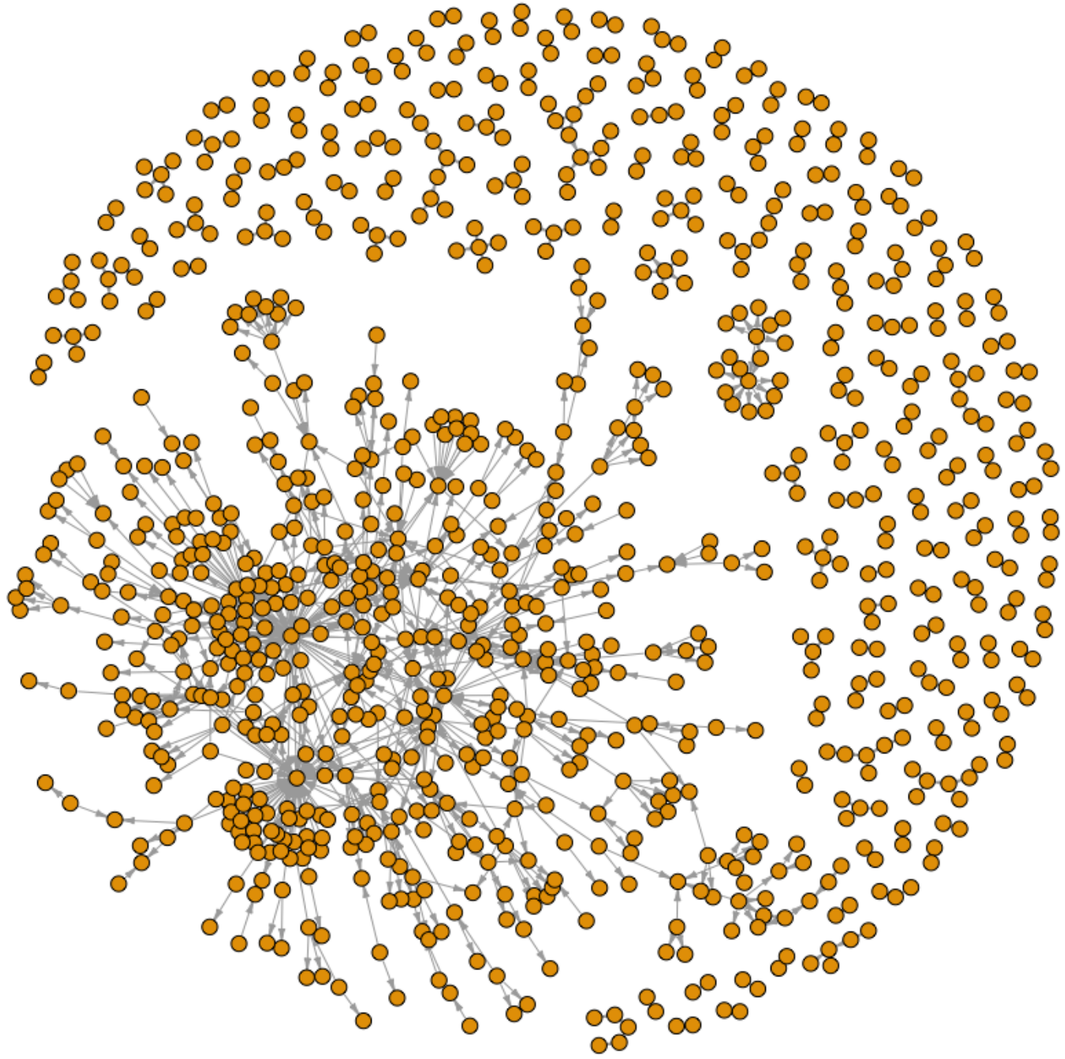
Build your mentions graph

```
ment_g <- graph.empty()
ment_g <- ment_g + vertices(all_sn)
for(i in 1:dim(raw_tweets)[1]) {
  ment_name <- mention_ext(raw_tweets$tweet_text[i])
  if(length(ment_name) > 0 ) {
    # Add the edge(s)
    for(j in ment_name) {
      # Check to make sure the vertex exists, if not, add it
      if(!j %in% all_sn) {
        ment_g <- ment_g + vertices(j)  }
      ment_g <- ment_g + edges(c(raw_tweets$screen_name[i], j))
    }
  }
}
ment_g <- simplify(ment_g)
ment_g <- delete.vertices(ment_g, degree(ment_g) == 0)
```

Retweet Graph



Mentions Graph



Let's practice!

CASE STUDIES: NETWORK ANALYSIS IN R

Finding communities

CASE STUDIES: NETWORK ANALYSIS IN R

Edmund Hart
Instructor

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Three different communities

```
undirected_ment_g <- as.undirected(ment_g)


ment_edg <- cluster_edge_betweenness(undirected_ment_g)
ment_eigen <- cluster_leading_eigen(undirected_ment_g)
ment_lp <- cluster_label_prop(undirected_ment_g)
```

Sizing the communities

```
length(ment_edg)
length(ment_eigen)
length(ment_lp)
```

```
173
168
212
```

```
table(sizes(ment_edg))
```

```
  2   3   4   5   6   7   8   9  11  12  18  19  20  23  24  26  28
103  21  14   7   3   3   1   2   1   2   2   1   1   1   1   2   1
 31  33  38  40  41  52  58
  1   1   1   1   1   1   1
```

```
table(sizes(ment_eigen))
```

```
  2   3   4   5   6   7   9  10  12  18  23  26  29  30  32  34  35  58
103  22  14   7   4   3   1   1   1   1   1   1   1   1   1   1   1   1
64  66 101
 1   1   1
```

```
table(sizes(ment_lp))
```

```
  2   3   4   5   6   7   8   9  10  11  12  13  16  25  26  67  70
103  32  22  19   8   5   4   3   5   1   2   3   1   1   1   1   1
```

Comparing communities

```
compare(ment_edg, ment_eigen, method = 'vi')
```

```
0.9761792
```

```
compare(ment_eigen, ment_lp, method = 'vi')
```

```
1.192238
```

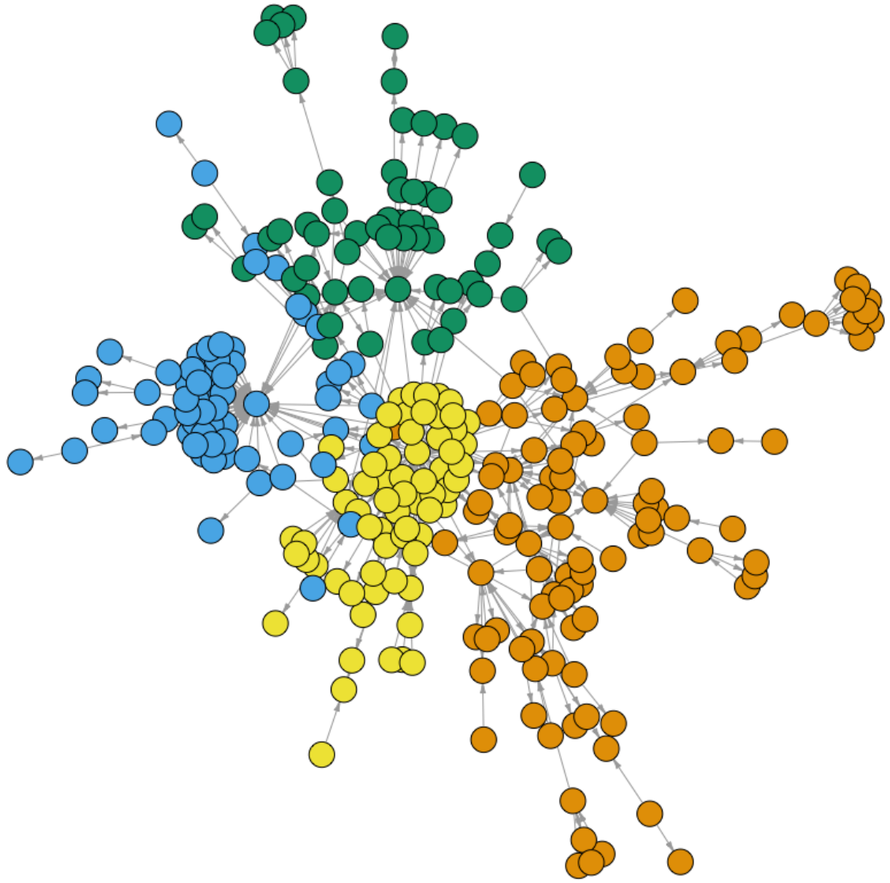
```
compare(ment_lp, ment_edg, method = 'vi')
```

```
0.9631608
```

Plotting community structure

```
lrg_eigen <- as.numeric(
                names(ment_eigen[which(sizes(ment_eigen) > 45)])
             )
eigen_sg <- induced.subgraph(ment_g,
      V(ment_g)[ eigen %in% lrg_eigen])
plot(eigen_sg, vertex.label = NA, edge.arrow.width = .8,
     edge.arrow.size = 0.2,
     coords = layout_with_fr(ment_sg), margin = 0,
     vertex.size = 6, vertex.color =
     as.numeric(as.factor(V(eigen_sg)$eigen)))
```

Mentions subgraph communities



Let's practice!

CASE STUDIES: NETWORK ANALYSIS IN R

Exploring our data

CASE STUDIES: NETWORK ANALYSIS IN R

Edmund Hart
Instructor

```r
library(igraph)
library(dplyr)
library(lubridate)
bike_dat <- read.csv("datasets/bike2_test3.csv", stringsAsFactors = FALSE)
str(bike_dat)
```

```
'data.frame':    52800 obs. of  13 variables:
 $ tripduration     : int  295 533 1570 2064 2257 296 412...
 $ from_station_id  : int  49 165 25 300 85 174 75 45 85 99 ...
 $ from_station_name: chr  "Dearborn St & Monroe St" ...
 $ to_station_id    : int  174 308 287 296 313 198 56 147 174 99 ...
 $ to_station_name  : chr  "Canal St & Madison St" ...
 $ usertype         : chr  "Subscriber" "Subscriber" "Customer"...
 $ gender           : chr  "Male" "Male" "" "" ...
 $ birthyear        : int  1964 1972 NA NA 1963 1973 1989 1965 1983 1983 ...
 $ from_latitude    : num  41.9 42 41.9 41.9 41.9 ...
 $ from_longitude   : num  -87.6 -87.7 -87.6 -87.6 -87.6 ...
 $ to_latitude      : num  41.9 41.9 41.9 41.9 41.9 ...
 $ to_longitude     : num  -87.6 -87.7 -87.6 -87.6 -87.6 ...
 $ geo_distance     : num  859 1882 2159 288 3044 ...
```

Creating the bike sharing graph

```
trip_df <- bike_dat %>%
    group_by(from_station_id, to_station_id) %>%
    summarize(weights = n())
head(trip_df)
```

```
# A tibble: 6 x 3
# Groups: from_station_id [1]
  from_station_id to_station_id weights
            <int>         <int>   <int>
1               5             5       2
2               5            14       1
3               5            16       1
4               5            25       3
5               5            29       3
6               5            33       1
```

Creating the bike sharing graph

```
trip_g <- graph_from_data_frame(trip_df[, 1:2])
# add edge weights
E(trip_g)$weight <- trip_df$weights
# Quick exploration of our graph
gsize(trip_g)
```

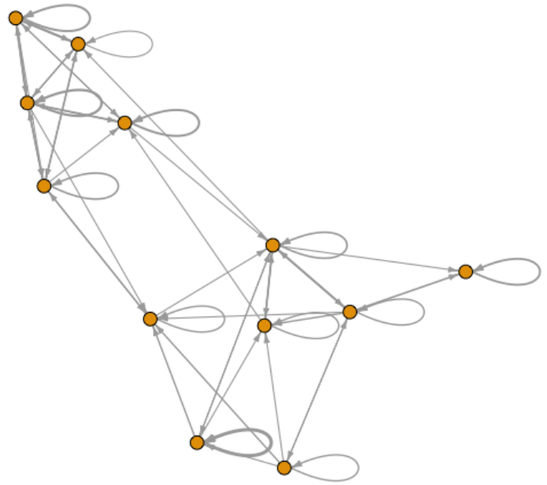
```
19052
```

```
gorder(trip_g)
```

```
300
```

Explore the graph

```
sg <- induced_subgraph(trip_g, 1:12)
plot(sg, vertex.label = NA, edge.arrow.width = 0.8,
     edge.arrow.size = 0.6,
      margin = 0,
     vertex.size = 6,
     edge.width = log(E(sg)$weight + 2))
```



Let's practice!

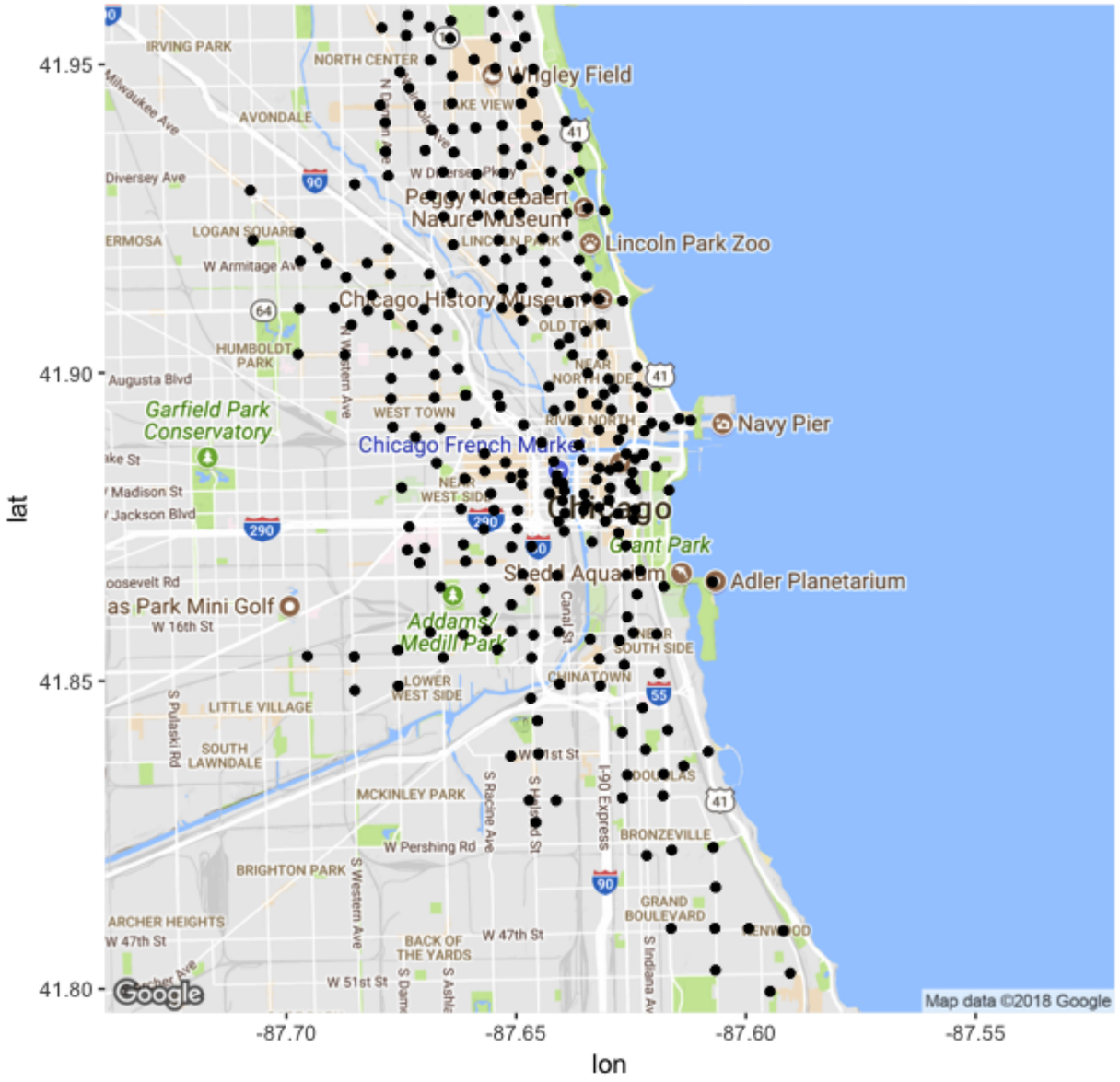
CASE STUDIES: NETWORK ANALYSIS IN R

Compare graph distance vs. geographic distance

CASE STUDIES: NETWORK ANALYSIS IN R

Edmund Hart
Instructor

datacamp


41.95
41.90
41.85
41.80
lat
-87.70
-87.65
-87.60
-87.55
lon
Wrigley Field
Peggy Notebaert Nature Museum
Lincoln Park Zoo
Chicago History Museum
Navy Pier
Chicago French Market
Garfield Park Conservatory
Grant Park
Shedd Aquarium
Adler Planetarium
Addams/Medill Park
Map data ©2018 Google

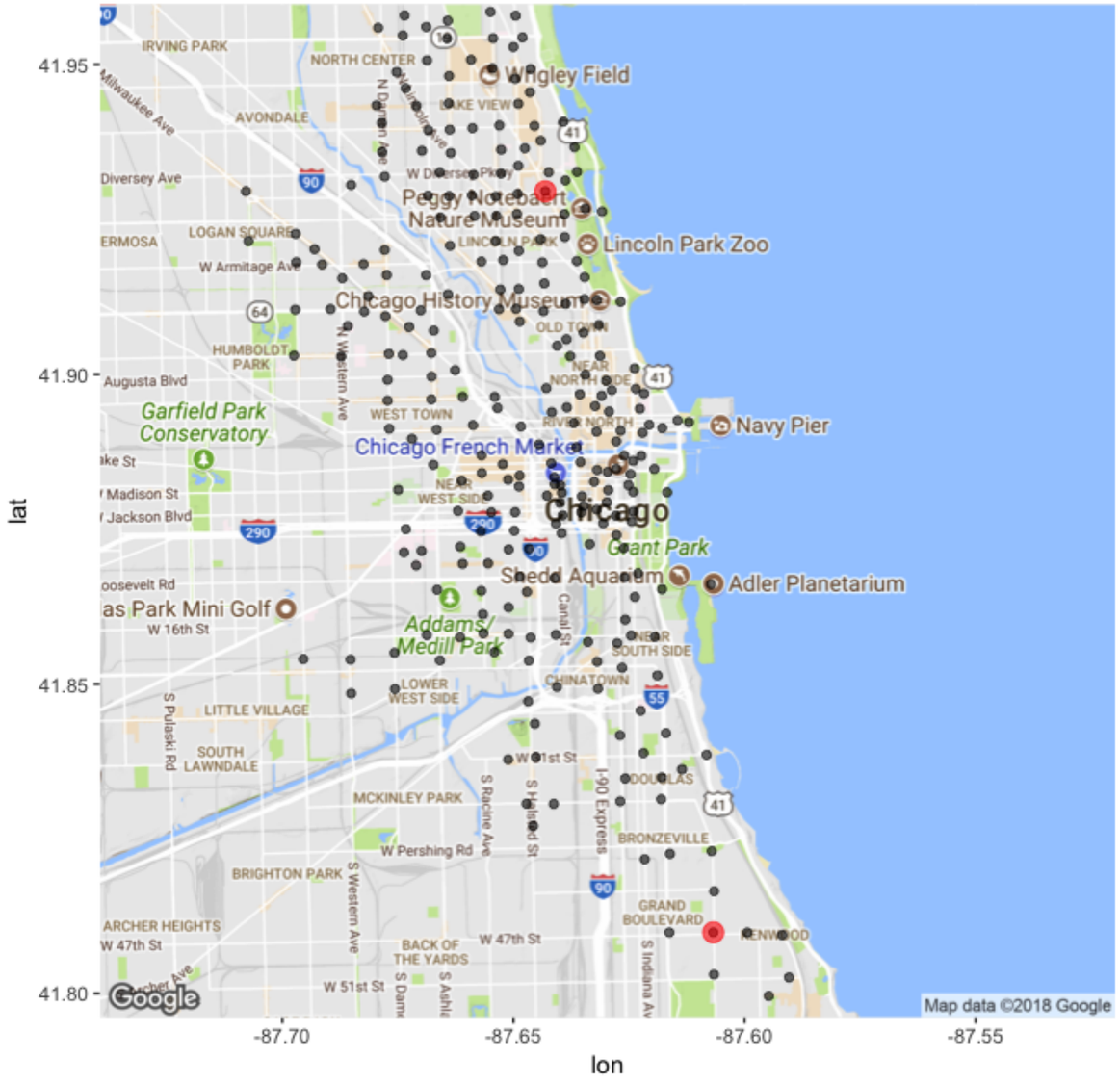
Graph distance

```
farthest_vertices(trip_g_simp)
```

```
$vertices
+ 2/300 vertices, named, from 20dcfff:
[1] 336 340

$distance
[1] 5
```

```
get_diameter(trip_g_simp)
```

```
+ 4/300 vertices, named, from 20dcfff:
[1] 336 267 76  340
```


41.95
41.90
41.85
41.80
lat
-87.70
-87.65
-87.60
-87.55
lon
Wrigley Field
Peggy Notebaert Nature Museum
Lincoln Park Zoo
Chicago History Museum
Navy Pier
Chicago French Market
Chicago
Grant Park
Shedd Aquarium
Adler Planetarium
Garfield Park Conservatory
Addams/ Medill Park
Map data ©2018 Google

Geographic distance

```
library(geosphere)
# Get the to stations coordinates
st_to <- bike_dat %>%
            filter(from_station_id == 336) %>%
            sample_n(1) %>%
            select(from_longitude, from_latitude)
# Get the from stations coordinates
st_from <- bike_dat %>%
            filter(from_station_id == 340) %>%
            sample_n(1) %>%
            select(from_longitude, from_latitude)
# find the geographic distance
farthest_dist <- distm(st_from, st_to, fun = distHaversine)
farthest_dist
```

```
[1, ] 13660.66
```

Geographic distance

```
bike_dist <- function(station_1, station_2, divy_bike_df){
    st1 <- divy_bike_df %>%
                filter(from_station_id == station_1) %>%
                sample_n(1) %>%
                select(from_longitude, from_latitude)
    st2 <- divy_bike_df %>%
                filter(from_station_id == station_2) %>%
                sample_n(1) %>%
                select(from_longitude, from_latitude)

    farthest_dist <- distm(st1, st2, fun = distHaversine)
    return(farthest_dist)
}
```

Let's practice!

CASE STUDIES: NETWORK ANALYSIS IN R

Connectivity

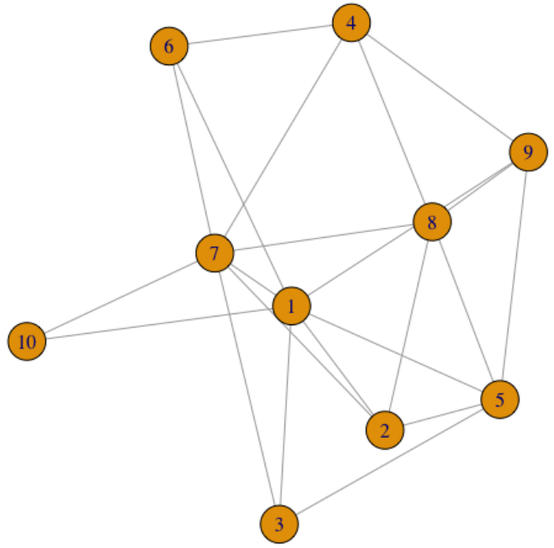
CASE STUDIES: NETWORK ANALYSIS IN R

Edmund Hart
Instructor

datacamp

Measuring connectivity

```
rand_g <- erdos.renyi.game(10, 0.4, "gnp", directed = FALSE)
plot(rand_g)
```



Measuring connectivity

```
rand_g <- erdos.renyi.game(10, 0.4, "gnp", directed = FALSE)
vertex_connectivity(rand_g)
```

```
2
```

```
edge_connectivity(rand_g)
```

```
2
```

Minimum number of cuts

```
min_cut(rand_g, value.only = FALSE)
```

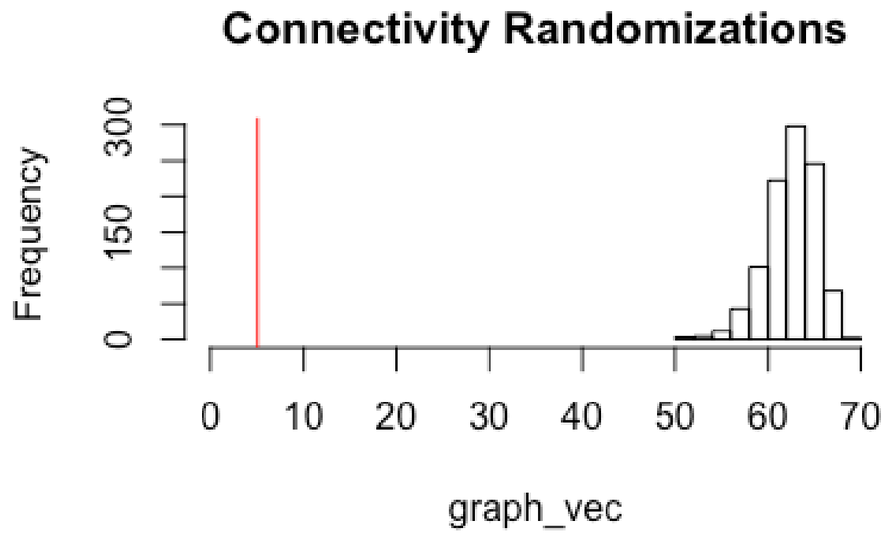
```
$value
[1] 2

$cut
+ 2/18 edges from 17a8fad:
[1] 10--7 10--1

$partition1
+ 1/10 vertex, from 17a8fad:
[1] 10

$partition2
+ 9/10 vertices, from 17a8fad:
[1]  1 2 3  4  5  6  7  8  9
```

Connectivity randomizations

```
# Get parameters to simulate graph
nv <- gorder(trip_g_ud)
ed <- edge_density(trip_g_ud)

# Empty vector to store output
graph_vec <- rep(NA, 1000)
# Generate 1000 random graphs and find the edge connectivity
for(i in 1:1000) {
  w1 <- erdos.renyi.game(nv, ed, "gnp", directed = TRUE)
  graph_vec[i] <- edge_connectivity(w1)
}
```

Connectivity randomizations

```
# Find actual connectivity
econn <- edge_connectivity(trip_g_ud)
hist(graph_vec, xlim = c(0, 140))
abline(v = edge_connectivity(trip_g_ud))
```



Let's practice!

CASE STUDIES: NETWORK ANALYSIS IN R

Other packages for plotting graphs

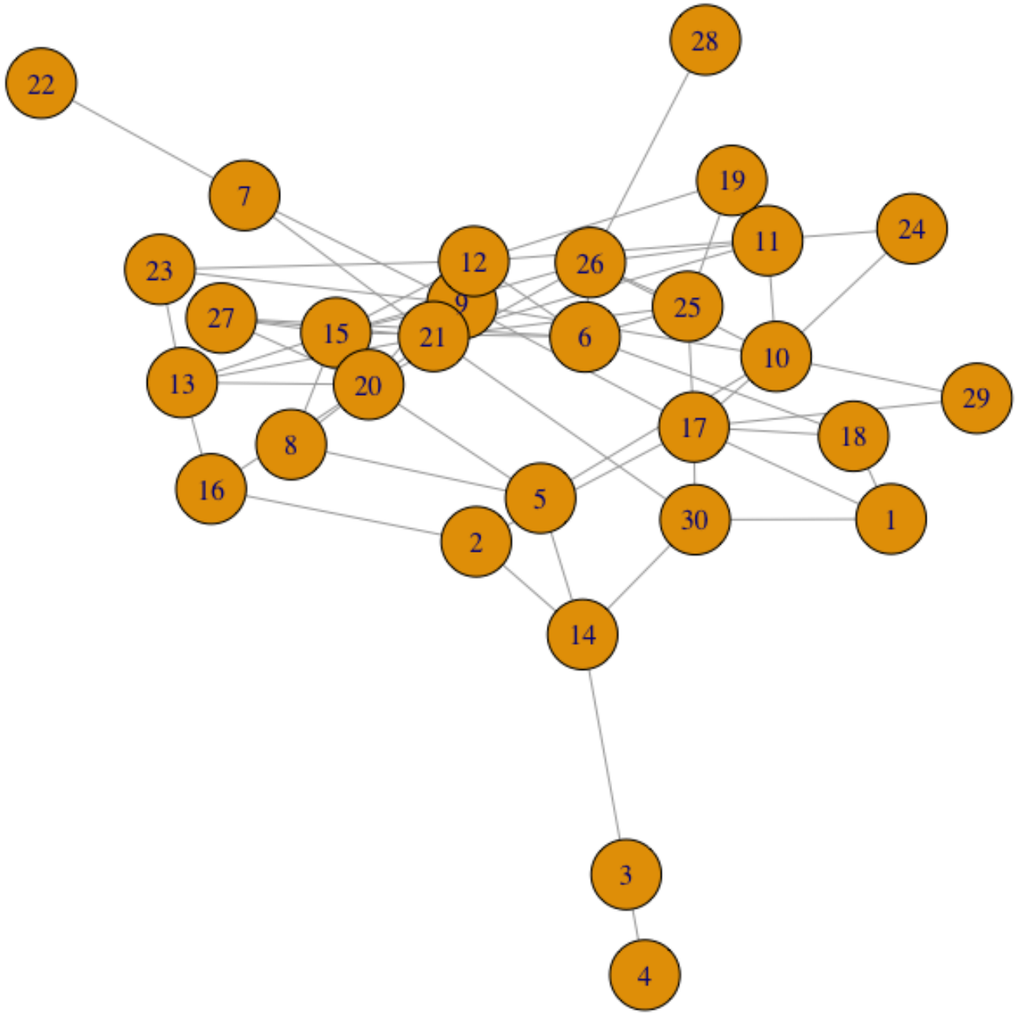
CASE STUDIES: NETWORK ANALYSIS IN R

Edmund Hart
Instructor

datacamp

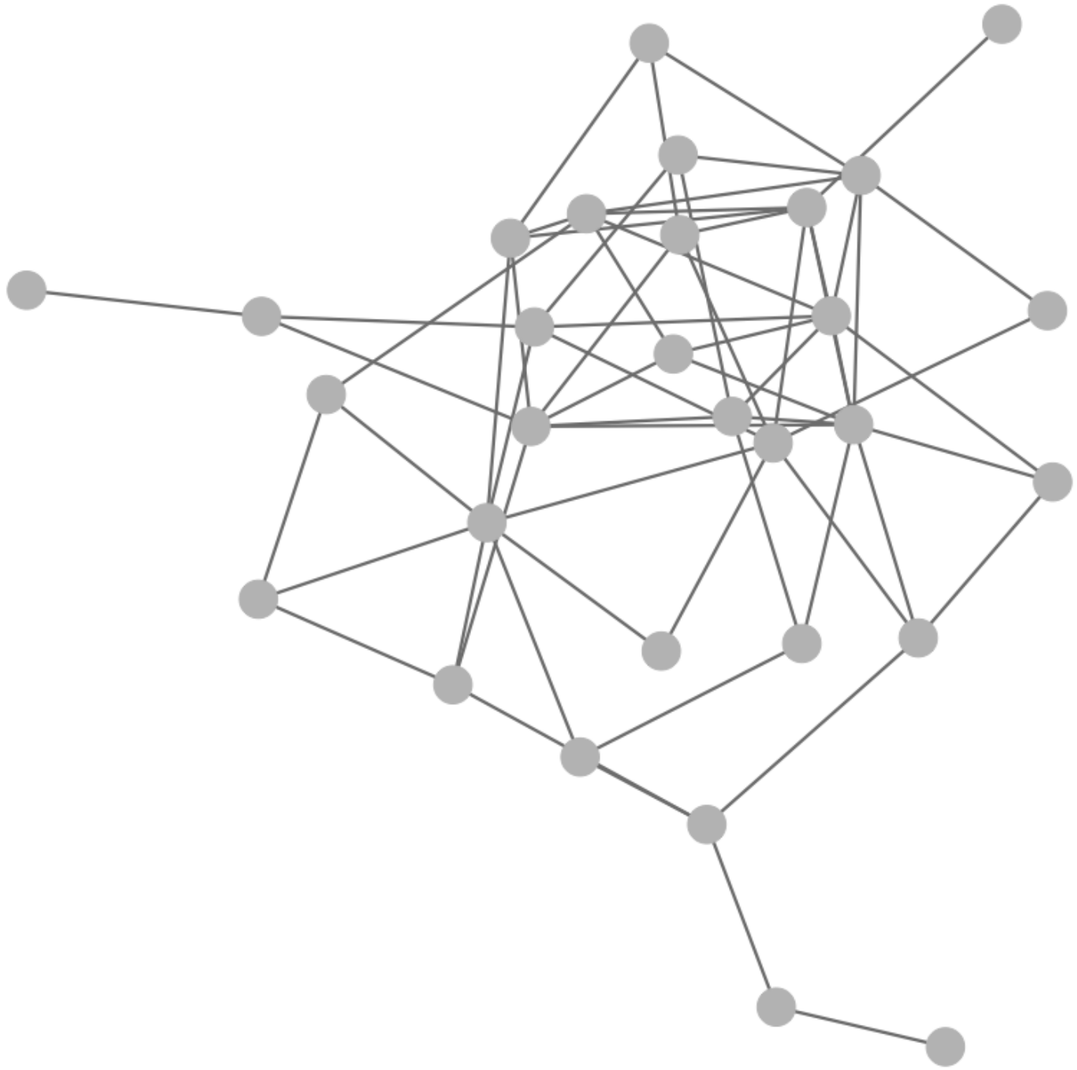
Generating data to plot

```
library(ggnetwork)
library(igraph)
library(GGally)
library(intergraph)

rand_g <- erdos.renyi.game(30, .15, "gnp", directed = F)
rand_g <- simplify(rand_g)

plot(rand_g)
```


28
22
7
19
24
11
23
12
26
9
25
27
15
21
6
10
13
20
29
17
18
8
16
5
30
1
2
14
3
4

Basic ggnet2

```
net <- asNetwork(rand_g)
ggnet2(net)
```

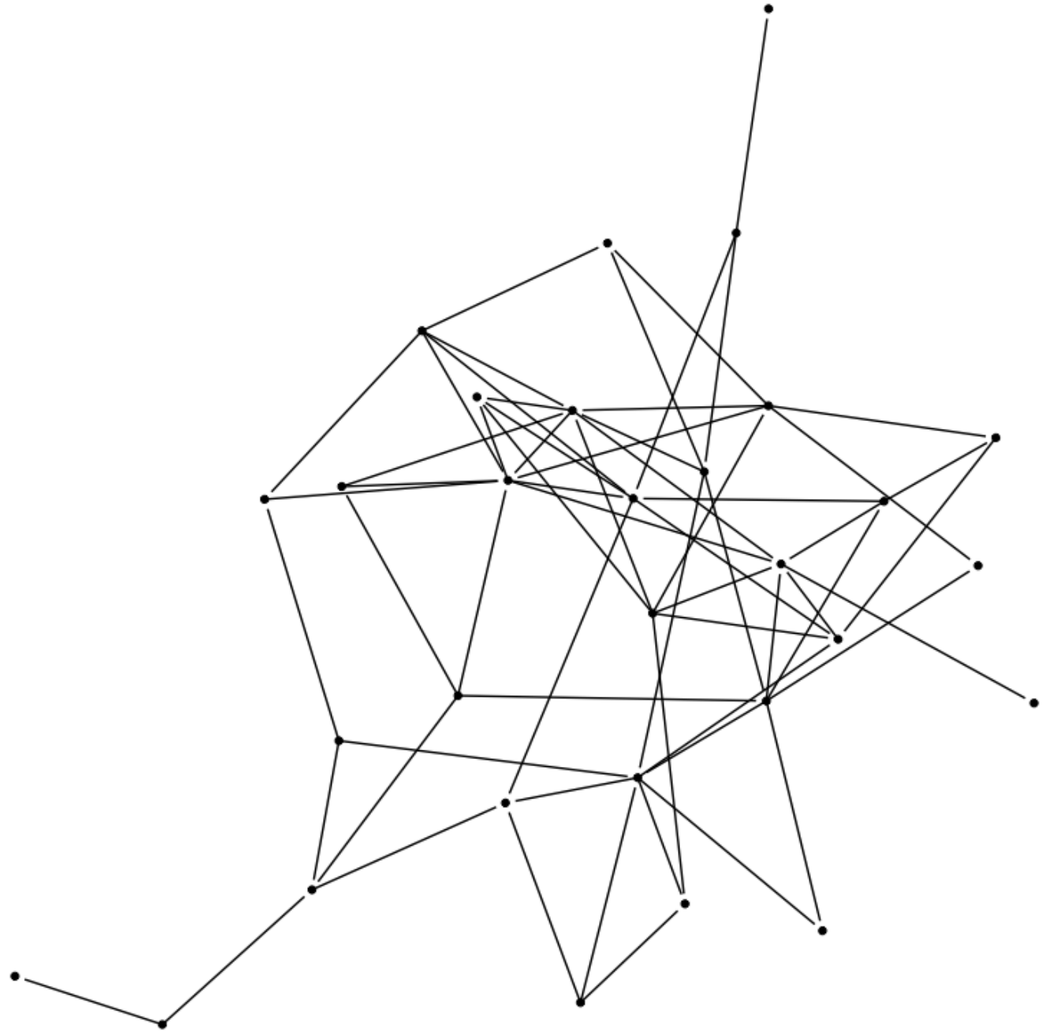


Basic ggnetwork

```
gn <- ggnetwork(rand_g)
g <- ggplot(gn, aes(x = x, y = y, xend = xend, yend = yend)) +
        geom_edges() +
        geom_nodes() +
        theme_blank()
head(gn)
```

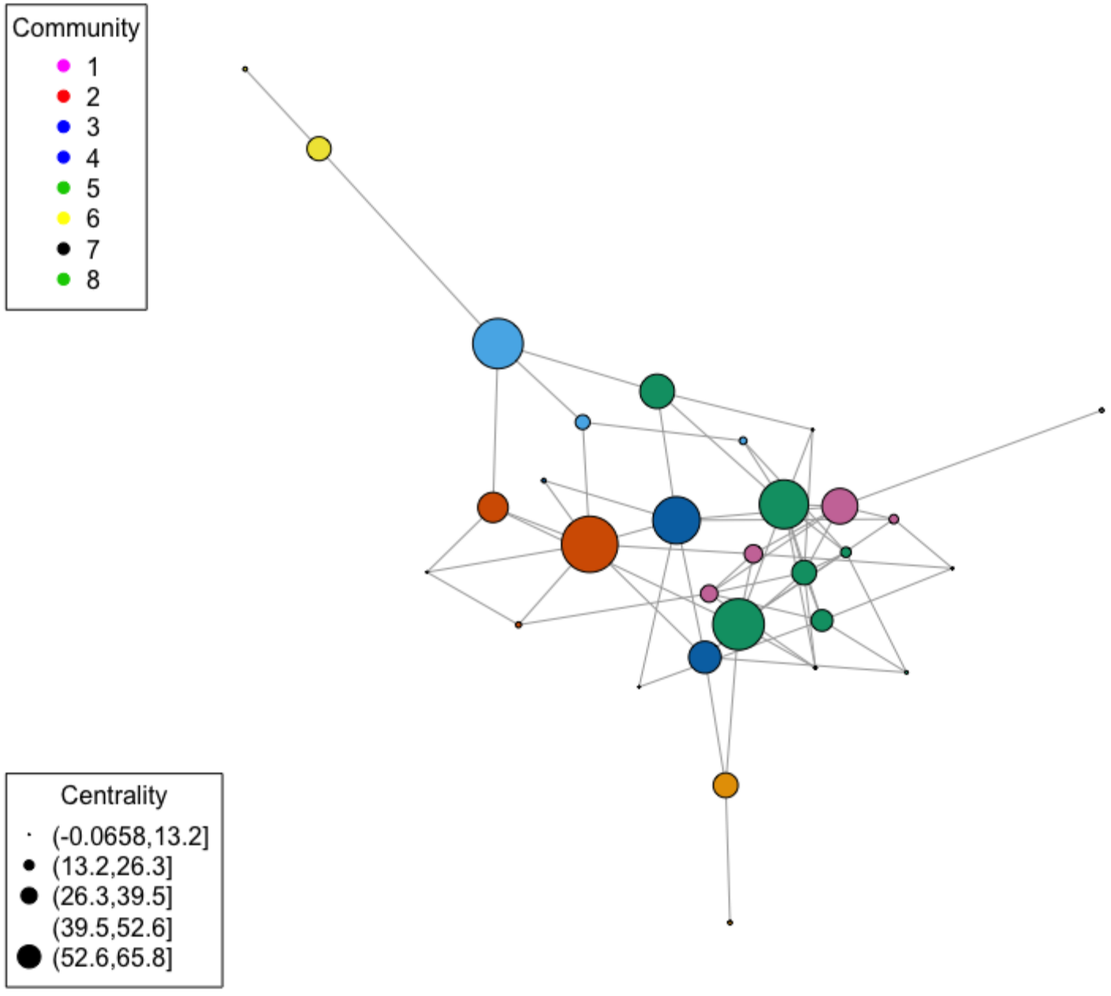
```
          x          y  na.x vertex.names      xend       yend na.y
1 0.4729841 0.01697675 FALSE            1 0.4729841 0.01697675   NA
2 0.1883442 0.42284666 FALSE            2 0.1883442 0.42284666   NA
3 0.3485247 0.82865654 FALSE            3 0.3485247 0.82865654   NA
4 0.3905894 1.00000000 FALSE            4 0.3905894 1.00000000   NA
```

```
plot(g)
```



Plotting graphs with attributes

```
# Add attributes
V(rand_g)$cent <- betweenness(rand_g)
V(rand_g)$comm <- membership(cluster_walktrap(rand_g))
# Make plot
plot(rand_g, vertex.label = NA, margin = 0,
     vertex.color = V(rand_g)$comm,
     vertex.size = V(rand_g)$cent / 6)
# Add legend for community membership
legend('topleft', legend= sort(unique( V(rand_g)$comm)),
col=  sort(unique(V(rand_g)$comm)), pch = 19, title = "Community")
# Add cuts and then get quantiles for size legend
cc <- cut(V(rand_g)$cent, 5)
scaled <- quantile(V(rand_g)$cent, seq(0.3, 0.9, length = 5)) / 25
# Add size legend for centrality
legend('bottomleft', legend= levels(cc),
  pt.cex = scaled, pch = 19, title = "Centrality")
```


Community
1
2
3
4
5
6
7
8
Centrality
(-0.0658,13.2]
(13.2,26.3]
(26.3,39.5]
(39.5,52.6]
(52.6,65.8]

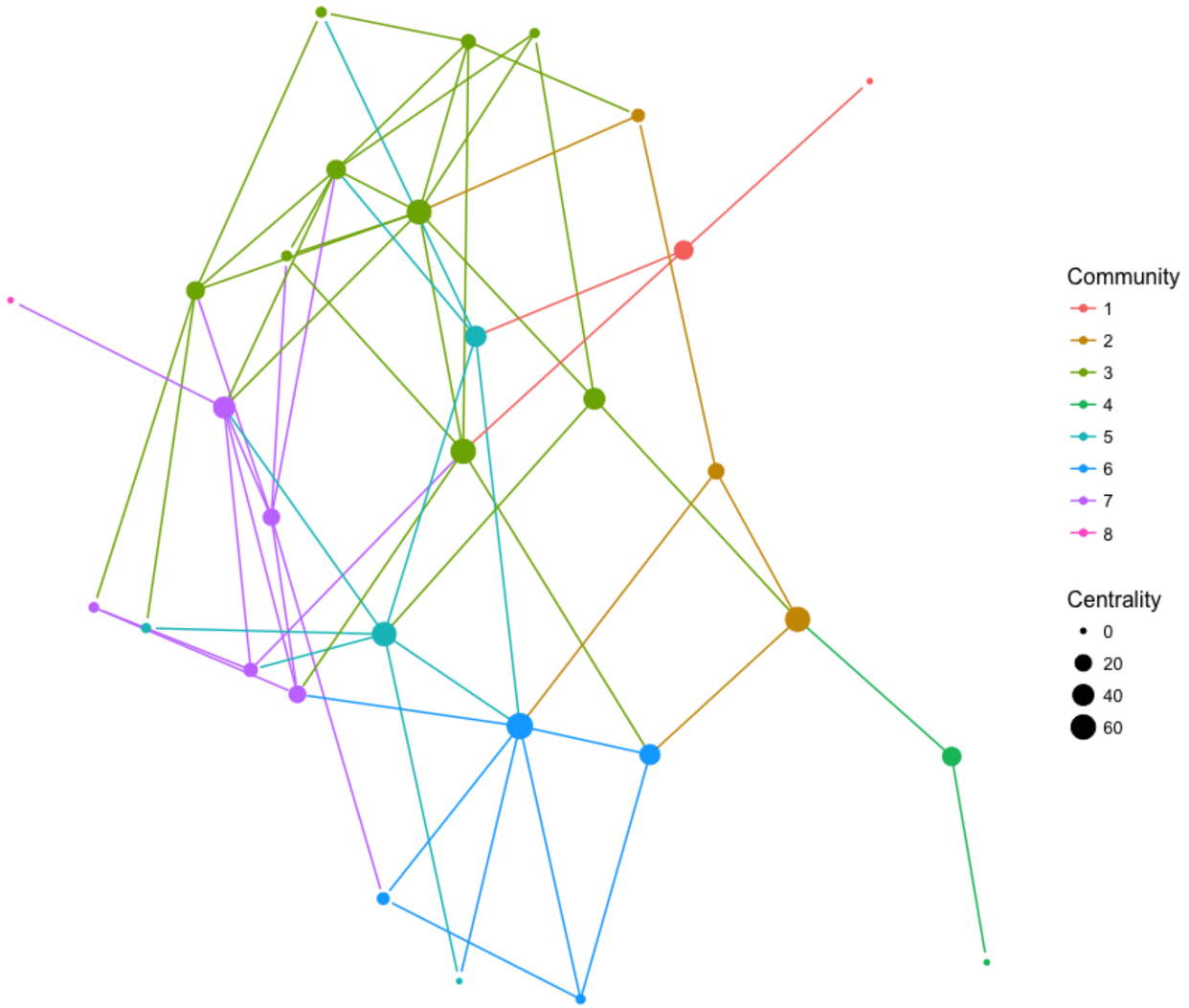
ggnet2 plot with attributes

```
net <- asNetwork(rand_g)

ggnet2(net,
       node.size = "cent",
       node.color = "comm",
       edge.size = 0.8,
       color.legend = "Community Membership",
       color.palette = "Spectral",
       edge.color = c("color", "gray88"),
       size.cut = TRUE,
       size.legend = "Centrality")
```


Community Membership
1
2
3
4
5
6
7
8
cent
[0,2.99]
(2.99,18.6]
(18.6,37]
(37,65.8]

ggnetwork plot with attributes

```
gn <- ggnetwork(rand_g)

g <- ggplot(gn, aes(x = x, y = y, xend = xend, yend = yend)) +
  geom_edges(aes(color = as.factor(comm))) +
  geom_nodes(aes(color = as.factor(comm), size = cent)) +
  theme_blank()  +
  guides(
    color = guide_legend(title = "Community"),
    size = guide_legend(title = "Centrality"))

plot(g)
```


Community
1
2
3
4
5
6
7
8
Centrality
0
20
40
60

Let's practice!

CASE STUDIES: NETWORK ANALYSIS IN R

Interactive visualizations

CASE STUDIES: NETWORK ANALYSIS IN R

Edmund Hart
Instructor

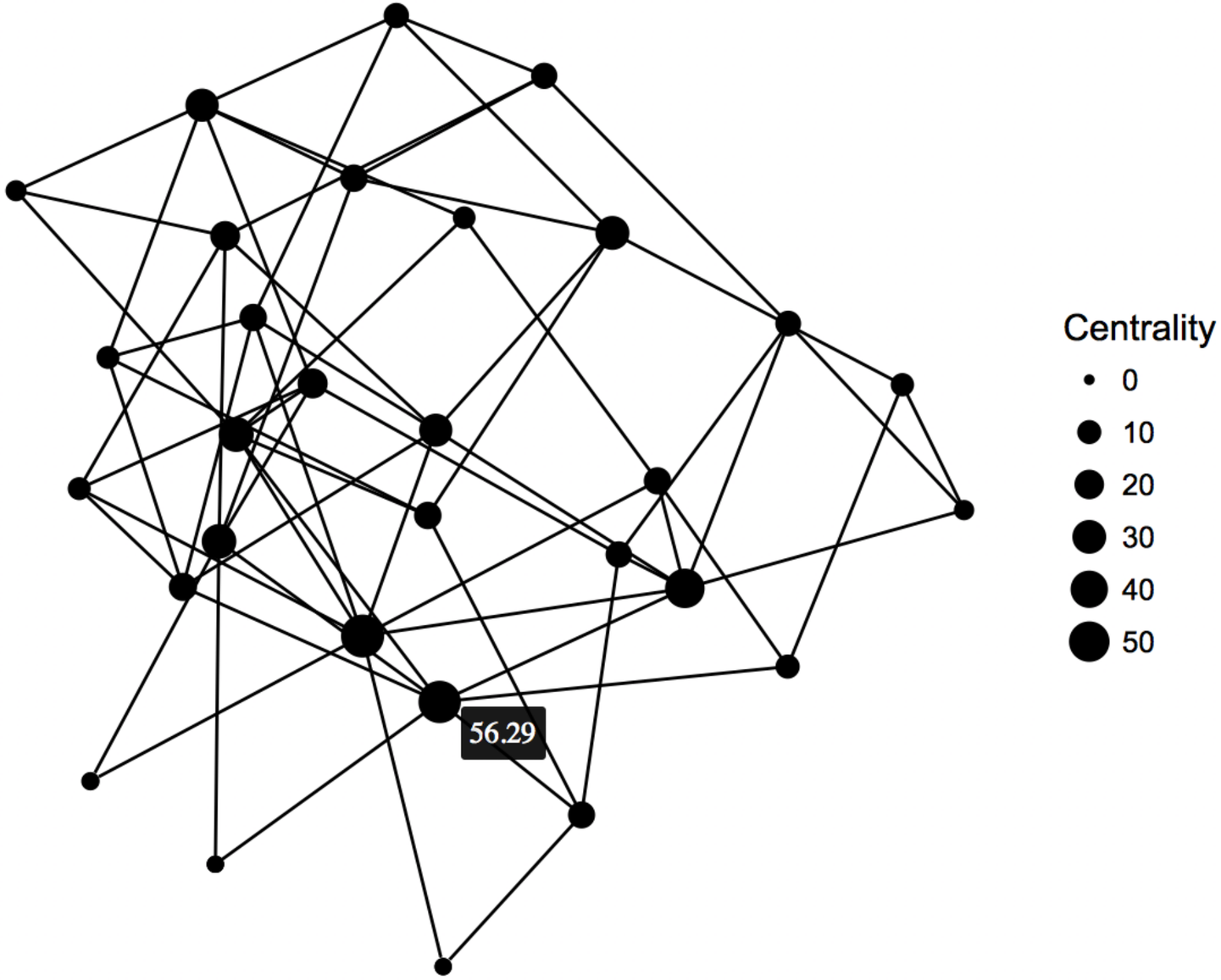
datacamp

Generating some data

```
library(igraph)
library(ggnetwork)
library(ggiraph)
library(htmlwidgets)
library(networkD3)

# Create random graph
rand_g <- erdos.renyi.game(30, 0.12, "gnp", directed = FALSE)
rand_g <- simplify(rand_g)

V(rand_g)$cent <- betweenness(rand_g)
```

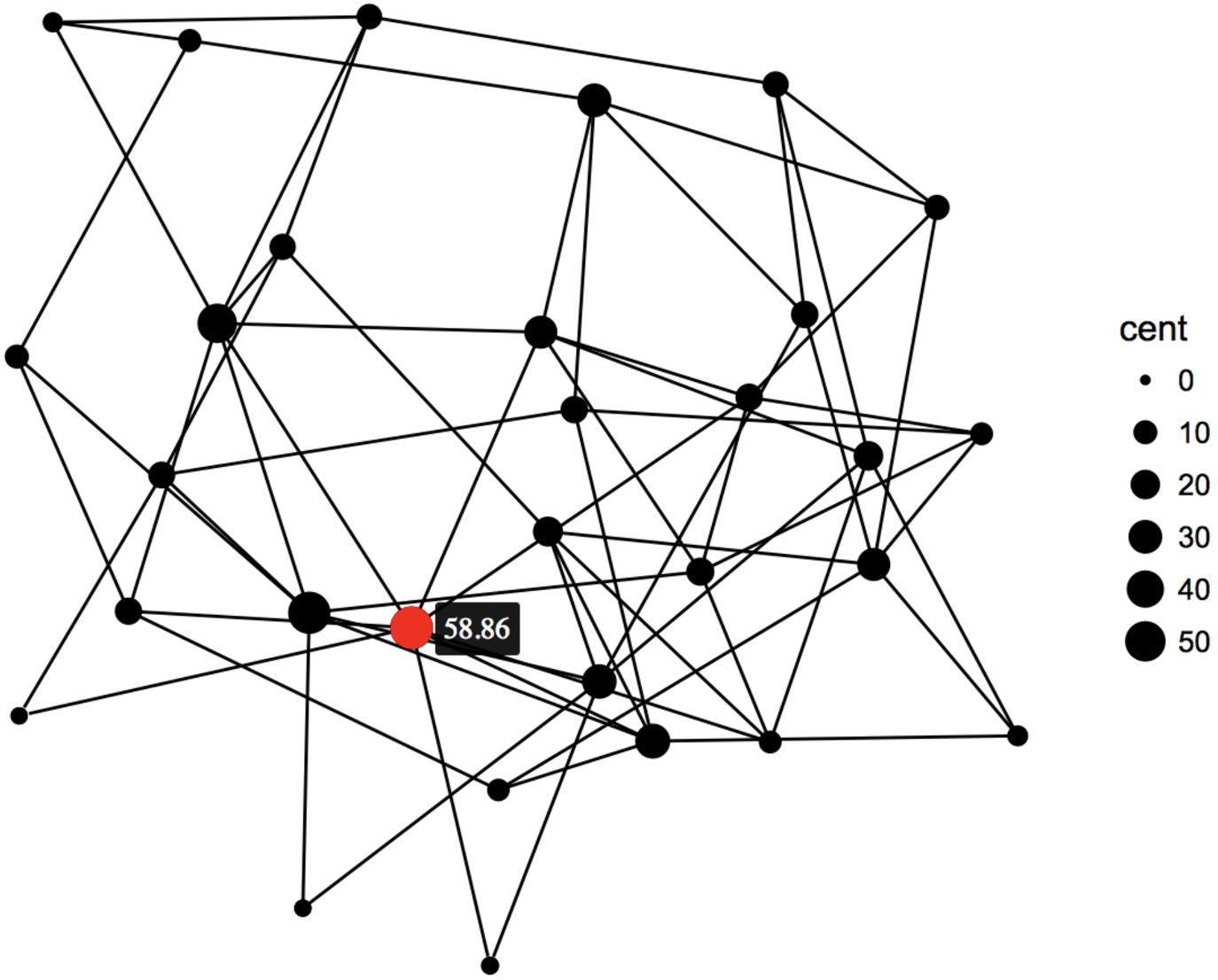
Interactive plots with ggiraph

```
# Plot graph with ggplot2 and ggnetwork
g <- ggplot(ggnetwork(rand_g),
            aes(x = x, y = y, xend = xend, yend = yend)) +
     geom_edges(color = "black") +
     geom_nodes(aes(size = cent))+ theme_blank() +
     guides(size = guide_legend(title = "Centrality"))
# Create ggiraph object
my_gg <- g + geom_point_interactive(aes(tooltip = round(cent, 2)),
        size = 2)
# Display ggiraph object
ggiraph(code = print(my_gg))
```


56.29
Centrality
0
10
20
30
40
50

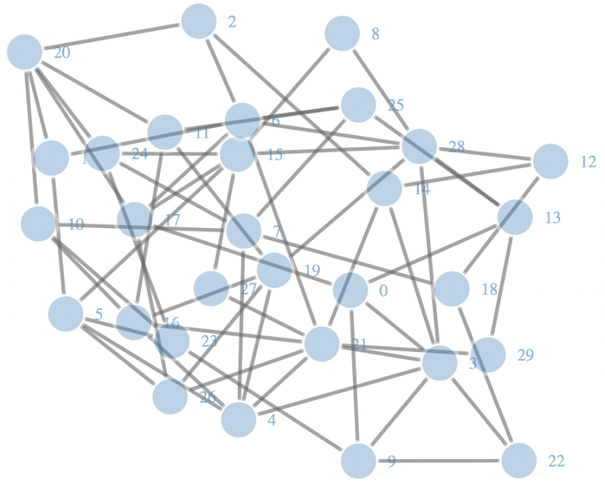
ggiraph customization

```
my_gg <- g + geom_point_interactive(aes(tooltip = round(cent, 2),
                                        data_id = round(cent, 2)),
                                    size = 2)

hover_css = "cursor:pointer;fill:red;stroke:red;r:5pt"

ggiraph(code = print(my_gg),
        hover_css = hover_css,
        tooltip_offx = 10,
        tooltip_offy = -10)
```


58.86
cent
0
10
20
30
40
50

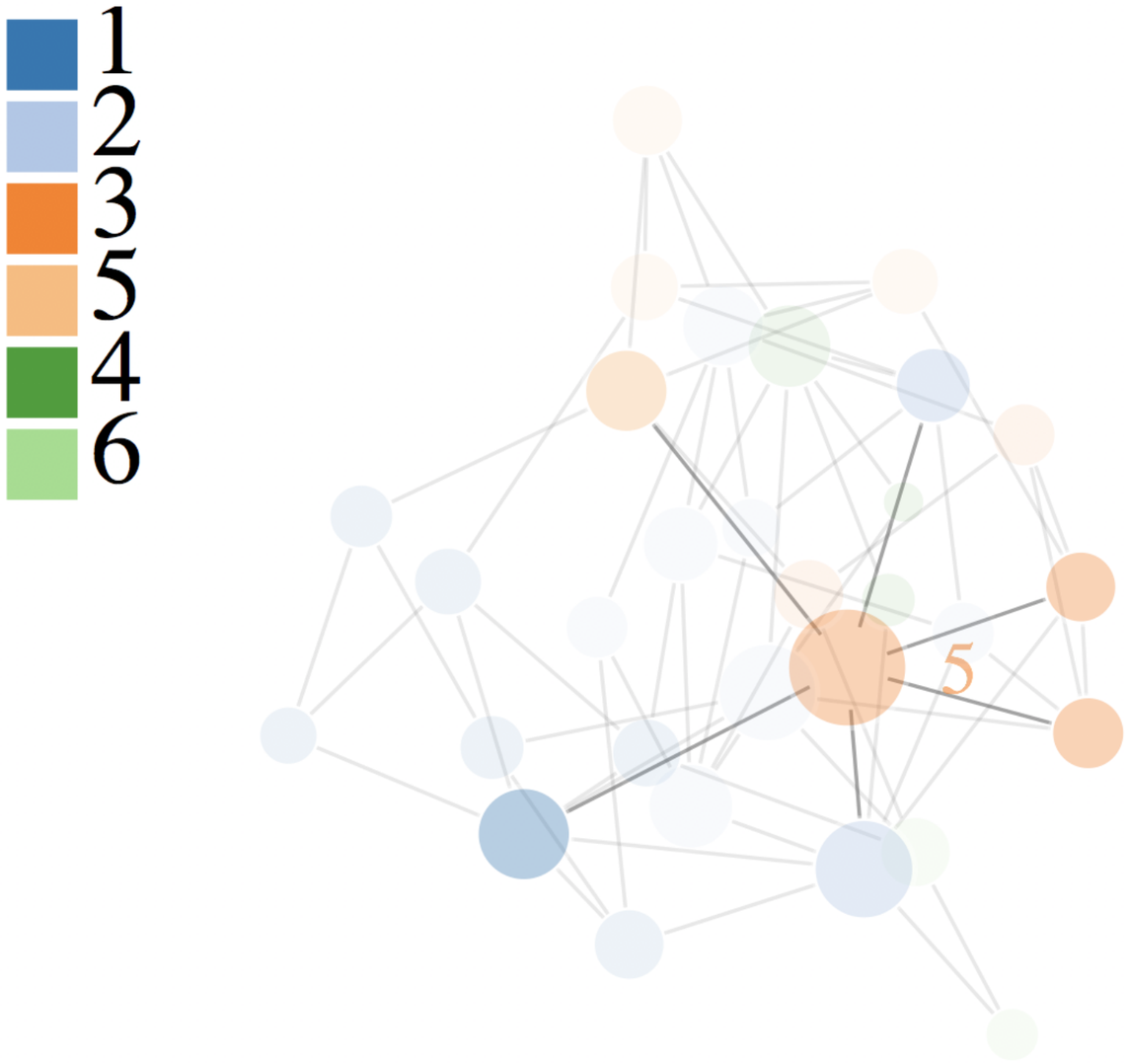
Plotting with networkD3

```
# Convert the igraph object
nd3 <- igraph_to_networkD3(rand_g)

# Create a simple network
simpleNetwork(nd3$links)
```



More complex networkD3

```
# Add attributes, group is community, and cent is centrality.
nd3$nodes$group = V(rand_g)$comm
nd3$nodes$cent = V(rand_g)$cent
# Plot the graph
forceNetwork(Links = nd3$links,
             Nodes = nd3$nodes,
             Source = 'source',
             Target = 'target',
             NodeID = 'name',
             Group = 'group',
             Nodesize = 'cent',
             legend = T,
             fontSize = 20)
```


1
2
3
5
4
6
5

Let's practice!

CASE STUDIES: NETWORK ANALYSIS IN R

Alternative visualizations

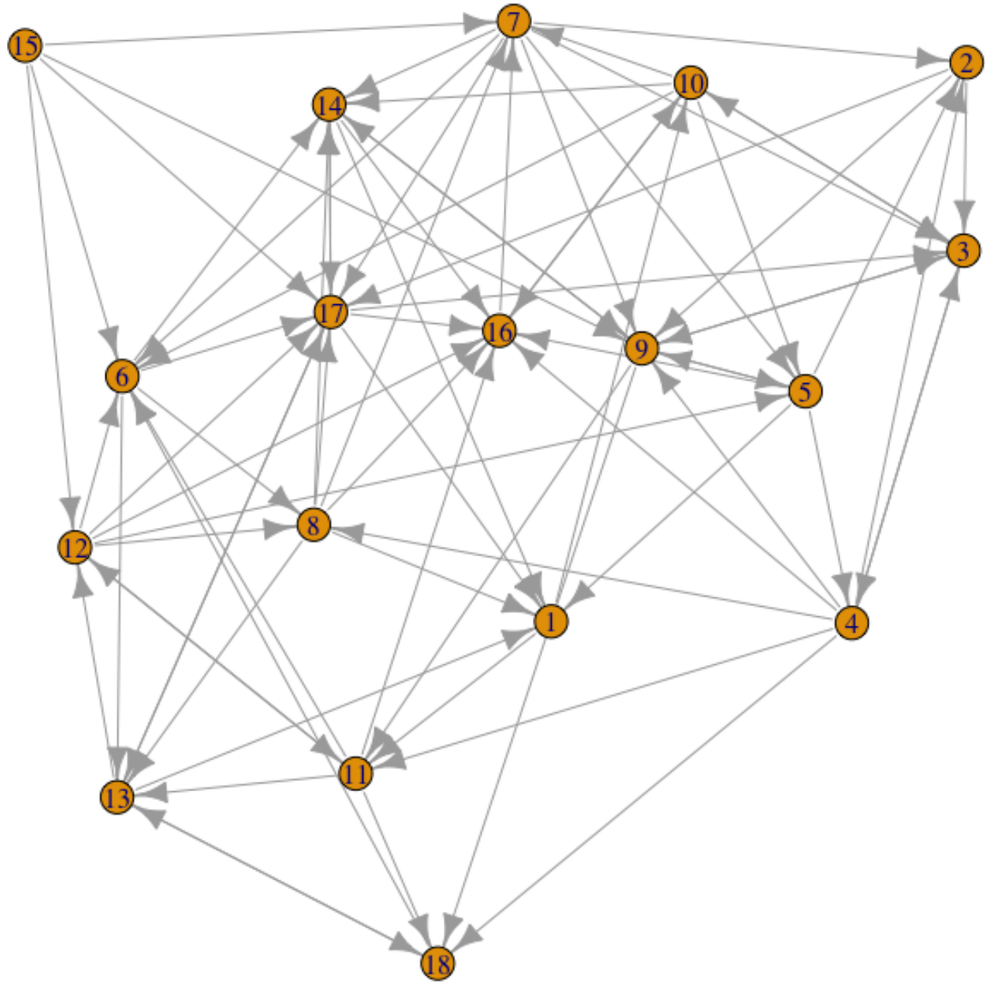
CASE STUDIES: NETWORK ANALYSIS IN R

Edmund Hart
Instructor

datacamp

Introduction to hive plots

```
library(HiveR)
library(igraph)

# Create random graph
rand_g <- erdos.renyi.game(18, 0.3, "gnp", directed = TRUE)

# Plot random graph
plot(rand_g, vertex.size = 7)
```


15
7
2
14
10
3
17
16
9
6
5
8
12
1
4
11
13
18

Introduction to hive plots

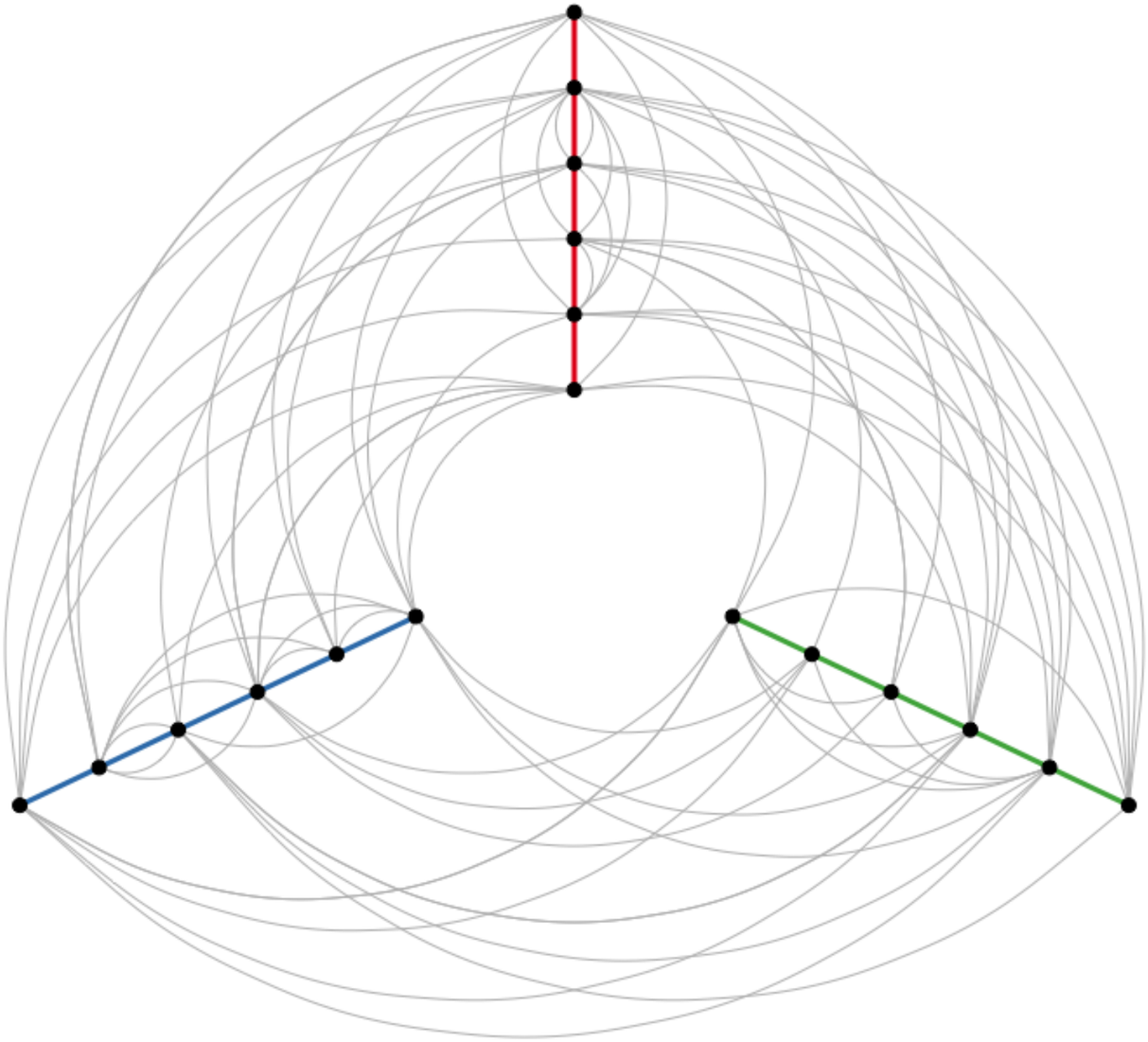
```
# Convert to dataframe for hive plots and add weights
rand_g_df <- as.data.frame(get.edgelist(rand_g))
rand_g_df$weight <- 1
# Convert to hive object
rand_hive <- edge2HPD(edge_df = rand_g_df)
# Set the axis and the radius of each node
rand_hive$nodes$axis <- sort(rep(1:3, 6))
rand_hive$nodes$radius <- as.double(rep(1:6, 3))
```

Introduction to hive plots

```
# See how nodes are modified
rand_hive$nodes
```

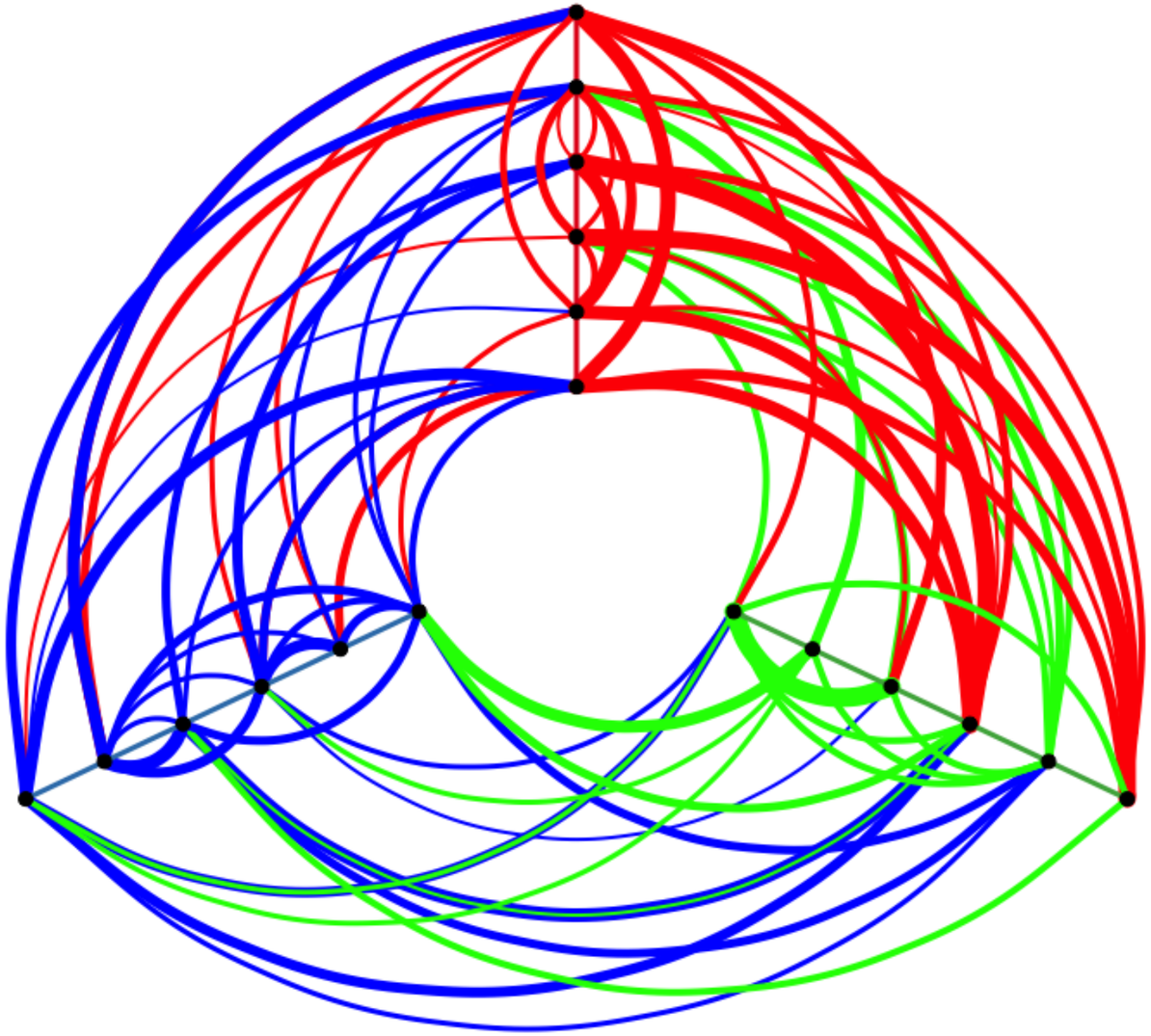
```
id lab axis radius size color
1   2    1      1    1 black
2   8    1      2    1 black
3   9    1      3    1 black
4   3    1      4    1 black
5   4    1      5    1 black
6   7    1      6    1 black
7  11    2      1    1 black
8  14    2      2    1 black
9  18    2      3    1 black
```

```
# See hive plot
plotHive(rand_hive, method = "abs", bkgnd = "white")
```



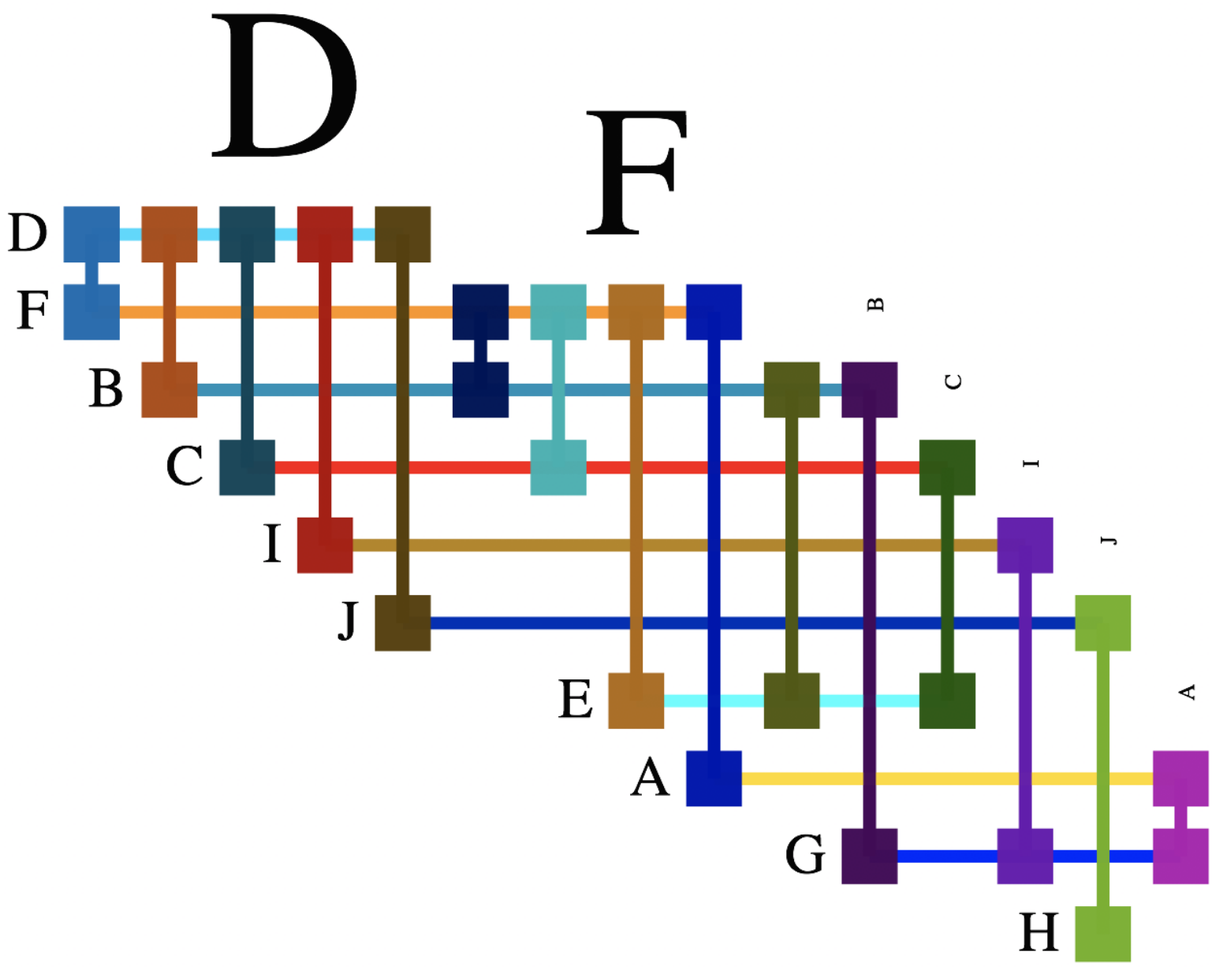
Modifying hive plots

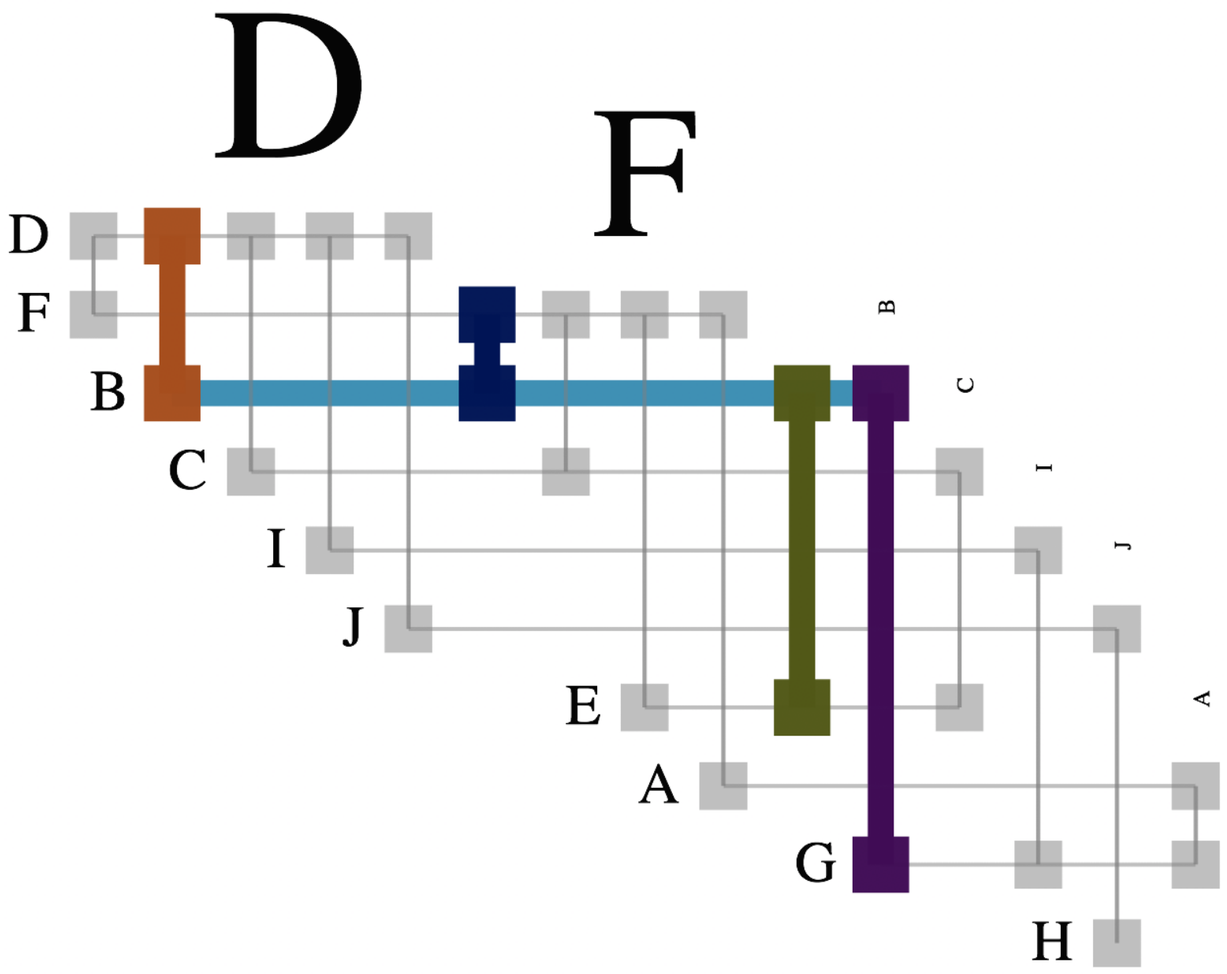
```
# Setting location of each node
rand_hive$nodes$axis <- sort(rep(1:3, 6))
rand_hive$nodes$radius <- as.double(rep(1:6, 3))
# Add weights to each edge
rand_hive$edges$weight <- as.double(
                      rpois(length(rand_hive$edges$weight), 5)
                          )

# Add color based on edge origination
rand_hive$edges$color[rand_hive$edges$id1 %in% 1:6] <- 'red'
rand_hive$edges$color[rand_hive$edges$id1 %in% 7:12] <- 'blue'
rand_hive$edges$color[rand_hive$edges$id1 %in% 13:18] <- 'green'
# Plot
plotHive(rand_hive, method = "abs", bkgnd = "white")
```



Biofabric plots

```
# Create random graph
rand_g <- erdos.renyi.game(10, 0.3, "gnp", directed = FALSE)
rand_g <- simplify(rand_g)
# Add names to vertices
V(rand_g)$name <- LETTERS[1:length(V(rand_g))]
# Create biofabric plot
biofbc <- bioFabric(rand_g)
bioFabric_htmlwidget(biofbc)
```


D
F
D
F
B
C
I
J
E
A
G
H
B
C
I
J
A


D
F
D
F
B
C
I
J
E
A
G
H
B
C
I
J
A

Let's practice!

CASE STUDIES: NETWORK ANALYSIS IN R