



PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Extract a dataset

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Post-doctoral researcher

Getting the dataset

```
V(g)$degree<-degree(g)
V(g)$triangles<-count_triangles(g)
V(g)$betweenness<-betweenness(g,normalized=TRUE)
V(g)$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):
  [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
 [15] G--I G--H H--I H--J I--J
```



Getting the dataset

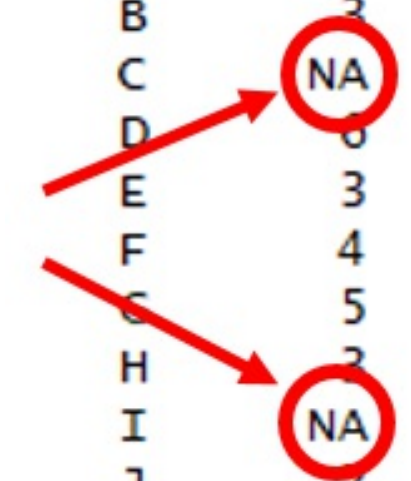
```
g
IGRAPH UN-- 10 19 --
  attr: name (v/c), degree (v/n), triangles (v/n), transitivity
| (v/n), rNeighbors (v/n), averageAge (v/n), pageRank (v/n),
| pPageRank (v/n), label (e/c)
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 [15] G--I G--H H--I H--J I--J
```

```
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	NA	2	0.6666667	0	39.33333	0.08675903	0.03285162
I	3	3	0.5000000	1	37.25000	0.10994175	0.04785657
J	2	1	1.0000000	0	31.00000	0.06294435	0.01947748

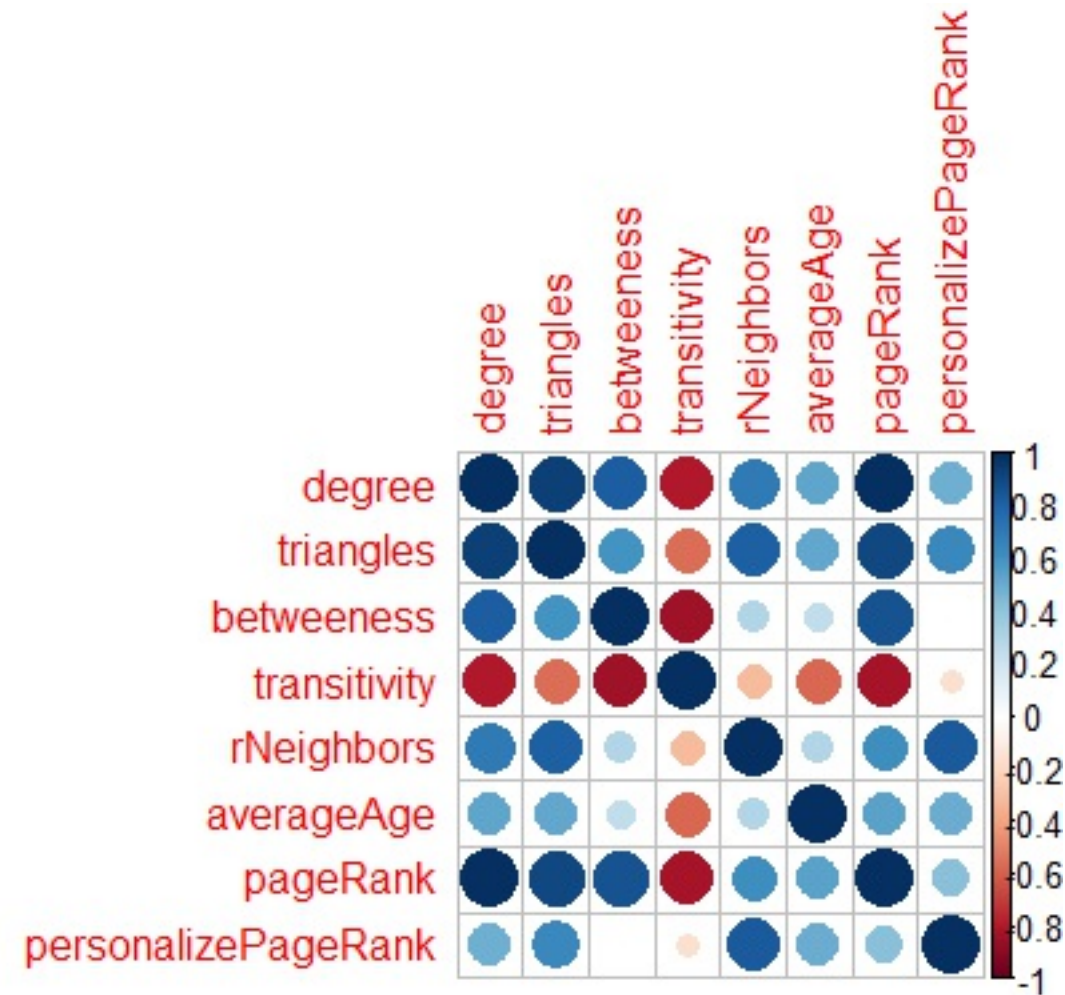
```
sum(is.na(dataset$degree))  
[1] 2
```

Preprocessing - Correlated variables

```
library(corrplot)

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

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





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Let's practice!



PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

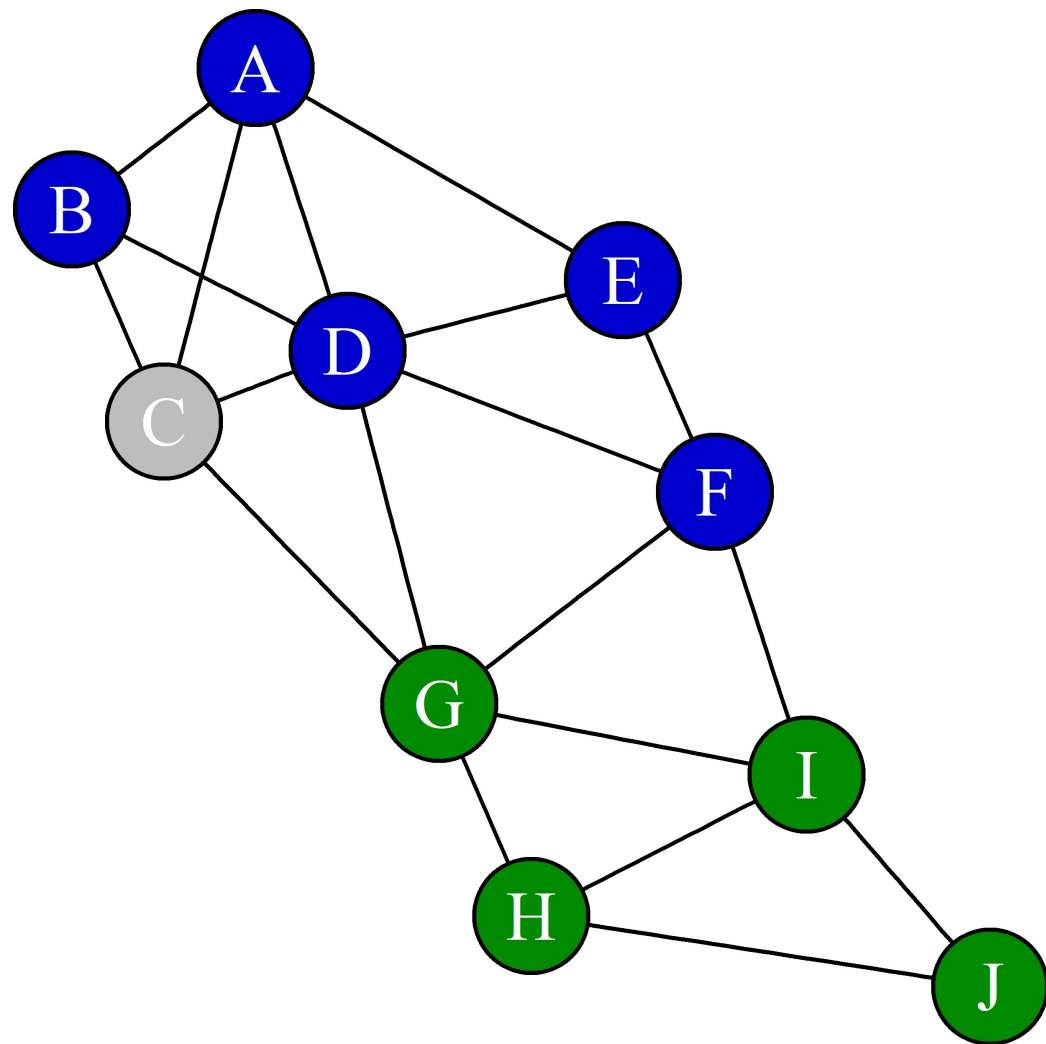
Building a predictive model

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Post-doctoral researcher



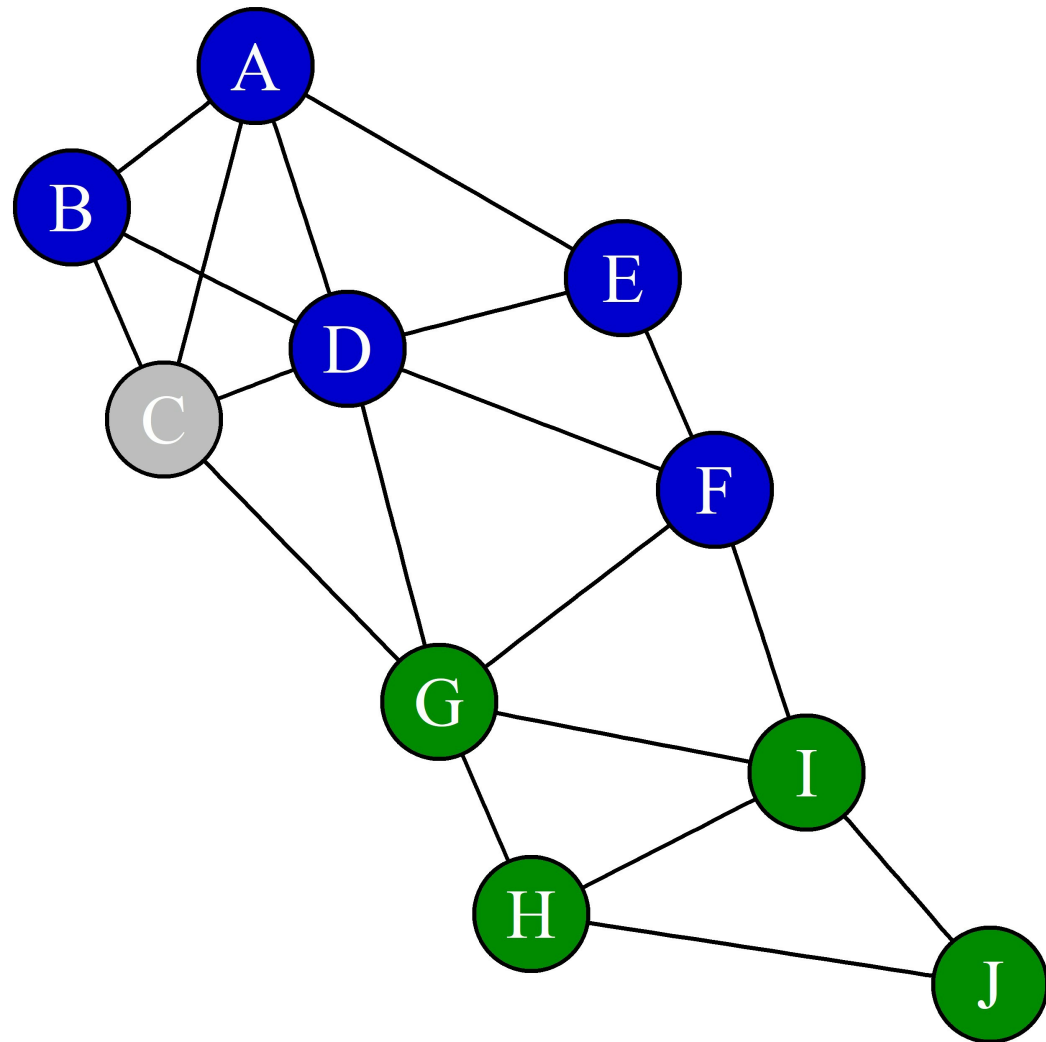
Predictive modeling



```
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
```



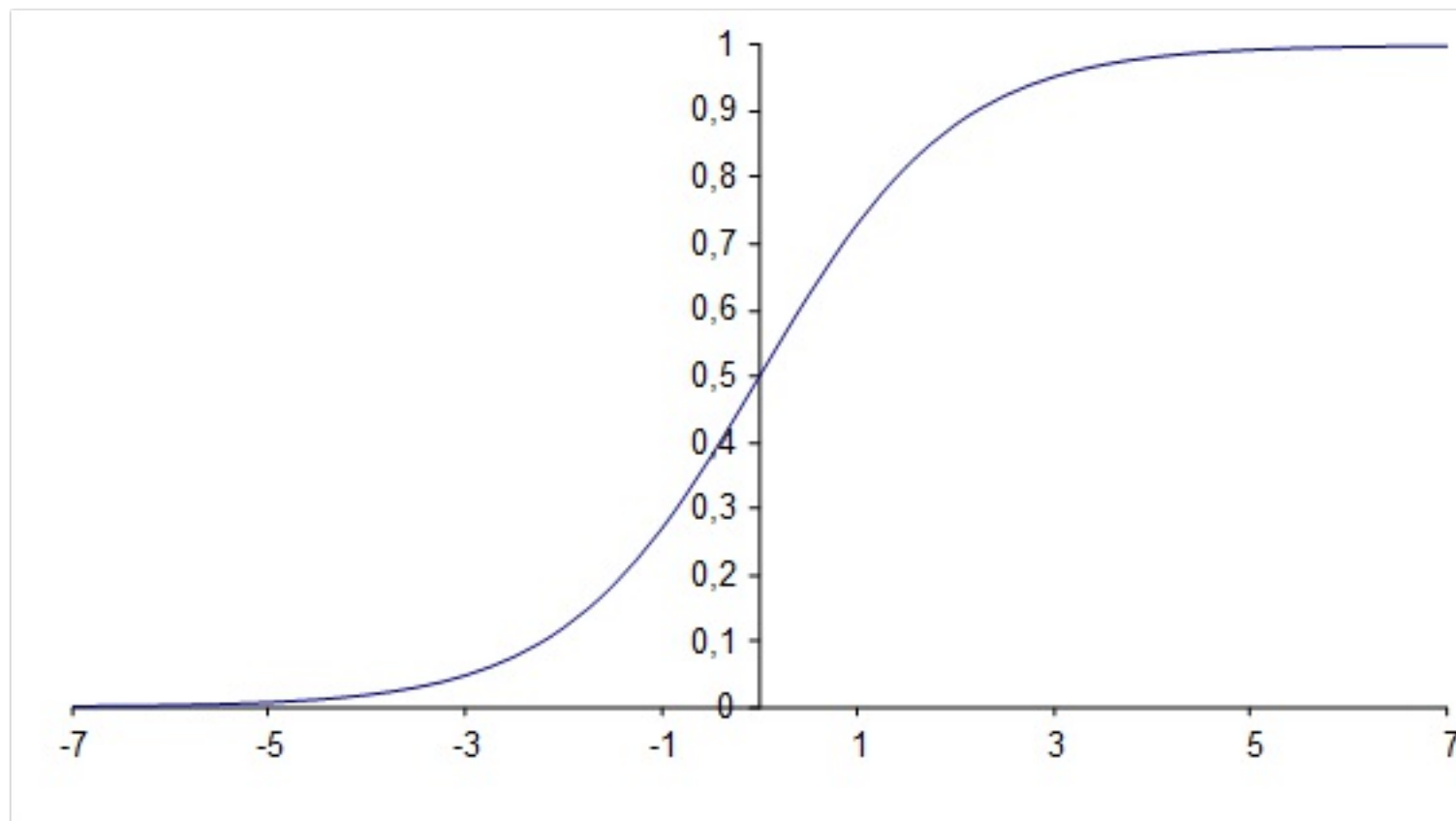

Predictive modeling



```
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')
```

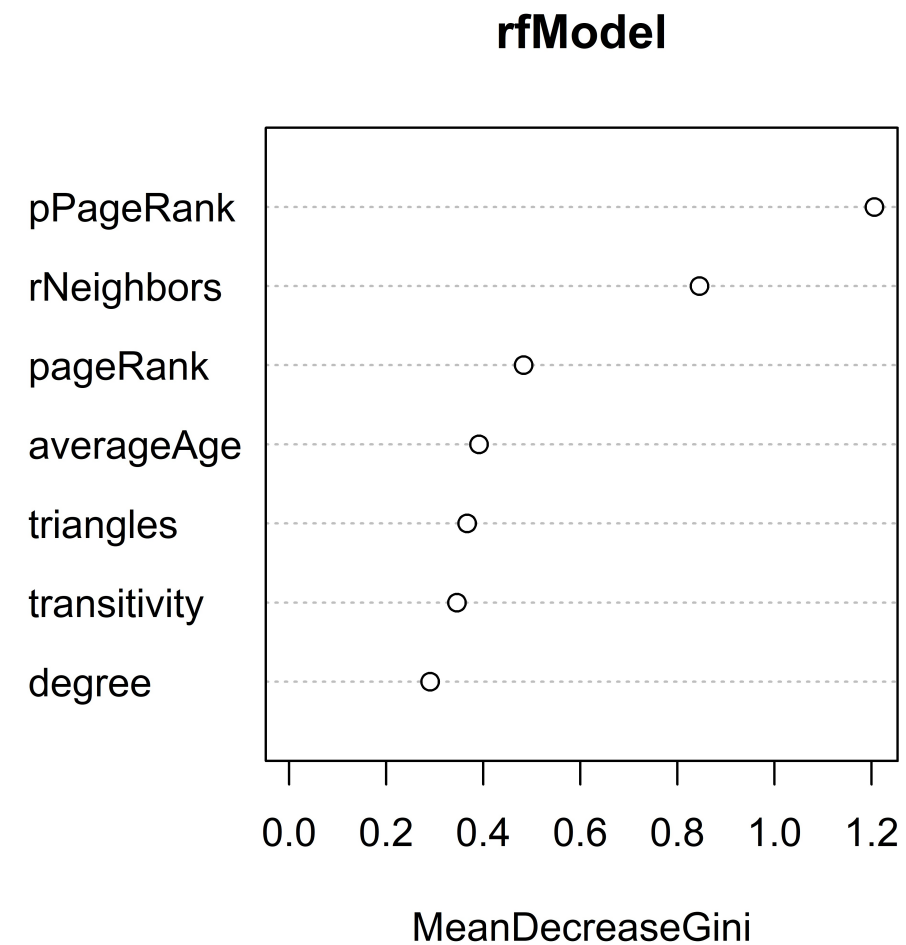
```
glm(R~., dataset=training_set,family='binomial')
```



Random forests

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

```
varImpPlot(rfModel)
```





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Let's practice!



PREDICTIVE ANALYTICS USING NETWORKED DATA IN R

Evaluating model performance

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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
      0      1
C 0.136 0.864
attr(,"class")
[1] "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)
```



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Let's practice!



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Summary and final thoughts

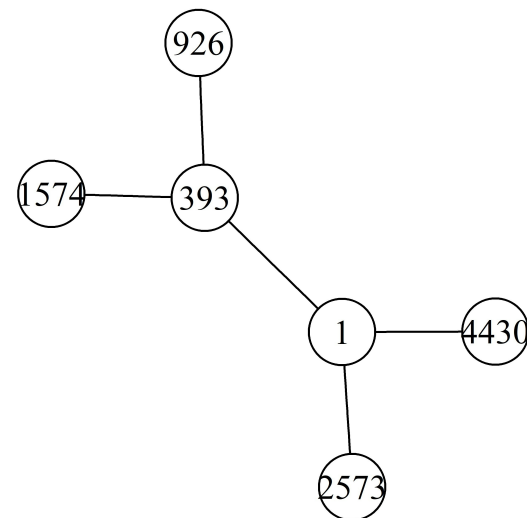
Bart Baesens, Ph.D.

Professor of Data Science, KU Leuven and University of Southampton

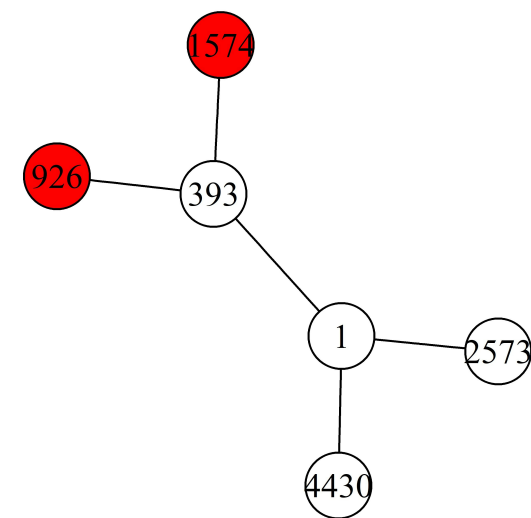


Labeled networks

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

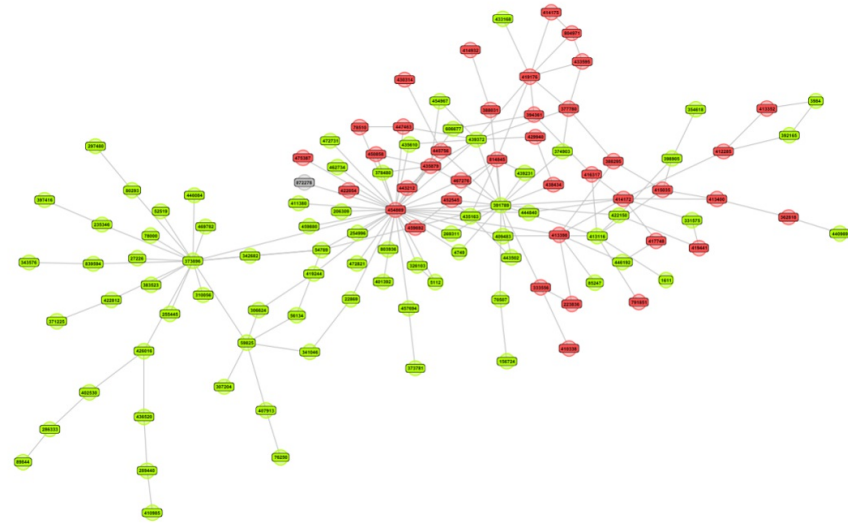


```
> customers
  id churn
1    1    0
2  393    0
3 2573    0
4 4430    0
5  926    1
6 1574    1
```





Homophily



Birds of a feather flock together

Dyadicity: connectedness between nodes with same label

Heterophilicity: connectedness between nodes with opposite labels



Network Featurization

```
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 [15] 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),
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 [15] G--I G--H H--I H--J I--J
```



Model building and evaluation

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)
```




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Congratulations!