

R-EndSem

May 29, 2020

I have referred the official bnlearn documentation for implementing the Bayesian network.

<https://www.bnlearn.com/>

<https://www.bnlearn.com/examples/useR19-tutorial/>

<https://www.bnlearn.com/examples/custom/>

```
[59]: # install.packages("BiocManager")
# BiocManager::install("Rgraphviz")
# install.packages("bnlearn")
# install.packages("ggplots")
# install.packages("GGally")
# install.packages("polycor")
# install.packages("dplyr")
```

Installing package into ‘/home/maddy/R/x86_64-pc-linux-gnu-library/3.6’
(as ‘lib’ is unspecified)

also installing the dependencies ‘purrr’, ‘tidyselect’, ‘BH’, ‘plogr’

```
[61]: library(bnlearn)
library(gplots)
library(GGally)
library(polycor)
library(dplyr)
```

```
[62]: col_names = ␣
      ↪ "age,sex,cp,trestbps,chol,fb,restecg,thalach,exang,oldpeak,slope,ca,thal,num"
col_names = strsplit(col_names, ",")
col_names = as.vector(col_names)
col_names = unlist(col_names)
```

```
[64]: test_data = sample_n(data, 50)
```

```
[3]: data = read.csv("processed.cleveland.data",header = FALSE,sep = ",", col.names=␣
      ↪ col_names)
```

```
[4]: my_col_names = "age,cp,trestbps,chol,thalach,exang,oldpeak,ca,thal,num"
my_col_names = strsplit(my_col_names, ",")
my_col_names = as.vector(my_col_names)
my_col_names = unlist(my_col_names)
```

Randomly selected attributes

```
[5]: my_col_names
```

1. 'age' 2. 'cp' 3. 'trestbps' 4. 'chol' 5. 'thalach' 6. 'exang' 7. 'oldpeak' 8. 'ca' 9. 'thal' 10. 'num'

```
[6]: data = data[,my_col_names]
```

```
[7]: dim(data)

head(data)
```

1. 303 2. 10

A data.frame: 6 × 10

		age <dbl>	cp <dbl>	trestbps <dbl>	chol <dbl>	thalach <dbl>	exang <dbl>	oldpeak <dbl>	ca <dbl>	thal <dbl>	num <dbl>
1	63	1	145	233	150	0	2.3	0	6	0	
2	67	4	160	286	108	1	1.5	3	3	2	
3	67	4	120	229	129	1	2.6	2	7	1	
4	37	3	130	250	187	0	3.5	0	3	0	
5	41	2	130	204	172	0	1.4	0	3	0	
6	56	2	120	236	178	0	0.8	0	3	0	

```
[8]: my_col_names = "age,cp,trestbps,chol,thalach,exang,oldpeak,ca,thal,num"
my_col_names = strsplit(my_col_names, ",")
my_col_names = as.vector(my_col_names)
my_col_names = unlist(my_col_names)
```

```
continous_col_names = "age,trestbps,chol,thalach,oldpeak"
continous_col_names = strsplit(continous_col_names, ",")
continous_col_names = as.vector(continous_col_names)
continous_col_names = unlist(continous_col_names)
```

```
discrete_col_names = "cp,exang,ca,thal,num"
discrete_col_names = strsplit(discrete_col_names, ",")
discrete_col_names = as.vector(discrete_col_names)
discrete_col_names = unlist(discrete_col_names)
```

```
x_col_names = "age,cp,trestbps,chol,thalach,exang,oldpeak"
x_col_names = strsplit(x_col_names, ",")
x_col_names = as.vector(x_col_names)
```

```
x_col_names = unlist(x_col_names)
```

```
[9]: data[, "num"][data[, "num"] > 0] = 1
```

```
[10]: data[, discrete_col_names] <- lapply(data[, discrete_col_names], as.factor)
data[, continous_col_names] <- lapply(data[, continous_col_names], as.numeric)
```

```
[11]: head(data)
```

A data.frame: 6 × 10

	age <dbl>	cp <fct>	trestbps <dbl>	chol <dbl>	thalach <dbl>	exang <fct>	oldpeak <dbl>	ca <fct>	thal <fct>	num <fct>
1	63	1	145	233	150	0	2.3	0	6	0
2	67	4	160	286	108	1	1.5	3	3	1
3	67	4	120	229	129	1	2.6	2	7	1
4	37	3	130	250	187	0	3.5	0	3	0
5	41	2	130	204	172	0	1.4	0	3	0
6	56	2	120	236	178	0	0.8	0	3	0

0.0.1 Dataset understanding

There is no missing value in the dataframe which is evident from -

```
[12]: sum(is.na(data))
```

6

For all the continous variables, we do the histogram plot to see if they are Gaussian

```
[13]: head(data[, continous_col_names])
dim(data[, continous_col_names])
```

A data.frame: 6 × 5

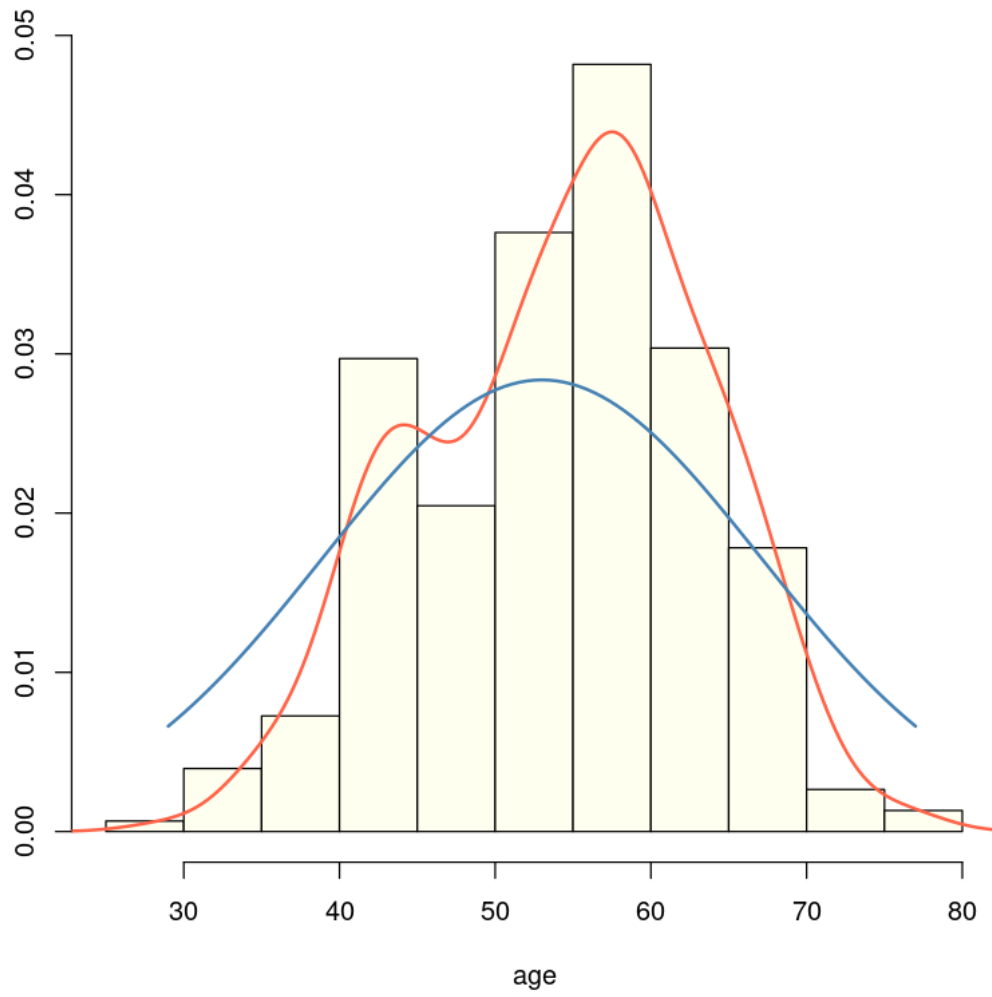
	age <dbl>	trestbps <dbl>	chol <dbl>	thalach <dbl>	oldpeak <dbl>
1	63	145	233	150	2.3
2	67	160	286	108	1.5
3	67	120	229	129	2.6
4	37	130	250	187	3.5
5	41	130	204	172	1.4
6	56	120	236	178	0.8

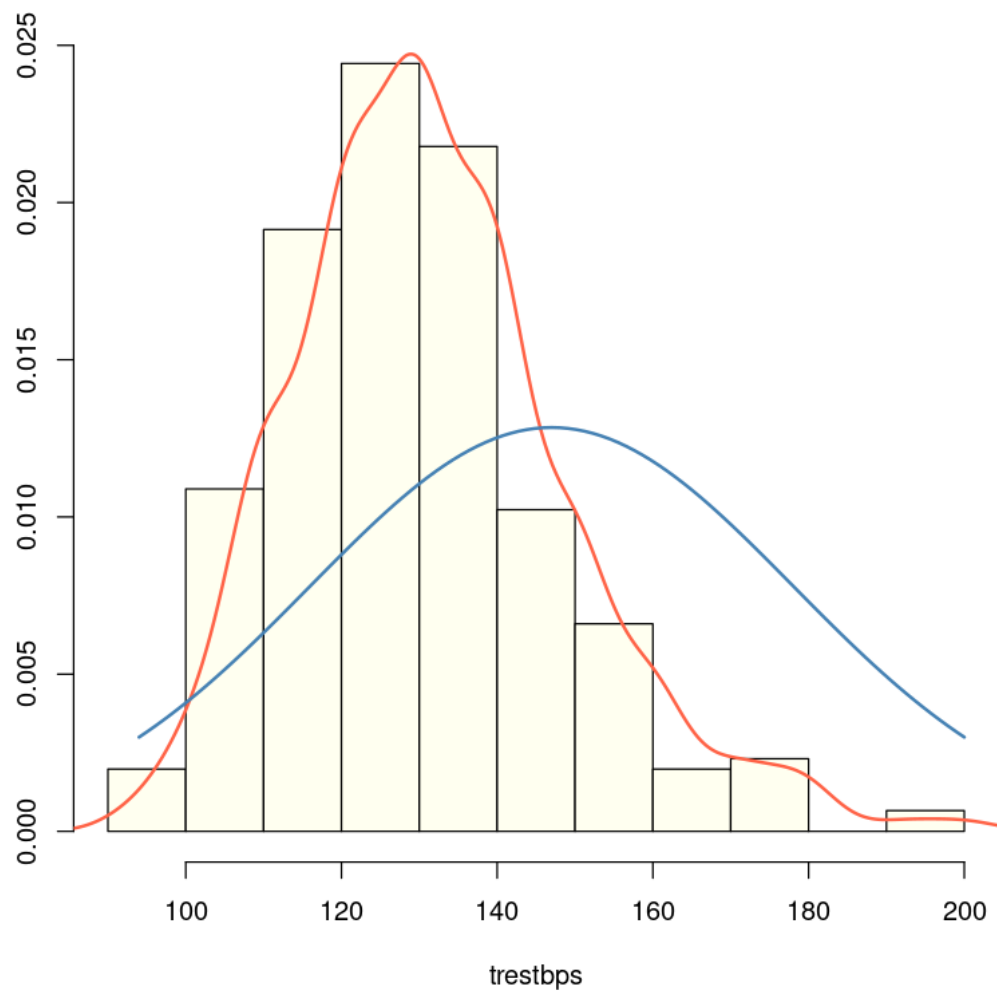
1. 303 2. 5

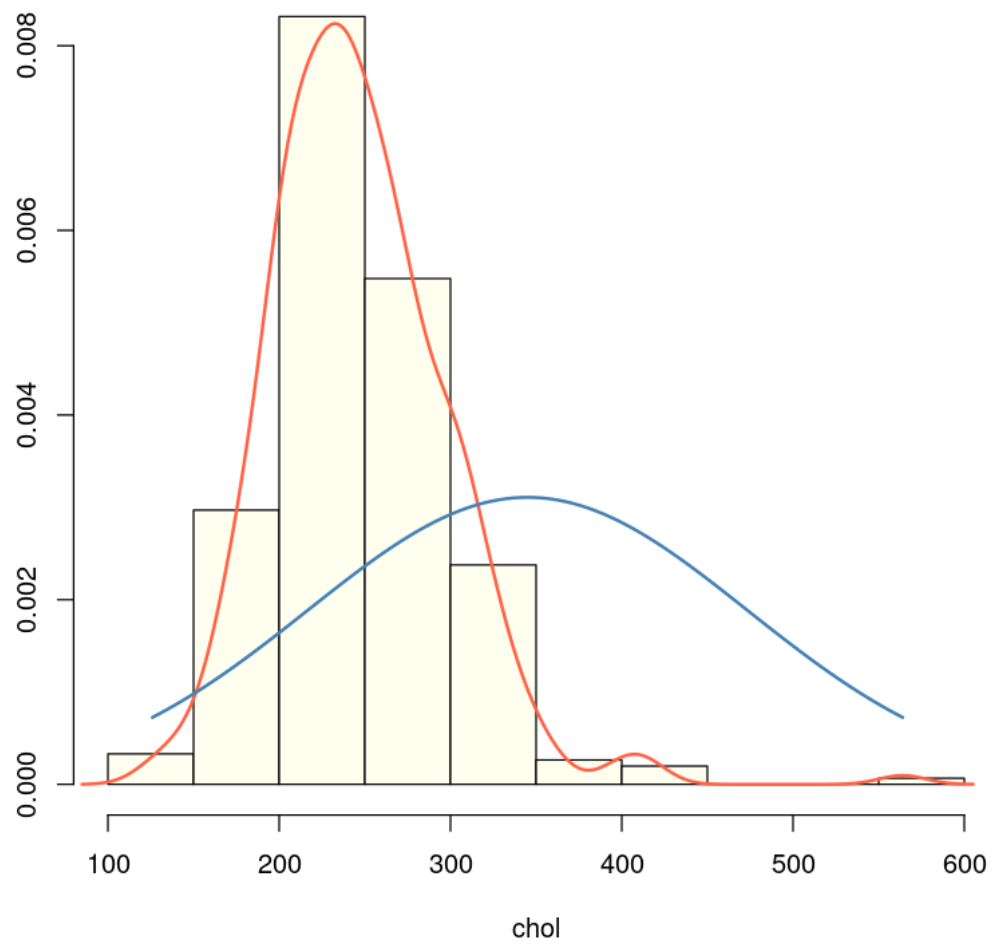
```
[14]: for (var in continous_col_names) {

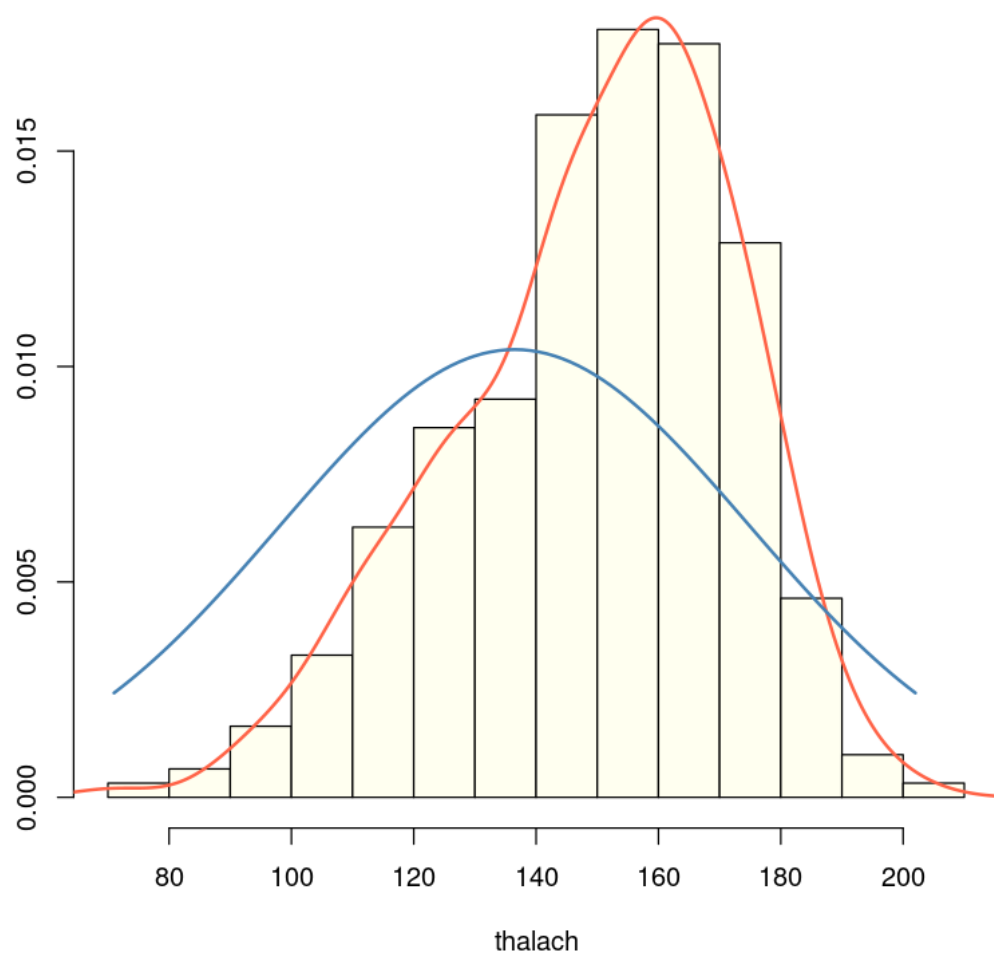
  x = data[, var]
  hist(x, prob = TRUE, xlab = var, ylab = "", main = "", col = "ivory")
  lines(density(x), lwd = 2, col = "tomato")
  curve(dnorm(x, mean = mean(x), sd = sd(x)), from = min(x), to = max(x), add_
  ↪ = TRUE, lwd = 2, col = "steelblue")
}
```

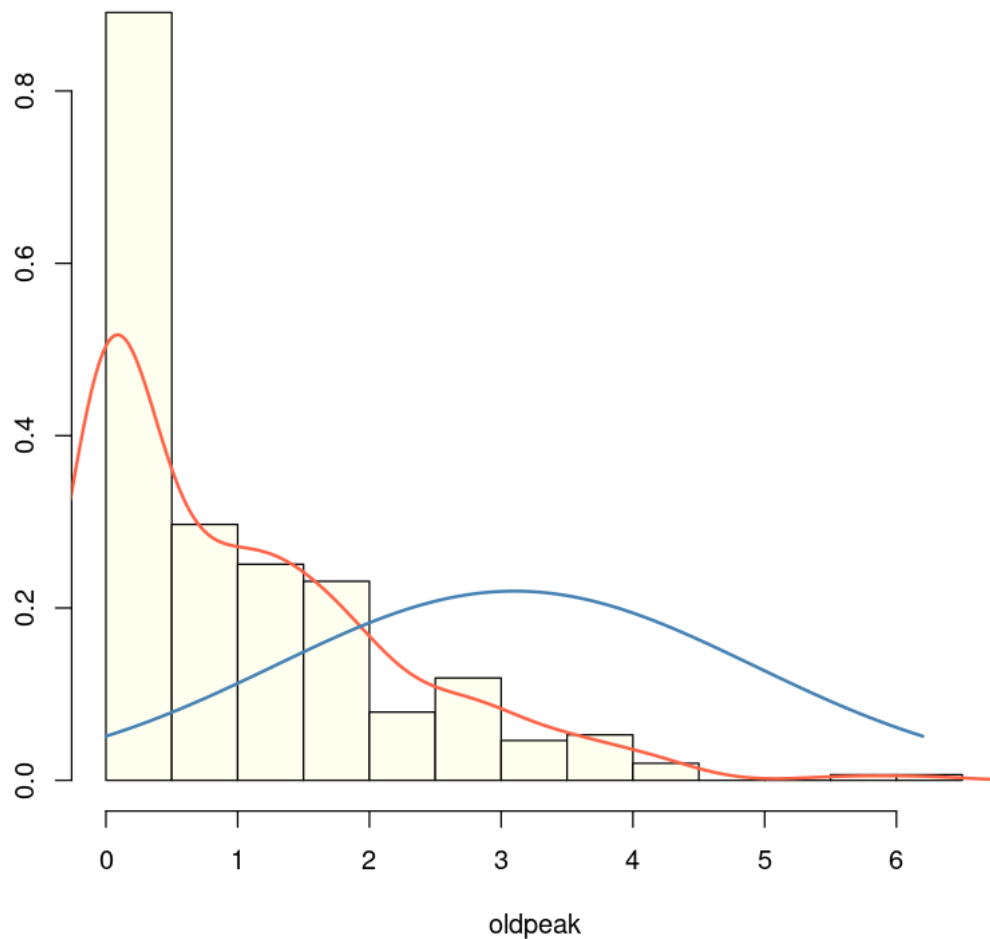
```
}
```











Most of the continuous attributes are close to a Gaussian distribution, but some e.g. oldpeak are not.

We will deal with that later.

Checking relationship between all the feature-pairs

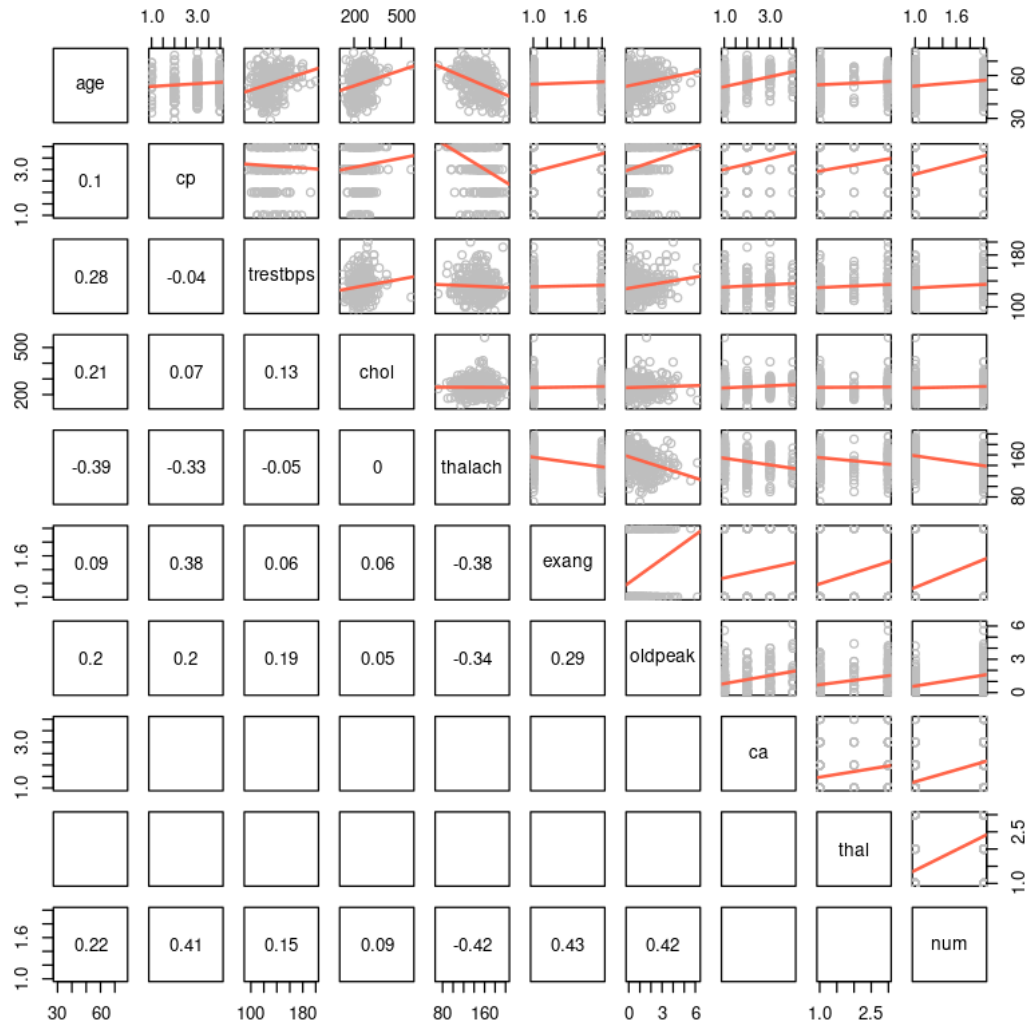
```
[15]: pairs(data,
upper.panel = function(x, y, ...) {
  points(x = x, y = y, col = "grey")
  abline(coef(lm(y ~ x)), col = "tomato", lwd = 2)
},
lower.panel = function(x, y, ...) {
  par(usr = c(0, 1, 0, 1))
```



```

text(x = 0.5, y = 0.5, round(cor(x, y), 2), cex = 1)
}
)

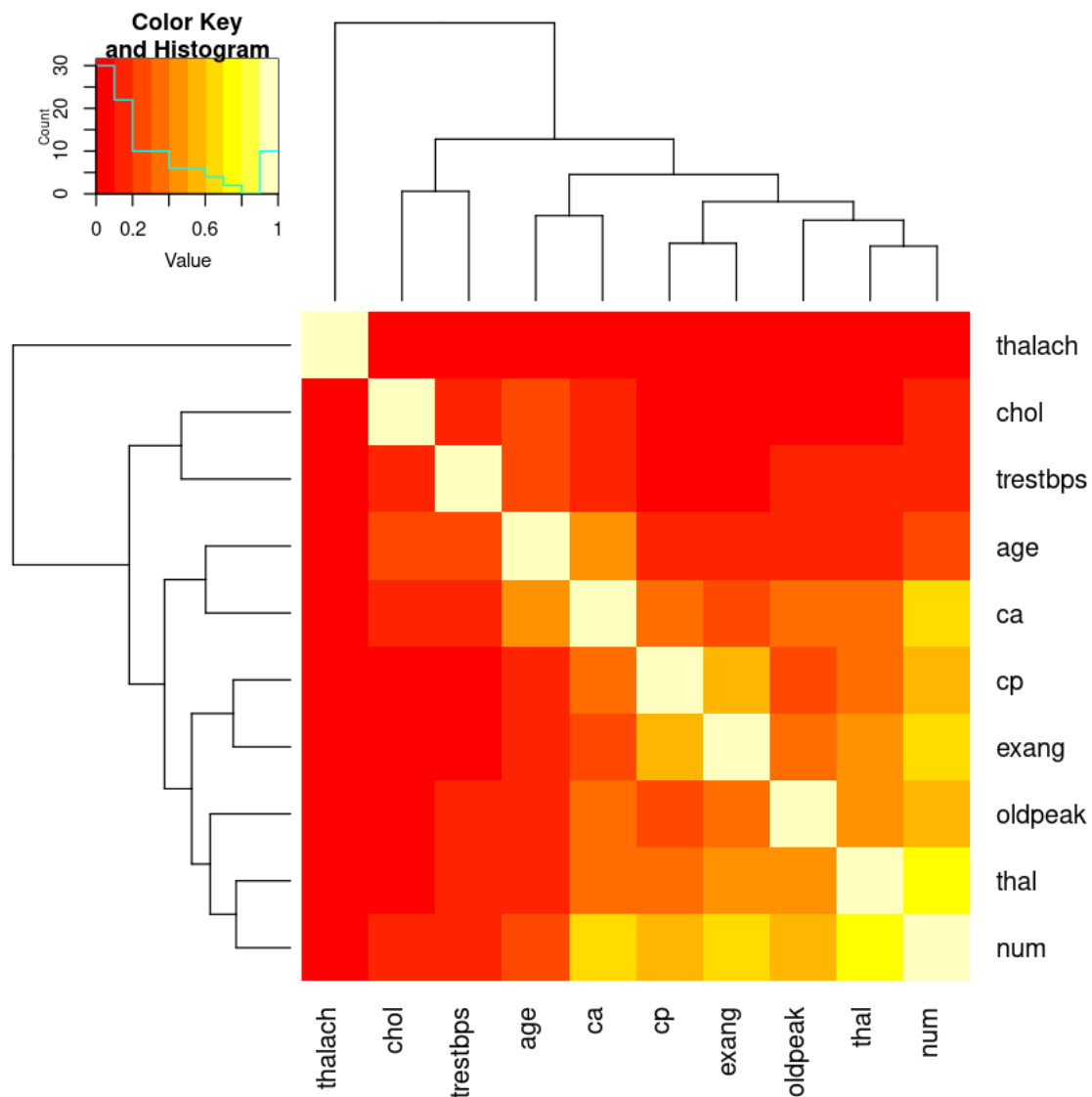
```



Checking correlations between features to get a raw idea of the bayesian-network

```
[16]: correlations_all = hetcor(data,std.err = FALSE)$correlations
```

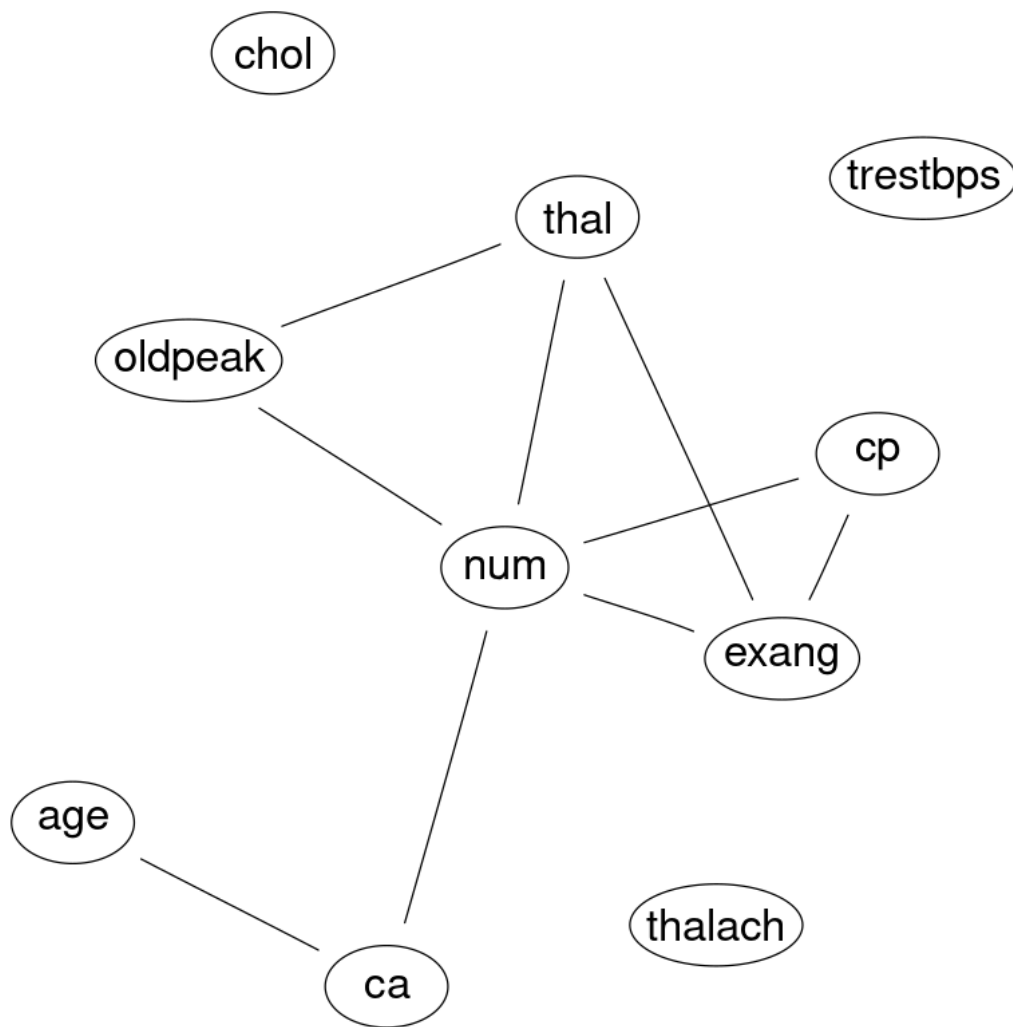
```
[17]: heatmap.2(correlations_all,scale = "none", trace = "none", revC = TRUE, breaks_
  ↪= seq(0, 1, 0.1))
```



There is definitely a cluster of variables as seen from the heatmap, same is visualized in the graph below.

```
[18]: ug = empty.graph(colnames(correlations_all))
      amat(ug) = (correlations_all > 0.4) + 0L - diag(1L, nrow(correlations_all))
      graphviz.plot(ug, layout = "fdp", shape = "ellipse")
```

Loading required namespace: Rgraphviz



0.0.2 Structure Learning

We will learn the structure of the Bayesian Network before learning the parameters. Using some information from <https://archive.ics.uci.edu/ml/datasets/Heart+Disease> one can say that these features should not change when one is changed, so adding a black-list in the network corresponding to these attributes.

```
[19]: b1 = tiers2blacklist(list("exang", c("chol", "trestbps")))
```

```
b1 = rbind(b1, c("exang", "chol"), c("chol", "exang"))
```

```
[20]: b1
```

	from	to
	chol	exang
A matrix: 4 × 2 of type chr	trestbps	exang
	exang	chol
	chol	exang

Similarly, adding a white-list for the attributes.

```
[21]: wl = matrix(c("thalach", "trestbps"), ncol = 2, byrow = TRUE, dimnames =
      ↪list(NULL, c("from", "to")))
```

```
[22]: wl
```

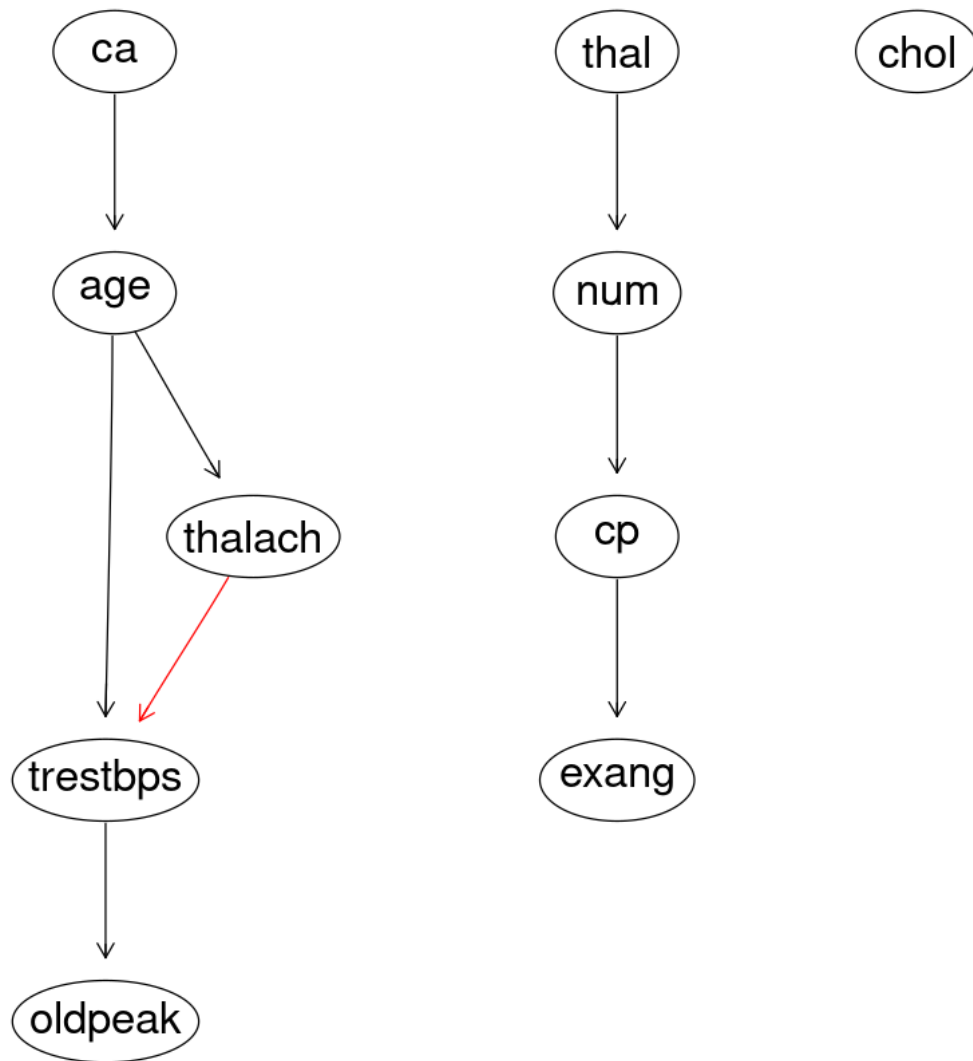
	from	to
A matrix: 1 × 2 of type chr	thalach	trestbps

```
[23]: x_data = data[, x_col_names]
```

```
[24]: data_no_na = data[complete.cases(data), ]
```

```
[25]: dag = mmhc(data_no_na, whitelist = wl, blacklist = bl)
```

```
[26]: graphviz.plot(dag, shape = "ellipse", highlight = list(arcs = wl))
```



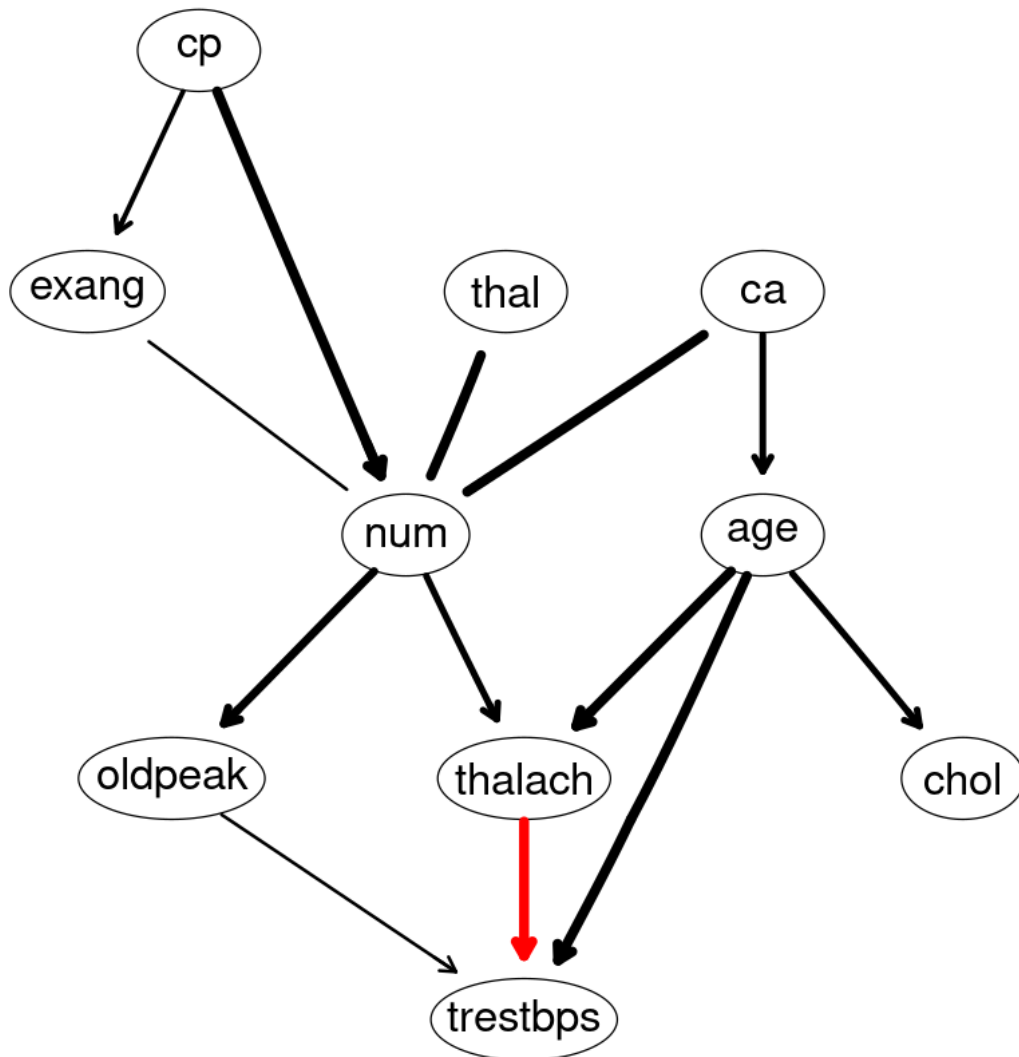
As we saw, above that some of the continuous attributes do not strictly follow the Gaussian distribution, so we use `boot.strength` to resample data using bootstrapping and to get a better representation of the bayesian-network.

```
[27]: strength = boot.strength(data_no_na, R = 200, algorithm = "hc",
                             algorithm.args = list(whitelist = wl, blacklist = bl))
```

```
[28]: avg = averaged.network(strength)
```

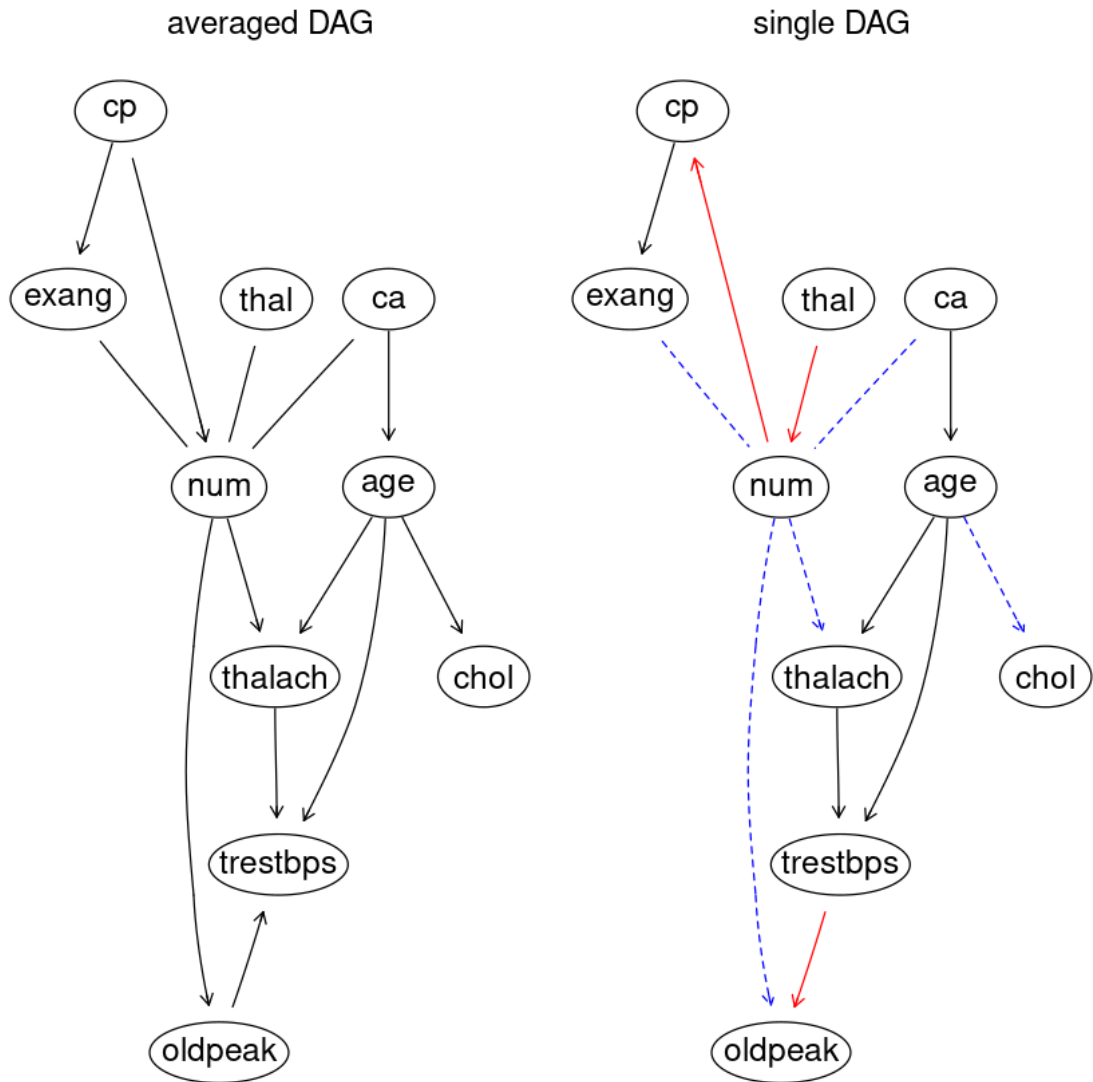
```
Warning message in averaged.network.backend(strength = strength, nodes = nodes,
:
"arc num -> cp would introduce cycles in the graph, ignoring."
```

```
[29]: strength.plot(avg, strength, shape = "ellipse", highlight = list(arcs = w1))
```



We try to compare both the networks - learned from data and learned using boot.strength

```
[30]: par(mfrow = c(1, 2))
graphviz.compare(avg, dag, shape = "ellipse", main = c("averaged DAG", "single DAG"))
```



```
[31]: compare(avg, dag)
```

```
$tp 5
```

```
$fp 3
```

```
$fn 8
```

```
[32]: compare(cpdag(avg, wlbl = TRUE), cpdag(dag, wlbl = TRUE))
```

```
$tp 7
```

```
$fp 1
```

```
$fn 6
```

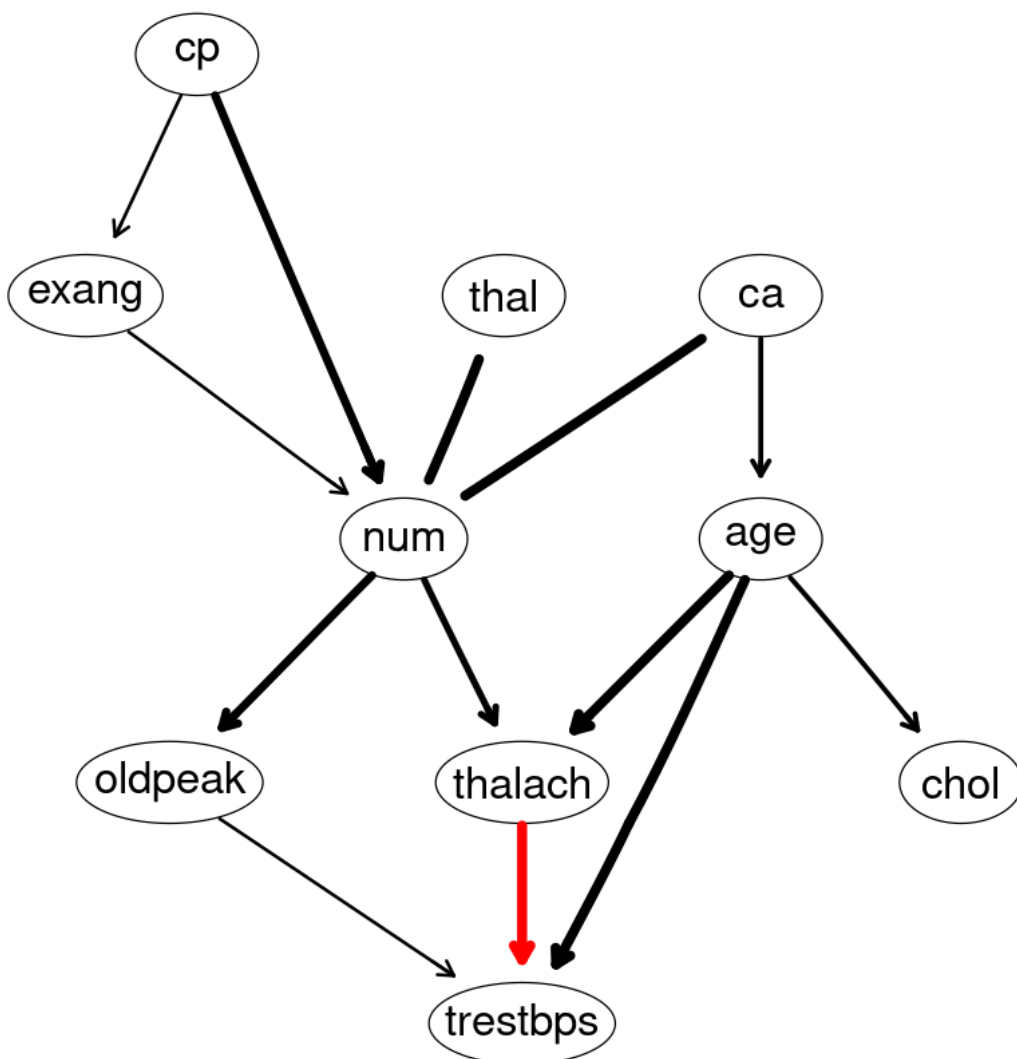
```
[33]: nrow(strength[strength$strength > 0.5 & strength$direction > 0.5, ])
```

9

```
[34]: simpler = averaged.network(strength, threshold = 0.6)
```

Warning message in averaged.network.backend(strength = strength, nodes = nodes,
:
"arc num -> cp would introduce cycles in the graph, ignoring."

```
[44]: strength.plot(simpler, strength, shape = "ellipse", highlight = list(arcs =  
↪wl), threshold = 0.6)
```




```
[47]: undirected.arcs(simpler)
```

A matrix: 4×2 of type chr

	from	to
ca	ca	num
thal	thal	num
num	num	ca
num	num	thal

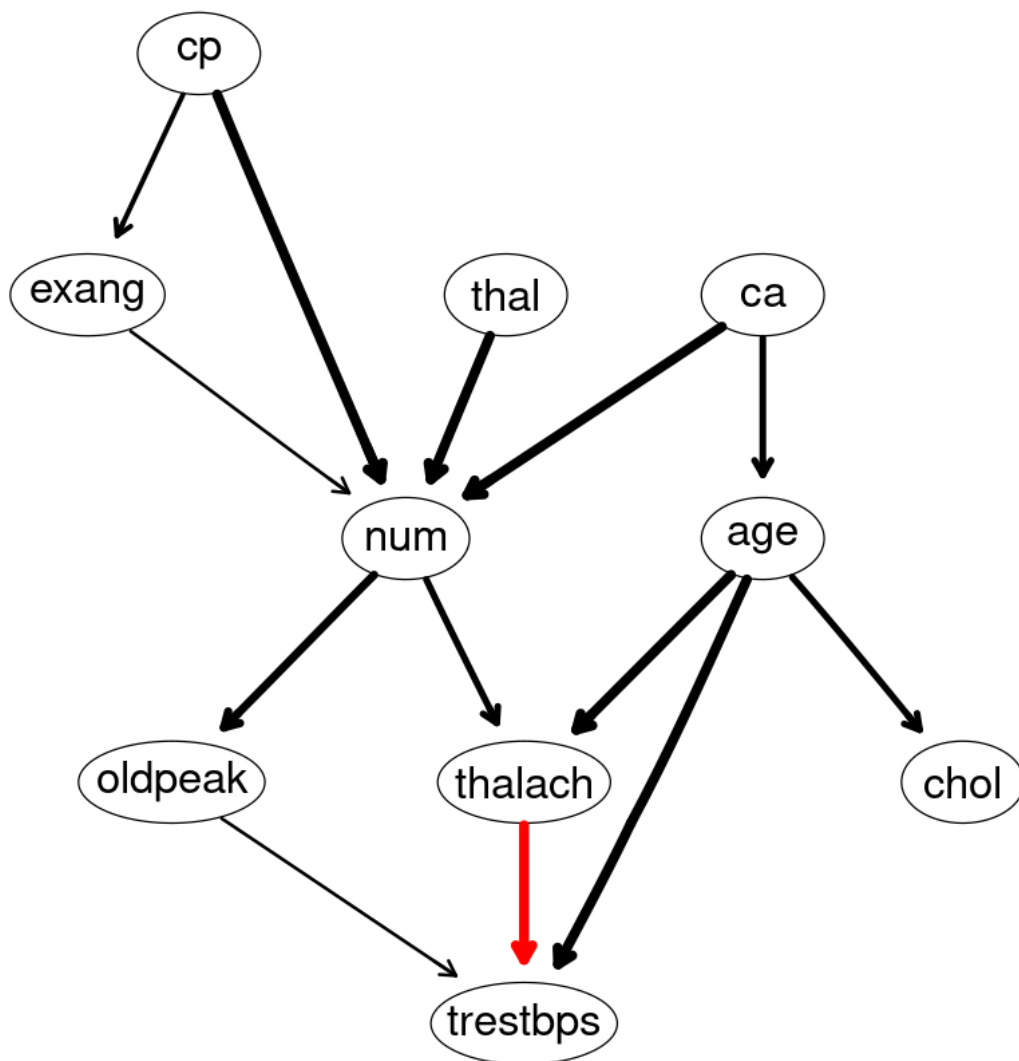
```
[48]: simpler = set.arc(simpler, from="ca", to="num")
simpler = set.arc(simpler, from="thal", to="num")
# simpler = set.arc(simpler, from="thal", to="num")
# simpler = set.arc(simpler, from="cp", to="num")
```

```
[38]: continous_col_names
discrete_col_names
```

1. 'age' 2. 'trestbps' 3. 'chol' 4. 'thalach' 5. 'oldpeak'

1. 'cp' 2. 'exang' 3. 'ca' 4. 'thal' 5. 'num'

```
[56]: strength.plot(simpler, strength, shape = "ellipse", highlight = list(arcs = wl))
```



0.0.3 Parameter Learning

[149]: fitted

Bayesian network parameters

Parameters of node age (conditional Gaussian distribution)

Conditional density: age | ca

Coefficients:

	0	1	2	3
(Intercept)	51.68391	57.47692	59.78947	59.90000

Standard deviation of the residuals:

	0	1	2	3
	9.226005	6.876381	6.576608	8.232797

Discrete parents' configurations:

	ca
0	0
1	1
2	2
3	3

Parameters of node cp (multinomial distribution)

Conditional probability table:

	1	2	3	4
	0.07744108	0.16498316	0.27946128	0.47811448

Parameters of node trestbps (Gaussian distribution)

Conditional density: trestbps | age + thalach + oldpeak

Coefficients:

(Intercept)	age	thalach	oldpeak
80.2769148	0.6055481	0.1038890	2.6972546

Standard deviation of the residuals: 16.77764

Parameters of node chol (Gaussian distribution)

Conditional density: chol | age

Coefficients:

(Intercept)	age
183.844602	1.164341

Standard deviation of the residuals: 51.005

Parameters of node thalach (conditional Gaussian distribution)

Conditional density: thalach | age + num

Coefficients:

	0	1
(Intercept)	213.9876303	159.6233506
age	-1.0524778	-0.3614196

Standard deviation of the residuals:

	0	1
	16.22507	22.61379

Discrete parents' configurations:

	num
0	0
1	1

Parameters of node exang (multinomial distribution)

Conditional probability table:

	cp				
exang	1	2	3	4	
0	0.82608696	0.91836735	0.86746988	0.45070423	
1	0.17391304	0.08163265	0.13253012	0.54929577	

Parameters of node oldpeak (conditional Gaussian distribution)

Conditional density: oldpeak | num

Coefficients:

	0	1
(Intercept)	0.598750	1.589051

Standard deviation of the residuals:

	0	1
	0.7871601	1.3050061

Discrete parents' configurations:

	num
0	0
1	1

Parameters of node ca (multinomial distribution)

Conditional probability table:

	0	1	2	3
	0.58585859	0.21885522	0.12794613	0.06734007

Parameters of node thal (multinomial distribution)

Conditional probability table:

	3	6	7
	0.55218855	0.06060606	0.38720539

Parameters of node num (multinomial distribution)

Conditional probability table:

, , exang = 0, ca = 0, thal = 3

	cp				
num	1	2	3	4	
0	0.80000000	0.96551724	0.90243902	0.86956522	
1	0.20000000	0.03448276	0.09756098	0.13043478	

, , exang = 1, ca = 0, thal = 3

	cp				
num	1	2	3	4	

```

0 1.00000000 1.00000000 1.00000000 0.60000000
1 0.00000000 0.00000000 0.00000000 0.40000000

```

```
, , exang = 0, ca = 1, thal = 3
```

```

cp
num      1      2      3      4
0 0.50000000 0.50000000 1.00000000 0.25000000
1 0.50000000 0.50000000 0.00000000 0.75000000

```

```
, , exang = 1, ca = 1, thal = 3
```

```

cp
num      1      2 3      4
0 1.00000000 1.00000000 0.00000000
1 0.00000000 0.00000000 1.00000000

```

```
, , exang = 0, ca = 2, thal = 3
```

```

cp
num      1      2      3      4
0 0.50000000 0.66666667 1.00000000 0.66666667
1 0.50000000 0.33333333 0.00000000 0.33333333

```

```
, , exang = 1, ca = 2, thal = 3
```

```

cp
num 1 2 3      4
0      0.00000000
1      1.00000000

```

```
, , exang = 0, ca = 3, thal = 3
```

```

cp
num 1 2      3      4
0      0.50000000 0.00000000
1      0.50000000 1.00000000

```

```
, , exang = 1, ca = 3, thal = 3
```

```

cp
num 1 2 3      4
0      0.00000000
1      1.00000000

```

```
, , exang = 0, ca = 0, thal = 6
```

```
cp
```

num	1	2 3	4
0	1.00000000	1.00000000	1.00000000
1	0.00000000	0.00000000	0.00000000

, , exang = 1, ca = 0, thal = 6

cp			
num	1 2 3	4	
0	0.33333333		
1	0.66666667		

, , exang = 0, ca = 1, thal = 6

cp			
num	1 2	3 4	
0	0.00000000		
1	1.00000000		

, , exang = 1, ca = 1, thal = 6

cp			
num	1 2	3	4
0	0.00000000	0.00000000	
1	1.00000000	1.00000000	

, , exang = 0, ca = 2, thal = 6

cp			
num	1 2 3	4	
0	0.00000000		
1	1.00000000		

, , exang = 1, ca = 2, thal = 6

cp			
num	1 2 3	4	
0	0.00000000		
1	1.00000000		

, , exang = 0, ca = 3, thal = 6

cp			
num	1 2 3	4	
0	0.00000000		
1	1.00000000		

, , exang = 1, ca = 3, thal = 6

```

      cp
num 1      2 3 4
    0 0.00000000
    1 1.00000000

, , exang = 0, ca = 0, thal = 7

```

```

      cp
num      1      2      3      4
    0 0.66666667 0.66666667 0.85714286 0.33333333
    1 0.33333333 0.33333333 0.14285714 0.66666667

, , exang = 1, ca = 0, thal = 7

```

```

      cp
num      1 2      3      4
    0 0.50000000 0.33333333 0.11111111
    1 0.50000000 0.66666667 0.88888889

, , exang = 0, ca = 1, thal = 7

```

```

      cp
num 1      2      3      4
    0 0.00000000 0.33333333 0.00000000
    1 1.00000000 0.66666667 1.00000000

, , exang = 1, ca = 1, thal = 7

```

```

      cp
num 1 2      3      4
    0 0.50000000 0.06250000
    1 0.50000000 0.93750000

, , exang = 0, ca = 2, thal = 7

```

```

      cp
num 1 2      3      4
    0 0.00000000 0.00000000
    1 1.00000000 1.00000000

, , exang = 1, ca = 2, thal = 7

```

```

      cp
num 1 2 3      4
    0 0.00000000
    1 1.00000000

, , exang = 0, ca = 3, thal = 7

```

```

      cp
num 1 2      3      4
  0      0.33333333 0.20000000
  1      0.66666667 0.80000000

```

```
, , exang = 1, ca = 3, thal = 7
```

```

      cp
num 1 2 3      4
  0      0.00000000
  1      1.00000000

```

```
[150]: fitted = bn.fit(simpler, data_no_na)
```

```
[151]: imputed_data = impute(fitted, data)
```

```
[152]: dim(data)
       dim(imputed_data)
```

```
1. 303 2. 10
```

```
1. 303 2. 10
```

```
[205]: imputed_data = imputed_data[sample(nrow(imputed_data)),]
```

```
[206]: test_data = tail(imputed_data,50)
       train_data = imputed_data
```

```
[207]: fitted_all = bn.fit(simpler, train_data)

       predicted_test = predict(fitted_all, node = "num", data = test_data)
       accuracy_test = sum(test_data[, "num"] == predicted_test) /
         ↳length(predicted_test)

       predicted_train = predict(fitted_all, node = "num", data = train_data)
       accuracy_train = sum(train_data[, "num"] == predicted_train) /
         ↳length(predicted_train)
```

```
[208]: accuracy_train
       accuracy_test
```

```
0.867986798679868
```

```
0.84
```