

TDDE15 - Lab 1

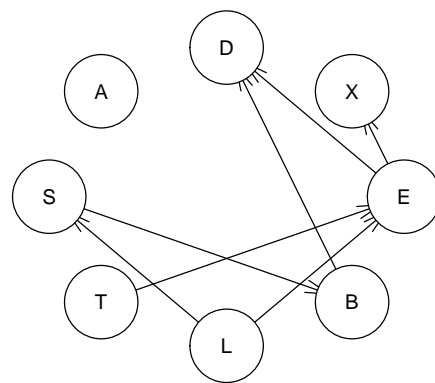
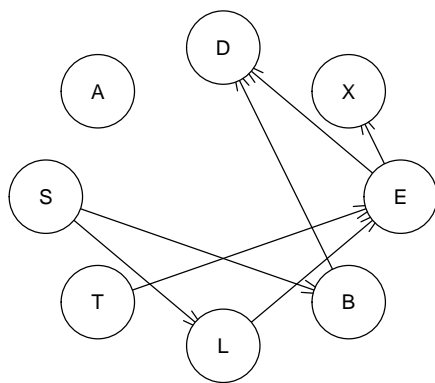
Question 1

```
library(bnlearn)
data("asia")
structure = hc(asia, restart = 3)

b=T
for (i in 1:100) {
  structure2 = hc(asia, restart = 1)
  b = all.equal(structure, structure2)
  if (b!=TRUE) {
    print("Different network found")
    break
  }
}
```

```
## [1] "Different network found"
```

```
plot(structure)
plot(structure2)
```



The HC return two different networks, because it can get trapped in a local optimum. In this case an edge is reversed, which would give the same score in the HC algorithm, therefore HC will evaluate these two networks as equal and not move between them.

Question 2

```
library(gRain)
N = dim(asia)[1]

train = asia[1:floor(N*0.8),]
test = asia[(floor(N*0.8)+1):N,]

structure = hc(train, restart = 0)

# Learn conditional probabilities given the nodes parents
fit = bn.fit(structure, data=train)

# Create Graphical independence network ( grain object )
fit_grain = as.grain(fit)

# create a junction tree and est. potential clique ( grain object )
# junc_tree = compile(fit_grain)
# print(junc_tree$cptlist)

# Remove S from test-data
test_ans = test[, "S"]
test_evid = subset(test, select = -2)

# Predict S
pred_s = c()
for (j in 1:dim(test_evid[1])) {

# Finding/evidence or potentials
# Need to extract observed values correctly.
  obs = c()
  for (i in 1:7) {
    obs = c(obs, as.character(test_evid[j,i]))
  }

  nodes_ev = names(test_evid)
  evid = setEvidence(fit_grain, nodes_ev, states = obs)

# Querygrain to get conditional distributon
  node = c("S")
  prob_s = querygrain(evid, nodes = node)

  if (prob_s$S[1]>prob_s$S[2]) {
    pred_s=c(pred_s, "no")
  }else{
    pred_s=c(pred_s, "yes")
  }
}

misc_table = table(pred_s, test_ans)

# Correct DAG
dag = model2network("[A] [S] [T|A] [L|S] [B|S] [D|B:E] [E|T:L] [X|E]")
```

```

# Learn conditional probabilities given the nodes parents
fit = bn.fit(dag, data=train)

# Create Graphical independence network ( grain object )
fit_grain = as.grain(fit)

# create a junction tree and est. potential clique ( grain object )
# junc_tree = compile(fit_grain)
# print(junc_tree$cptlist)

# Remove S from test-data
test_ans = test[, "S"]
test_evid = subset(test, select = -2)

#Predict S
pred_s = c()
for (j in 1:dim(test_evid[1])) {

# Finding/evidence or potentials
# Need to extract observed values correctly.
obs = c()
  for (i in 1:7) {
    obs = c(obs, as.character(test_evid[j,i]))
  }

nodes_ev = names(test_evid)
evid = setEvidence(fit_grain, nodes_ev, states = obs)

# Quergrain to get conditional distributon
node = c("S")
prob_s = querygrain(evid, nodes = node)

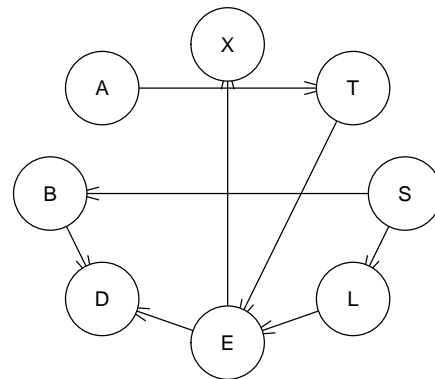
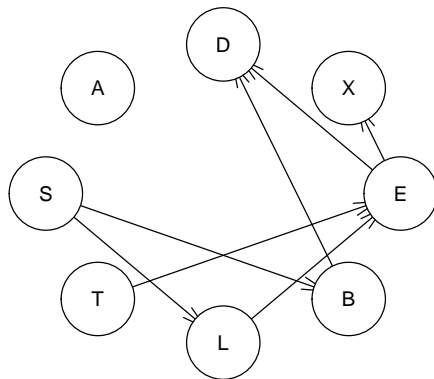
  if (prob_s$S[1]>prob_s$S[2]) {
    pred_s=c(pred_s, "no")
  }else{
    pred_s=c(pred_s, "yes")
  }
}

corr_table = table(pred_s, test_ans)

miss_class = function(conf_matr){
  return(1-sum(diag(conf_matr))/sum(conf_matr))
}

plot(structure)
plot(dag)

```



```
misc_table
```

```
##      test_ans
## pred_s no yes
##    no 358 120
##    yes 147 375
```

```
miss_class(misc_table)
```

```
## [1] 0.267
```

```
corr_table
```

```
##      test_ans
## pred_s no yes
##    no 358 120
##    yes 147 375
```

```
miss_class(corr_table)
```

```
## [1] 0.267
```

We get the same classification from the correct network. That's because "S" is independent given the Markov blanket ("B" & "L"). The subgraph containing "S", "B" and "L" is learned correctly.

Question 3

```
marc_blanc = mb(fit, node = c("S" ))
marc_blanc
```

```
## [1] "B" "L"
```

```
test_evid = subset(test_evid, select=marc_blanc)

pred_s =c()
for (j in 1:dim(test_evid[1])) {

# finding/evidence or potentials
#need to extract observed values correctly.....
  obs = c()
  for (i in 1:dim(test_evid)[2]) {
    obs = c(obs, as.character(test_evid[j,i]))
  }

  nodes_ev = names(test_evid)
  evid = setEvidence(fit_grain, nodes_ev, states = obs)
#pEvidence(evid)

# quergrain to get conditional distributon
  node = c("S")
  prob_s = querygrain(evid, nodes = node)

  if (prob_s$S[1]>prob_s$S[2]) {
    pred_s=c(pred_s,"no")
  }else{
    pred_s=c(pred_s,"yes")
  }
}

marcov_table = table(pred_s,test_ans)
misc_table
```

```
##      test_ans
## pred_s  no yes
##    no  358 120
##    yes 147 375
```

```
miss_class(misc_table)
```

```
## [1] 0.267
```

```
marcov_table
```

```
##      test_ans
## pred_s  no yes
##    no  358 120
##    yes 147 375
```

```
miss_class(marcov_table)
```

```
## [1] 0.267
```

The classification turns out to be the same. Because “S” given the marcov blanket, is independent on the rest of the variables given.

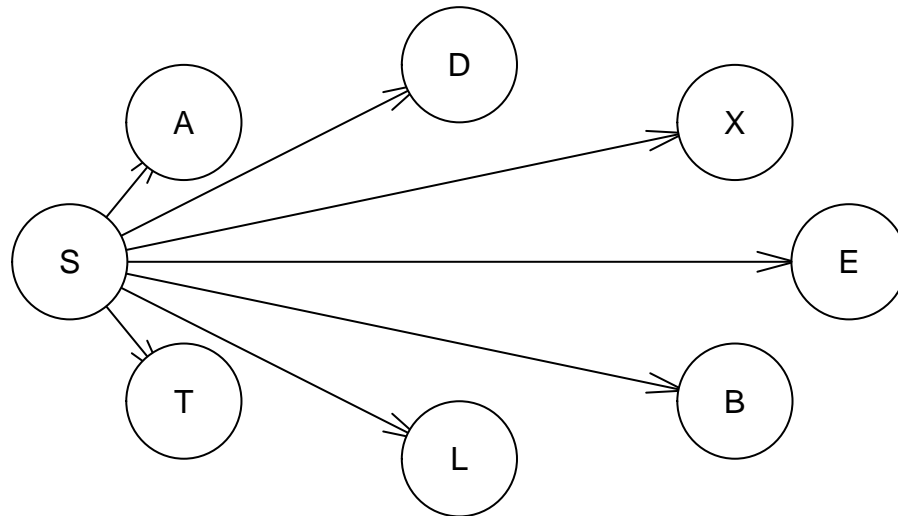
Question 4

```
N = dim(asia)[1]
train = asia[1:floor(N*0.8),]
test = asia[floor(N*0.8)+1:N,]
test_ans = test[, "S"]
test_evid = subset(test, select = -2)

#Crating an empty network
library(bnlearn)
b_net = empty.graph(names(asia))

# Adjacency matrix (0L ensures that the number is stored as an integer instead of a double)
adj = matrix(0L, ncol = 8, nrow = 8,
             dimnames = list(names(asia), names(asia)))
amat(b_net) = adj

# Add edges in BN
for (i in names(test_evid)) {
  adj["S", i] = 1L
}
amat(b_net) = adj
plot(b_net)
```



```

bn_pot = bn.fit(b_net, data=train)
bn_grain = as.grain(bn_pot)

pred_s = c()
for (j in 1:dim(test_evid[1])) {
  # finding/evidence or potentials
  obs = c()
  for (i in 1:dim(test_evid)[2]) {
    obs = c(obs, as.character(test_evid[j,i]))
  }

  nodes_ev = names(test_evid)
  evid = setEvidence(bn_grain, nodes_ev, states = obs)

  # quergrain to get conditional distributon
  node = c("S")
  prob_s = querygrain(evid, nodes = node)

  if (prob_s$S[1]>prob_s$S[2]) {
    pred_s=c(pred_s,"no")
  }else{
    pred_s=c(pred_s,"yes")
  }
}
naive_table = table(pred_s,test_ans)

```

```
misc_table
```

```
##      test_ans
## pred_s  no yes
##    no  358 120
##    yes  147 375
```

```
miss_class(misc_table)
```

```
## [1] 0.267
```

```
naive_table
```

```
##      test_ans
## pred_s  no yes
##    no  389 180
##    yes  116 315
```

```
miss_class(naive_table)
```

```
## [1] 0.296
```

Answer

The classification of the naive bayes classifier is predicting worse, with a higher missclassification rate, than the BN generated from the HC-algorithm. That is because Naive Bayes assumes that all variables are independent given “S” and that there is a possible dependence between “S” and all other variables. And in the correct DAG we saw that S is only dependent on “B” and “L”.