Bayesian Networks and Causal Inference Assignment 1 Code Notebook

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Import packages

```
library(semPlot)
library(bayesianNetworks)
library(funModeling)
library(tidyverse)
library(Hmisc)
library(bnlearn)
library(naivebayes)
library(dagitty)
library(dataPreparation)
library(lavaan)
library(summarytools)
library(OneR)
library(corrplot)
library(knitr)
library(readxl)
library(dplyr)
library(kableExtra)
```

*s1057895
†s1011065
‡s4363779

Import dataset

Assuming the "heart_failure_clinical_records_dataset.csv"-file from this Kaggle page is present in the current working directory.

```
d1=read.table("./heart_failure_clinical_records_dataset.csv", sep=',', header=TRUE)
```

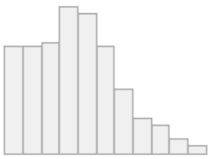
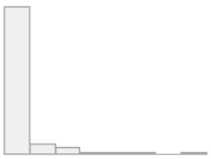
Exploration

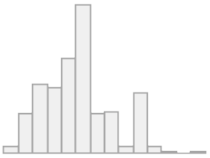
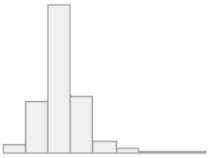
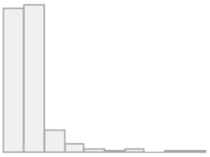
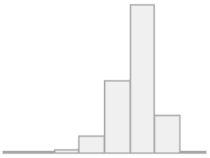
```
dfSummary(d1, plain.ascii  = FALSE,
          style        = 'grid',
          graph.magnif = 0.85,
          varnumbers = FALSE,
          valid.col    = FALSE, tmp.img.dir = "/tmp")
```

```
## temporary images written to 'C:\tmp'
```

Data Frame Summary

d1 Dimensions: 299 x 13
Duplicates: 0

Variable	Stats / Values	Freqs (% of Valid)	Graph	Missing
age [numeric]	Mean (sd) : 60.8 (11.9) min < med < max: 40 < 60 < 95 IQR (CV) : 19 (0.2)	47 distinct values		0 (0.0%)
anaemia [integer]	Min : 0 Mean : 0.4 Max : 1	0 : 170 (56.9%) 1 : 129 (43.1%)		0 (0.0%)
creatinine_phosphokinase [integer]	Mean (sd) : 581.8 (970.3) min < med < max: 23 < 250 < 7861 IQR (CV) : 465.5 (1.7)	208 distinct values		0 (0.0%)

Variable	Stats / Values	Freqs (% of Valid)	Graph	Missing
diabetes [integer]	Min : 0 Mean : 0.4 Max : 1	0 : 174 (58.2%) 1 : 125 (41.8%)		0 (0.0%)
ejection_fraction [integer]	Mean (sd) : 38.1 (11.8) min < med < max: 14 < 38 < 80 IQR (CV) : 15 (0.3)	17 distinct values		0 (0.0%)
high_blood_pressure [integer]	Min : 0 Mean : 0.4 Max : 1	0 : 194 (64.9%) 1 : 105 (35.1%)		0 (0.0%)
platelets [numeric]	Mean (sd) : 263358 (97804.2) min < med < max: 25100 < 262000 < 850000 IQR (CV) : 91000 (0.4)	176 distinct values		0 (0.0%)
serum_creatinine [numeric]	Mean (sd) : 1.4 (1) min < med < max: 0.5 < 1.1 < 9.4 IQR (CV) : 0.5 (0.7)	40 distinct values		0 (0.0%)
serum_sodium [integer]	Mean (sd) : 136.6 (4.4) min < med < max: 113 < 137 < 148 IQR (CV) : 6 (0)	27 distinct values		0 (0.0%)
sex [integer]	Min : 0 Mean : 0.6 Max : 1	0 : 105 (35.1%) 1 : 194 (64.9%)		0 (0.0%)

Variable	Stats / Values	Freqs (% of Valid)	Graph	Missing
smoking [integer]	Min : 0 Mean : 0.3 Max : 1	0 : 203 (67.9%) 1 : 96 (32.1%)		0 (0.0%)
time [integer]	Mean (sd) : 130.3 (77.6) min < med < max: 4 < 115 < 285 IQR (CV) : 130 (0.6)	148 distinct values		0 (0.0%)
DEATH_EVENT [integer]	Min : 0 Mean : 0.3 Max : 1	0 : 203 (67.9%) 1 : 96 (32.1%)		0 (0.0%)

All data is complete. Lets check data type:

```
describe(d1)  %>% html()
```

```
plot_num(d1)
```

Preprocessing

Shorten some long variable names.

```
d1 <- rename(d1, cpk = creatinine_phosphokinase)
d1 <- rename(d1, srm_creatinine = serum_creatinine)
d1 <- rename(d1, srm_sodium = serum_sodium)
```

Create extra dataset to perform processing on.

```
d1_proc = data.frame(d1)
```

Continuous and binary data Order binary variables

```
d1_proc$anaemia <- as.numeric(ordered(d1$anaemia))
d1_proc$sex <- as.numeric(ordered(d1$sex))
d1_proc$high_blood_pressure <- as.numeric(ordered(d1$high_blood_pressure))
d1_proc$diabetes <- as.numeric(ordered(d1$diabetes))
d1_proc$smoking <- as.numeric(ordered(d1$smoking))
d1_proc$DEATH_EVENT <- as.numeric(ordered(d1$DEATH_EVENT))
```

Bin all continuous Bin continuous variables using the histograms of the data to create regularly spaces bins

```
temp_age <- rep("<97", nrow(d1_proc)) #96 is max age
temp_age[d1_proc$age >=0 & d1_proc$age <50] <- "<50"
temp_age[d1_proc$age >=50 & d1_proc$age <60] <- "50-60"
temp_age[d1_proc$age >=60 & d1_proc$age <70] <- "60-70"
temp_age[d1_proc$age >=70 & d1_proc$age <80] <- "70-80"
temp_age[d1_proc$age >=80 & d1_proc$age<90] <- "80-90"
temp_age[d1_proc$age >=90] <- "90>"
#turn binned data into factor:
d1_proc$age <- ordered(temp_age, levels=c("<50","50-60","60-70","70-80","80-90",
                                          "90>"))

temp_cpk <- rep("<7862", nrow(d1_proc)) #96 is max cpk
temp_cpk[d1_proc$cpk >=0 & d1_proc$cpk <200] <- "0-200"
temp_cpk[d1_proc$cpk >=200 & d1_proc$cpk <400] <- "200-400"
temp_cpk[d1_proc$cpk >=400 & d1_proc$cpk <600] <- "400-600"
temp_cpk[d1_proc$cpk >=600 & d1_proc$cpk <800] <- "600-800"
temp_cpk[d1_proc$cpk >=800 & d1_proc$cpk <1000] <- "800-1000"
temp_cpk[d1_proc$cpk >=1000 & d1_proc$cpk <1200] <- "1000-1200"
temp_cpk[d1_proc$cpk >=1200 & d1_proc$cpk <1400] <- "1200-1400"
temp_cpk[d1_proc$cpk >=1400 & d1_proc$cpk <1600] <- "1400-1600"
temp_cpk[d1_proc$cpk >=1600 & d1_proc$cpk <1800] <- "1600-1800"
temp_cpk[d1_proc$cpk >=1800 & d1_proc$cpk <2000] <- "1800-2000"
temp_cpk[d1_proc$cpk >=2000] <- "2000>"
#turn binned data into factor:
d1_proc$cpk <- ordered(temp_cpk, levels=c("0-200", "200-400", "400-600",
                                          "600-800","800-1000","1000-1200",
                                          "1200-1400","1400-1600",
                                          "1600-1800","1800-2000",
                                          "2000>"))

temp_ef <- rep("<81", nrow(d1_proc)) #80 is max ef
temp_ef[d1_proc$ejection_fraction >=0  & d1_proc$ejection_fraction <20] <- "<20"
temp_ef[d1_proc$ejection_fraction >=20 & d1_proc$ejection_fraction <30] <- "20-30"
temp_ef[d1_proc$ejection_fraction >=30 & d1_proc$ejection_fraction <40] <- "30-40"
temp_ef[d1_proc$ejection_fraction >=40 & d1_proc$ejection_fraction <50] <- "40-50"
temp_ef[d1_proc$ejection_fraction >=50 & d1_proc$ejection_fraction <60] <- "50-60"
temp_ef[d1_proc$ejection_fraction >=60] <- "60>"
#turn binned data into factor:
d1_proc$ejection_fraction <- ordered(temp_ef, levels=c("<20","20-30","30-40",
                                                       "40-50","50-60","60>"))
```

```
temp_plt <- rep("<850k", nrow(d1_proc)) #850k is max platelets
temp_plt[d1_proc$platelets >=0  & d1_proc$platelets <50000] <- "<50k"
temp_plt[d1_proc$platelets >=50000  & d1_proc$platelets <100000] <- "50k-100k"
temp_plt[d1_proc$platelets >=100000  & d1_proc$platelets <150000] <- "100k-150k"
temp_plt[d1_proc$platelets >=150000  & d1_proc$platelets <200000] <- "150k-200k"
temp_plt[d1_proc$platelets >=200000  & d1_proc$platelets <250000] <- "200k-250k"
temp_plt[d1_proc$platelets >=250000  & d1_proc$platelets <300000] <- "250k-300k"
temp_plt[d1_proc$platelets >=300000  & d1_proc$platelets <350000] <- "300k-350k"
temp_plt[d1_proc$platelets >=350000  & d1_proc$platelets <400000] <- "350k-400k"
temp_plt[d1_proc$platelets >=400000  & d1_proc$platelets <450000] <- "400k-450k"
temp_plt[d1_proc$platelets >=450000  & d1_proc$platelets <500000] <- "450k-500k"
temp_plt[d1_proc$platelets >=500000] <- "500k>"
#turn binned data into factor
d1_proc$platelets <- ordered(temp_plt, levels=c("<50k","50k-100k","100k-150k",
                                                "150k-200k","200k-250k","250k-300k",
                                                "300k-350k","350k-400k",
                                                "400k-450k","450k-500k","500k>"))

temp_sc <- rep("<9.5", nrow(d1_proc)) #850k is max platelets
temp_sc[d1_proc$srm_creatinine >=0  & d1_proc$srm_creatinine <1.0] <- "<1.0"
temp_sc[d1_proc$srm_creatinine >=1.0  & d1_proc$srm_creatinine <1.5] <- "1.0-1.5"
temp_sc[d1_proc$srm_creatinine >=1.5  & d1_proc$srm_creatinine <2.0] <- "1.5-2.0"
temp_sc[d1_proc$srm_creatinine >=2.0  & d1_proc$srm_creatinine <2.5] <- "2.0-2.5"
temp_sc[d1_proc$srm_creatinine >=2.5  & d1_proc$srm_creatinine <3.0] <- "2.5-3.0"
temp_sc[d1_proc$srm_creatinine >=3.0  & d1_proc$srm_creatinine <3.5] <- "3.0-3.5"
temp_sc[d1_proc$srm_creatinine >=3.5  & d1_proc$srm_creatinine <4.0] <- "3.5-4.0"
temp_sc[d1_proc$srm_creatinine >=4.0] <- "4.0>"
d1_proc$srm_creatinine <- ordered(temp_sc, levels=c("<1.0","1.0-1.5","1.5-2.0",
                                                    "2.0-2.5","2.5-3.0","3.0-3.5","3.5-4.0","4.0>"))

temp_ss <- rep("<149", nrow(d1_proc)) #148 is max serum_sodium
temp_ss[d1_proc$srm_sodium >=0  & d1_proc$srm_sodium <125] <- "<125"
temp_ss[d1_proc$srm_sodium >=125  & d1_proc$srm_sodium <130] <- "125-130"
temp_ss[d1_proc$srm_sodium >=130  & d1_proc$srm_sodium <135] <- "130-135"
temp_ss[d1_proc$srm_sodium >=135  & d1_proc$srm_sodium <140] <- "135-140"
temp_ss[d1_proc$srm_sodium >=140  & d1_proc$srm_sodium <145] <- "140-145"
temp_ss[d1_proc$srm_sodium >=145] <- "145>"
d1_proc$srm_sodium <- ordered(temp_ss, levels=c("<125","125-130", "130-135",
                                                "135-140","140-145","145>"))

temp_time <- rep("<286", nrow(d1_proc)) #285 is max time
temp_time[d1_proc$time >=0  & d1_proc$time <30] <- "<30"
temp_time[d1_proc$time >=30  & d1_proc$time <60] <- "30-60"
temp_time[d1_proc$time >=60  & d1_proc$time <90] <- "60-90"
temp_time[d1_proc$time >=90  & d1_proc$time <120] <- "90-120"
temp_time[d1_proc$time >=120  & d1_proc$time <150] <- "120-150"
temp_time[d1_proc$time >=150  & d1_proc$time <180] <- "150-180"
temp_time[d1_proc$time >=180  & d1_proc$time <210] <- "180-210"
temp_time[d1_proc$time >=210  & d1_proc$time <240] <- "210-240"
temp_time[d1_proc$time >=240  & d1_proc$time <270] <- "240-270"
temp_time[d1_proc$time >=270] <- "270>"
d1_proc$time <- ordered(temp_time,  levels=c("<30","30-60","60-90","90-120",
                                             "120-150","150-180","180-210",
                                             "210-240","240-270","270>"))
```

Define model version 1

```
g1 <- graphLayout(dagitty('dag {
bb="0,0,1,1"
age [pos="0.213,0.767"]
anaemia [pos="0.913,0.191"]
cpk [pos="0.814,0.701"]
diabetes [pos="0.387,0.127"]
ejection_fraction [pos="0.526,0.237"]
DEATH_EVENT [pos="0.504,0.491"]
high_blood_pressure [pos="0.661,0.123"]
platelets [pos="0.761,0.379"]
sex [pos="0.385,0.926"]
smoking [pos="0.523,0.027"]
srm_creatinine [pos="0.677,0.933"]
srm_sodium [pos="0.128,0.495"]
time [pos="0.196,0.265"]
age -> DEATH_EVENT
anaemia -> platelets
cpk -> DEATH_EVENT
diabetes -> ejection_fraction
ejection_fraction -> DEATH_EVENT
DEATH_EVENT -> srm_sodium
DEATH_EVENT -> time
high_blood_pressure -> ejection_fraction
platelets -> DEATH_EVENT
sex -> DEATH_EVENT
smoking -> high_blood_pressure
srm_creatinine -> DEATH_EVENT
}
'))
```

Plot first model

```
plot(g1)
```

Test independent relationship of the first model using chi-squared test.

```
chi_square_test <- localTests(g1, d1_proc, type = 'cis.chisq')
top_rmsea <- chi_square_test[order(chi_square_test$p.value, decreasing = FALSE),]
knitr::kable(top_rmsea[1:10,1:4])%>%
  kable_styling(bootstrap_options = c("striped", "hover", "condensed"),latex_options = "HOLD_position")
```

	rmsea	x2	df	p.value
sex._.._.smkn	0.4428667	59.447006	1	0.0000000
cpk._.._.srm_...DEAT	0.0517796	192.718992	90	0.0000000
cpk._.._.time...DEAT	0.0662021	248.381072	154	0.0000022
srm_c._.._.srm_s...DEAT	0.0687494	126.431244	70	0.0000421
age._.._.srm_	0.0539983	65.412019	35	0.0013729
anam._.._.cpk	0.0759400	27.185334	10	0.0024341
dbts._.._.sex	0.1469911	7.438700	1	0.0063836
dbts._.._.smkn	0.1355618	6.476344	1	0.0109320
age._.._.hg___	0.0759849	13.602814	5	0.0183393
hg___._.._.time...ejc_	0.1295641	66.950393	45	0.0184953

- Sex and smoking are very dependent, research on this checks out; Men smoke way more than women.
- diabetes and sex are dependent
- diabetes and smoking are dependent

P_values not significant but somewhat high rmsea: - Death is not independent from smoking given ejection fraction. - Anaemia is not independent from serum_.. given platelets - Death is not independent from anaemia given platelets - Death is not independent from high blood pressure given ejection fraction etc.

Test conditional independencies using polychoric correlation matrix

This test serves as an extra method to compare with the chi-squared test results.

```
# Compute polychoric correlation
d1_proc_corr = lavCor(d1_proc)
```

Perform correlation tests

Highest coef estimates table Computes and plots the table ordered by estimate coefs, with the highest value first.

```
corrtest <- localTests(g1, sample.cov = d1_proc_corr, sample.nobs=nrow(d1_proc))
top_corr <- corrtest[order(corrtest$estimate,decreasing = TRUE),]
knitr::kable(top_corr[1:6,1:4])%>%
  kable_styling(bootstrap_options = c("striped", "hover", "condensed"),latex_options = "HOLD_position")
```

	estimate	p.value	2.5%	97.5%
sex._.._.smkn	0.4458917	0.0000000	0.3505396	0.5356125
age._.._.srm_	0.2663449	0.0000027	0.1576849	0.3691157
cpk._.._.time...DEAT	0.1853698	0.0012771	0.0732929	0.2929712
ejc_._.._.srm_...DEAT	0.1564557	0.0067391	0.0436102	0.2654492
age._.._.hg___	0.0962893	0.0965585	-0.0173303	0.2074798
DEAT._.._.hg___...ejc_	0.0908136	0.1177979	-0.0230450	0.2023694

Lowest coef estimates table Computes and plots the table ordered by estimate coefs, with the lowest value first.

```
down_corr <- corrtest[order(corrtest$estimate,decreasing = FALSE),]
knitr::kable(down_corr[1:6,1:4])%>%
  kable_styling(bootstrap_options = c("striped", "hover", "condensed"),latex_options = "HOLD_position")
```

	estimate	p.value	2.5%	97.5%
anam._.._.cpk	-0.2418198	0.0000219	-0.3461102	-0.1320132
srm_c._.._.srm_s...DEAT	-0.2272203	0.0000713	-0.3325441	-0.1166115
hg___._.._.time...ejc_	-0.2102628	0.0002463	-0.3165454	-0.0990080
hg___._.._.time...DEAT	-0.1971350	0.0006018	-0.3041265	-0.0854280
ejc_._.._.srm_	-0.1865432	0.0011645	-0.2939081	-0.0746935
dbts._.._.sex	-0.1577295	0.0062091	-0.2664854	-0.0451062

Positive correlations - Similar to the chi-squared test, sex and smoking are strongly correlated. - Creatine phosphokinase shows correlation with time and death_event. - Age and serum creatine also show significant correlations.

Negative correlations - Many given time, are negatively correlated - Anaemia and creatine-pk show negative correlation - Age and creatine-cpk - diabetes and sex

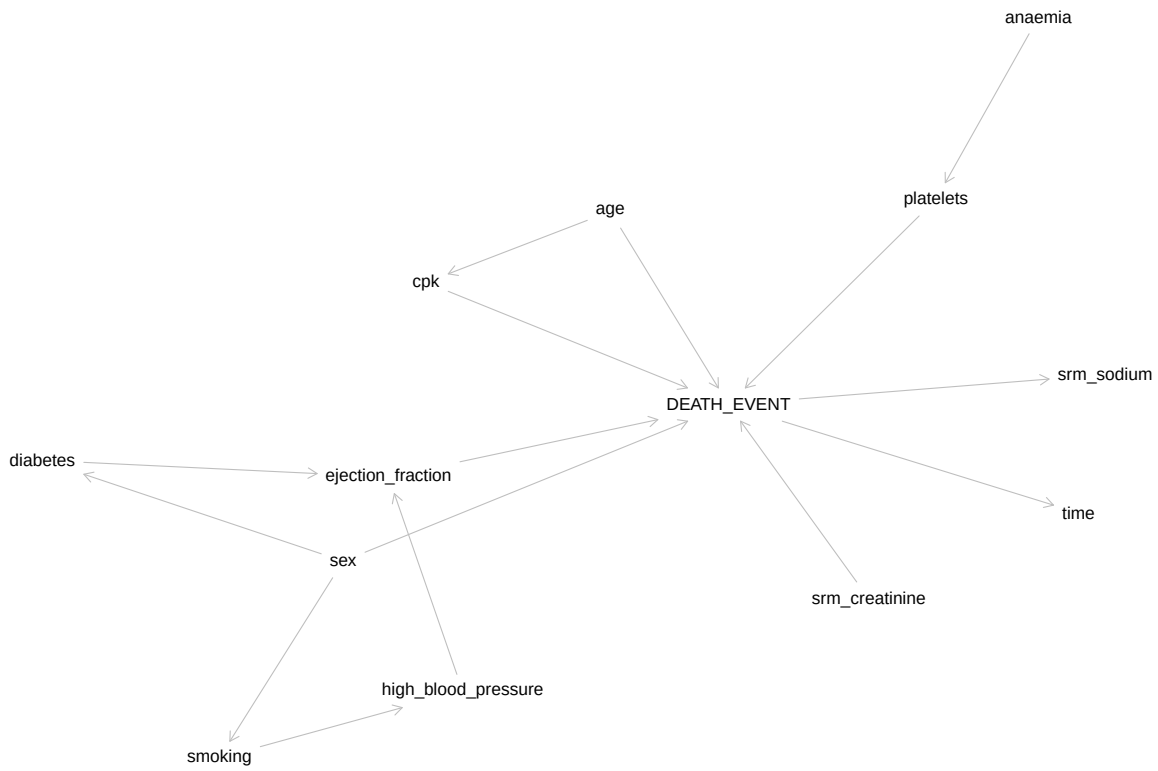
Define intermediate model with sex based changes.

Create dependencies in network for the implied gender relationships.

```
g2 <- graphLayout(dagitty('dag {
bb="0,0,1,1"
age [pos="0.213,0.767"]
anaemia [pos="0.913,0.191"]
cpk [pos="0.814,0.701"]
diabetes [pos="0.387,0.127"]
ejection_fraction [pos="0.526,0.237"]
DEATH_EVENT [pos="0.504,0.491"]
high_blood_pressure [pos="0.661,0.123"]
platelets [pos="0.761,0.379"]
sex [pos="0.385,0.926"]
smoking [pos="0.523,0.027"]
srm_creatinine [pos="0.677,0.933"]
srm_sodium [pos="0.128,0.495"]
time [pos="0.196,0.265"]
age -> DEATH_EVENT
age -> cpk
cpk -> DEATH_EVENT
diabetes -> ejection_fraction
ejection_fraction -> DEATH_EVENT
DEATH_EVENT -> srm_sodium
DEATH_EVENT -> time
high_blood_pressure -> ejection_fraction
anaemia -> platelets
platelets -> DEATH_EVENT
sex -> DEATH_EVENT
smoking -> high_blood_pressure
srm_creatinine -> DEATH_EVENT
sex -> smoking
sex -> diabetes
}
'))
```

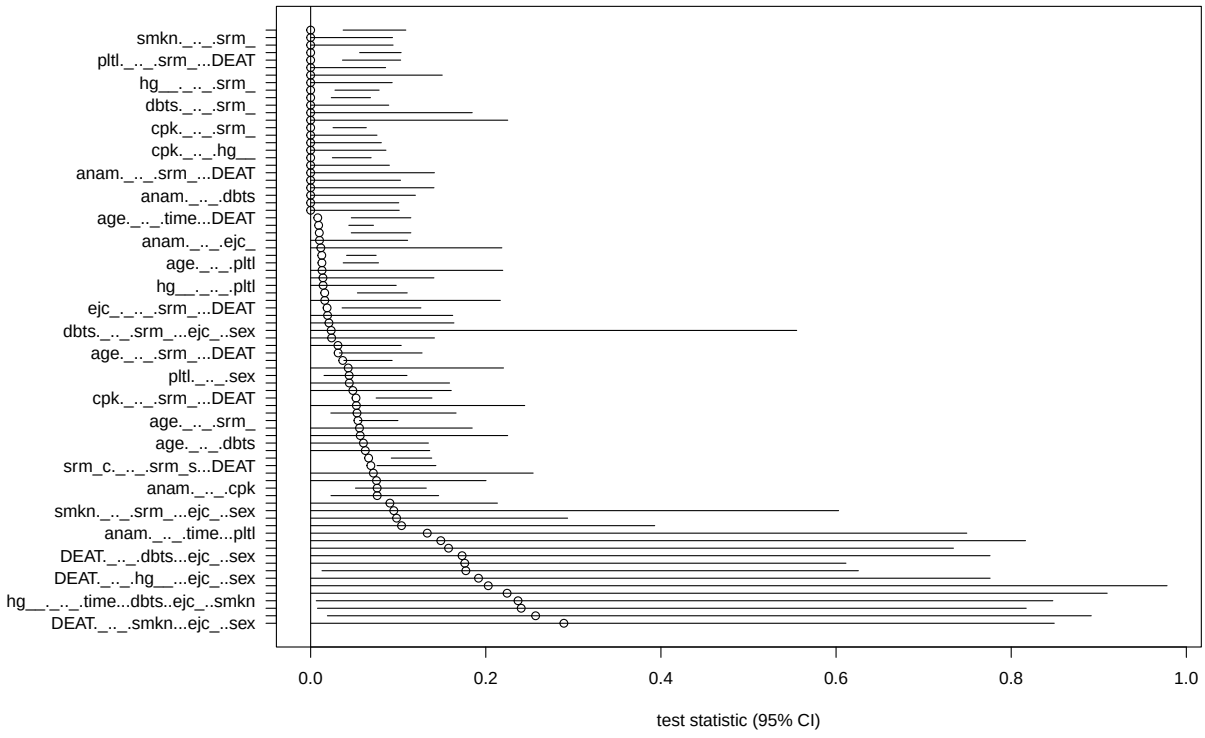
Plot intermediate model

```
plot(g2)
```



Test independent relationship of the intermediate model using chi-squared test.

```
chi_square_test <- localTests(g2, d1_proc, type = 'cis.chisq')
plotLocalTestResults(chi_square_test)
```




```
top_rmsea <- chi_square_test[order(chi_square_test$p.value, decreasing = FALSE),]
knitr::kable(top_rmsea[1:10,1:4])%>%
  kable_styling(bootstrap_options = c("striped", "hover", "condensed"),latex_options = "HOLD_position")
```

	rmsea	x2	df	p.value
cpk.__.._.srm_...DEAT	0.0517796	192.71899	90	0.0000000
cpk.__.._.time...DEAT	0.0662021	248.38107	154	0.0000022
srm_c.__.._.srm_s...DEAT	0.0687494	126.43124	70	0.0000421
age.__.._.srm_	0.0539983	65.41202	35	0.0013729
DEAT.__.._.hg___...dbts..ejc_..smkn	0.2568963	36.42911	15	0.0015324
anam.__.._.cpk	0.0759400	27.18533	10	0.0024341
DEAT.__.._.smkn...ejc_..sex	0.2891601	20.93410	8	0.0073246
age.__.._.hg___	0.0759849	13.60281	5	0.0183393
hg___.__.._.time...dbts..ejc_..smkn	0.2368054	127.40332	99	0.0287913
ejc_.__.._.sex...dbts..hg___	0.0715987	29.75973	19	0.0549370

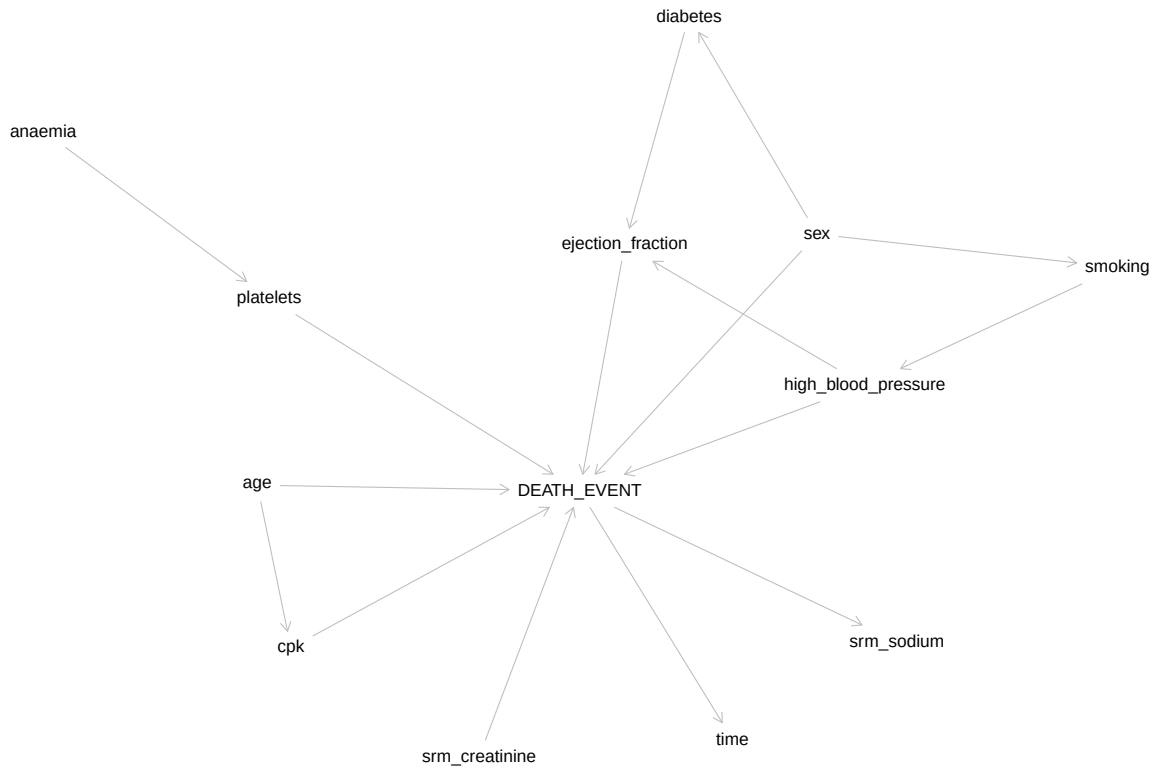
Results of the test suggest a significant dependence relationship between high blood pressure and death.

Define final model

```
g3 <- graphLayout(dagitty('dag {
bb="0,0,1,1"
age [pos="0.213,0.767"]
anaemia [pos="0.913,0.191"]
cpk [pos="0.814,0.701"]
diabetes [pos="0.387,0.127"]
ejection_fraction [pos="0.526,0.237"]
DEATH_EVENT [pos="0.504,0.491"]
high_blood_pressure [pos="0.661,0.123"]
platelets [pos="0.761,0.379"]
sex [pos="0.385,0.926"]
smoking [pos="0.523,0.027"]
srm_creatinine [pos="0.677,0.933"]
srm_sodium [pos="0.128,0.495"]
time [pos="0.196,0.265"]
age -> DEATH_EVENT
age -> cpk
cpk -> DEATH_EVENT
diabetes -> ejection_fraction
ejection_fraction -> DEATH_EVENT
DEATH_EVENT -> srm_sodium
DEATH_EVENT -> time
high_blood_pressure -> ejection_fraction
anaemia -> platelets
platelets -> DEATH_EVENT
sex -> DEATH_EVENT
smoking -> high_blood_pressure
srm_creatinine -> DEATH_EVENT
sex -> smoking
sex -> diabetes
high_blood_pressure -> DEATH_EVENT
}
'))
```

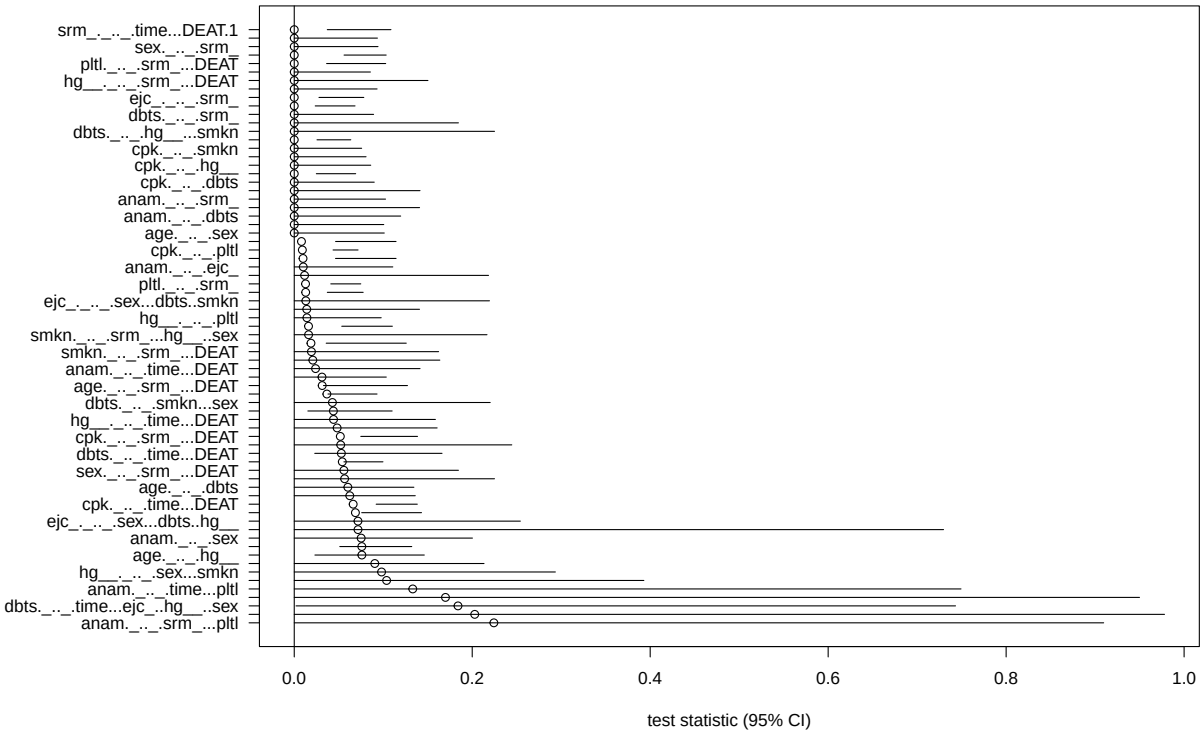
Plot final model

```
plot(g3)
```



Test independent relationship of the final model using chi-squared test.

```
chi_square_test <- localTests(g3, d1_proc, type = 'cis.chisq')
plotLocalTestResults(chi_square_test)
```




```
top_rmsea <- chi_square_test[order(chi_square_test$p.value, decreasing = FALSE),]
knitr::kable(top_rmsea[1:10,1:4])%>%
  kable_styling(bootstrap_options = c("striped", "hover", "condensed"),latex_options = "HOLD_position")
```

	rmsea	x2	df	p.value
cpk._.._.srm_...DEAT	0.0517796	192.718992	90	0.0000000
cpk._.._.time...DEAT	0.0662021	248.381072	154	0.0000022
srm_c._.._.srm_s...DEAT	0.0687494	126.431244	70	0.0000421
age._.._.srm_	0.0539983	65.412019	35	0.0013729
anam._.._.cpk	0.0759400	27.185334	10	0.0024341
age._.._.hg__	0.0759849	13.602814	5	0.0183393
ejc_._.._.sex...dbts..hg__	0.0715987	29.759733	19	0.0549370
age._.._.anam	0.0624170	10.804868	5	0.0553891
anam._.._.smkn	0.0905209	3.441822	1	0.0635656
age._.._.dbts	0.0602549	10.409667	5	0.0644256

Little significant high RMSEA test remain using this model. Therefore, we will use this model to fit our SEM using the polychoric correlation matrix and analyse it's path coefficients.

Fitting SEM using binned catagorical polychoric correlation matrix

```
# Define SEM model in lavaan syntax
sem_model <- "
            srm_sodium~DEATH_EVENT
            time~DEATH_EVENT
            DEATH_EVENT~age
            cpk~age
            platelets~anaemia
            DEATH_EVENT~cpk
            ejection_fraction~diabetes
            DEATH_EVENT~ejection_fraction
            DEATH_EVENT~high_blood_pressure
            ejection_fraction~high_blood_pressure
            DEATH_EVENT~platelets
            DEATH_EVENT~sex
            diabetes~sex
            smoking~sex
            high_blood_pressure~smoking
            DEATH_EVENT~srm_creatinine
           "

# Fit SEM
fit <- sem(sem_model, sample.cov = d1_proc_corr, sample.nobs = nrow(d1_proc), fixed.x = FALSE)

# Plot SEM network without exogenous covariances, minimum coef values of 0.1 and no residuals.
semPaths(fit, what="est", whatLabels = "par", style = "OpenMx", layout = "tree2",
         residuals = FALSE, nCharNodes=0, edge.label.cex = 1.5, asize = 6,
         sizeMan = 12,sizeMan2 = 5,minimum = 0.1,curvature = 1.5,
         rotation=1,curve=2, exoCov=FALSE)
```