Project 9

Richard Affolter

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Difficulty of this project: **2**

Problem 23: d-separation

For the following Bayesian network

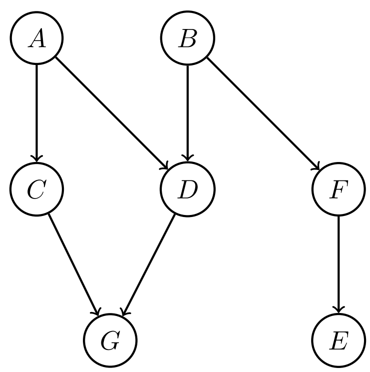


Figure 1

(i) Write down all the variables that are d-separated from A given $\{C, D\}$.

- $A \perp G \mid \{C, D\}$

(ii) Which of the following statements are true? If false, please explain why

- (a) B is conditionally independent of C given D
  FALSE, B is not d-separated from C given D. We have an active path C-A-D-B.
  Also we have

$$\begin{aligned} P(B, C|D) &= \frac{P(B, C, D)}{P(D)} \\ &= \frac{\sum_A P(A) \cdot P(B) \cdot P(C|A) \cdot P(D|A, B)}{\sum_A \sum_B P(D|A, B)} \end{aligned}$$

  in general this does not factorize to the product $P(B|D) \cdot P(C|D)$.

- (b) G is conditionally independent of E given D
  FALSE we have an active path G-C-A-D-B-F-E

- (c) C is conditionally independent of F given A.
  TRUE C is d-separated from F given A.

- (d) C is conditionally independent of E given its Markov blanket (of C).
  TRUE we have $MB(C) = \{A, D, G\}$, and C is d-separated from E given $\{A, D, G\}$.

Problem 24: Testing for marginal correlation

The covariance between two random variables X and Y captures their linear relationship, and is defined as $\text{Cov}(X,Y) := \mathbb{E}[(X - \mathbb{E}[X])(Y - \mathbb{E}[Y])]$. Their correlation $\rho_{X,Y} := \frac{\text{Cov}(X,Y)}{\sqrt{\text{Var}X\text{Var}Y}}$ is merely their covariance scaled by the product of their respective standard deviations. Note that for a multivariate normal distribution, uncorrelated variables are independent. However, it is important to keep in mind that this implication does not hold in general

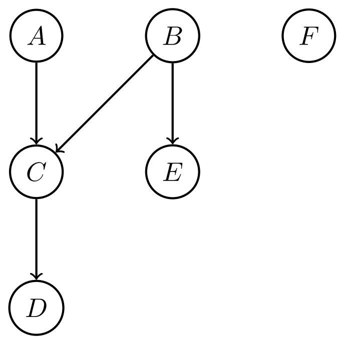
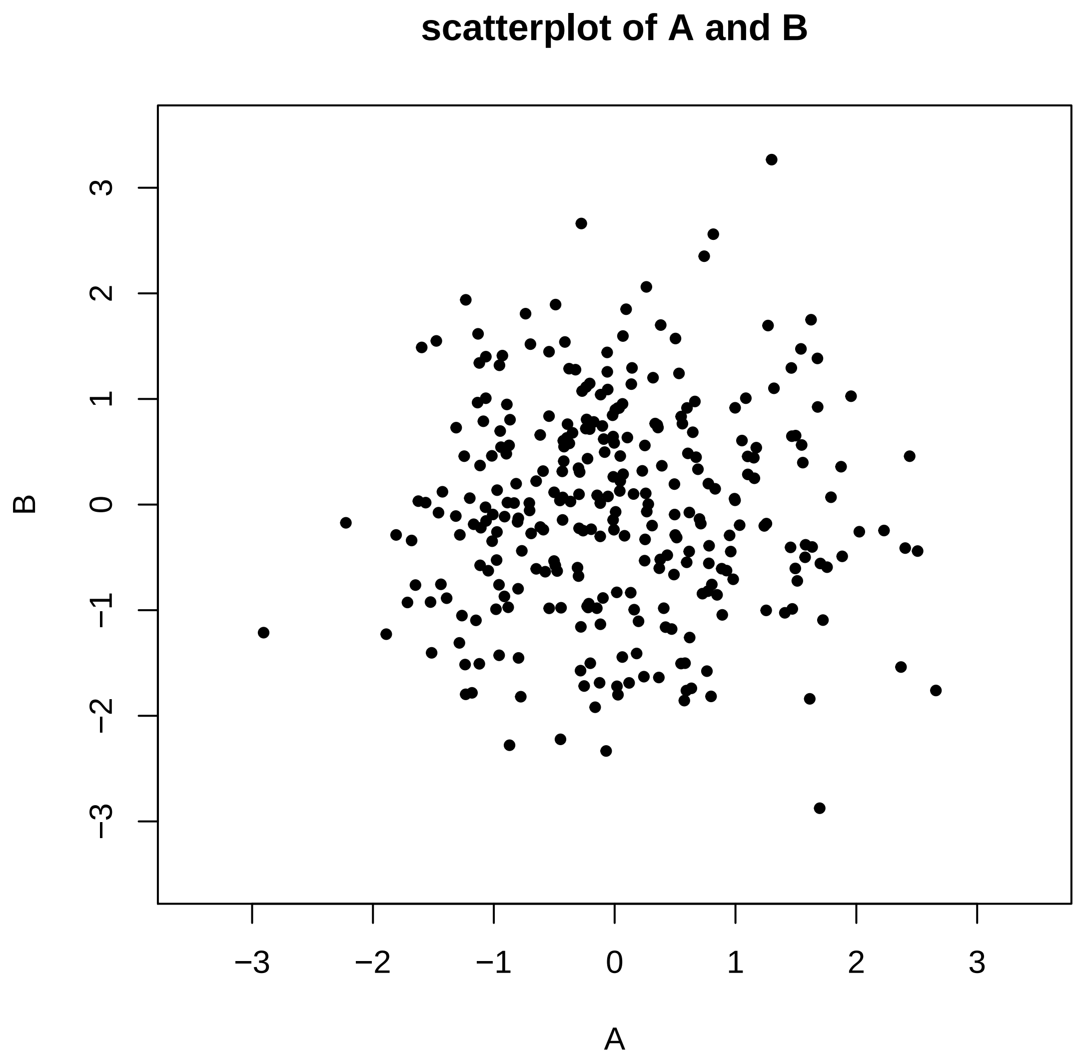


Figure 2

Using the data from `MVN_DAG.rds`, display the observations of A and B in a scatterplot. What does the plot suggest about their (marginal) correlation? Does it agree with Figure 2? Use the function `cor.test()` to test the null hypothesis of no correlation between A and B. What is your conclusion?

```
data = readRDS("MVN_DAG.rds")
plot(data$A, data$B, xlab = "A", ylab = "B", main = "scatterplot of A and B",
     xlim = c(-3.5,3.5), ylim = c(-3.5,3.5), pch=20)
```



The scatterplot suggests that there is no marginal covariance and therefore also no marginal correlation between A and B. This is also in agreement with Figure 2, since there is also marginal independence between A and B.

We can test this null-hypothesis (no correlation between A and B) with `cor.test()`:

```
cor.test(data$A, data$B)
```

```
##
##  Pearson's product-moment correlation
##
## data:  data$A and data$B
## t = 0.20194, df = 298, p-value = 0.8401
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.1016784  0.1247727
## sample estimates:
```

```
##        cor
## 0.01169715
```

We can see that our p-value (0.8401) is over the significance level $\alpha = 0.05$. Therefore we cannot reject the null-hypothesis.

So my conclusion is that A and B are (marginally) independent.

Problem 25: Testing for partial correlation

The partial correlation between two random variables X and Y given a random variable Z is

$$\rho_{X,Y|Z} = \frac{\rho_{X,Y} - \rho_{X,Z}\rho_{Y,Z}}{\sqrt{(1-\rho^2_{X,Z})(1-\rho^2_{Y,Z})}}$$

Alternatively, the partial correlation $\rho_{X,Y|Z}$ equals the correlation between residuals from the linear regressions of X on Z, and Y on Z, respectively. We will now compute the partial correlation $\rho_{A,B|C}$ to assess the association between A and B given C as follows:

- Linearly regress A on C (that is, with A as the response variable and C as the explanatory variable). Compute and store the residuals.

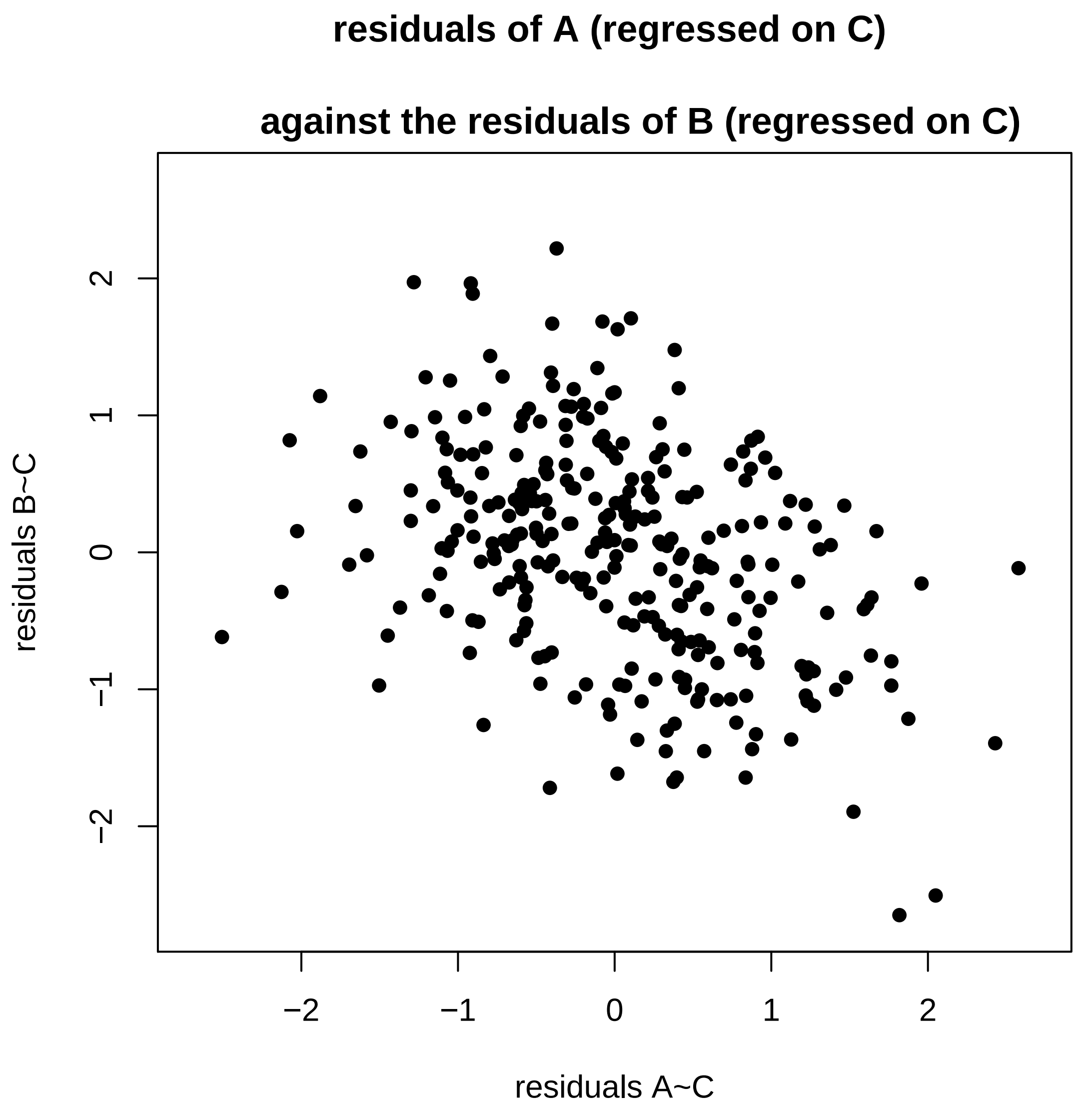
```r
lmFit = lm(A ~ C, data = data)
res_AC= residuals(lmFit)
```

- Linearly regress B on C. Compute and store the residuals.

```r
lmFit = lm(B ~ C, data = data)
res_BC= residuals(lmFit)
```

- Plot the residuals of A (regressed on C) against the residuals of B (regressed on C). What do you see?

```r
plot(res_AC, res_BC, xlab = "residuals A~C", ylab = "residuals B~C",
     main = "residuals of A (regressed on C) \n
     against the residuals of B (regressed on C)",
     xlim = c(-2.7,2.7), ylim = c(-2.7,2.7), pch=16)
```



There seems to be a negative correlation between the residuals of A (regressed on C) against the residuals of B (regressed on C). Higher residuals of A tend to be lower residuals of B. This indicates that the partial correlation $\rho_{A,B|C}$ is negative as well.

- Use the function `cor.test()` to test the null hypothesis of no correlation between the residuals of A (regressed on C) and the residuals of B (regressed on C). What is your conclusion? Does this agree with your expectation based on the underlying DAG in Figure 2?

```
cor.test(res_AC, res_BC)
```

```
##
##  Pearson's product-moment correlation
##
## data:  res_AC and res_BC
## t = -7.5173, df = 298, p-value = 6.6e-13
## alternative hypothesis: true correlation is not equal to 0
```

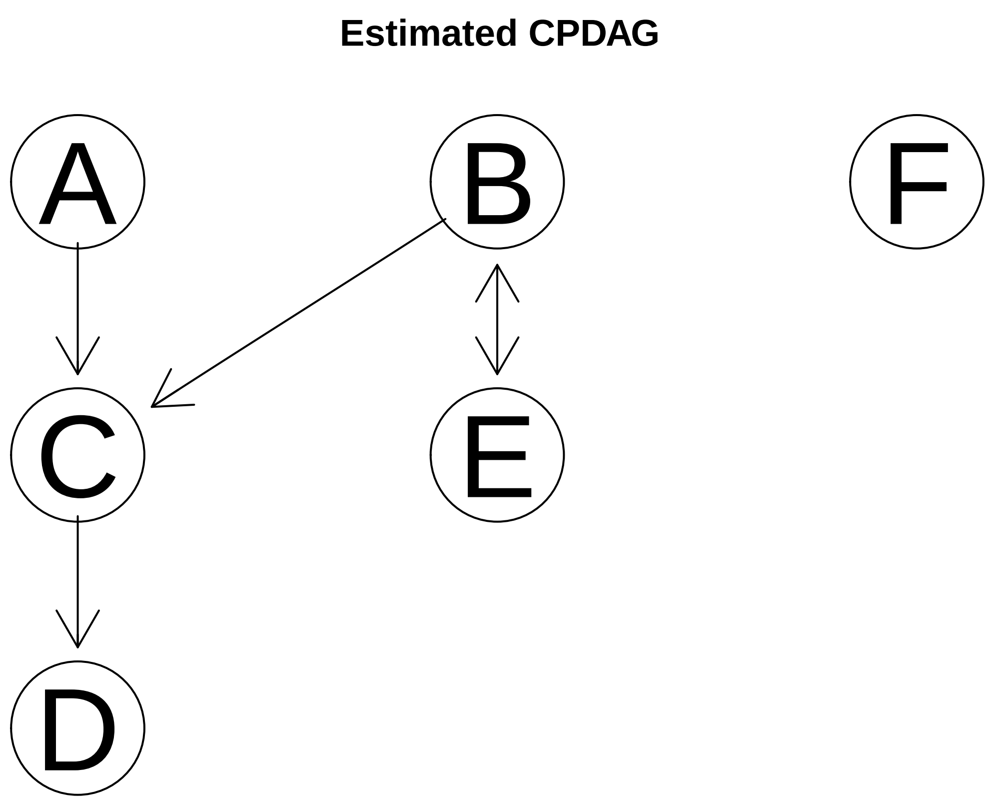
```
## 95 percent confidence interval:
##  -0.4903245 -0.2995546
## sample estimates:
##        cor
## -0.3992521
```

We can see that our p-value ($6.6 \cdot 10^{-13}$) is smaller than the significance level $\alpha = 0.05$. Therefore we reject the null-hypothesis. There is a negative correlation between the residuals. This leads to the conclusion, that there is a partial correlation $\rho_{A,B|C}$. This is also in agreement with figure 2. We can see that A is not d-separated from B given C.

Problem 26: Running the PC algorithm

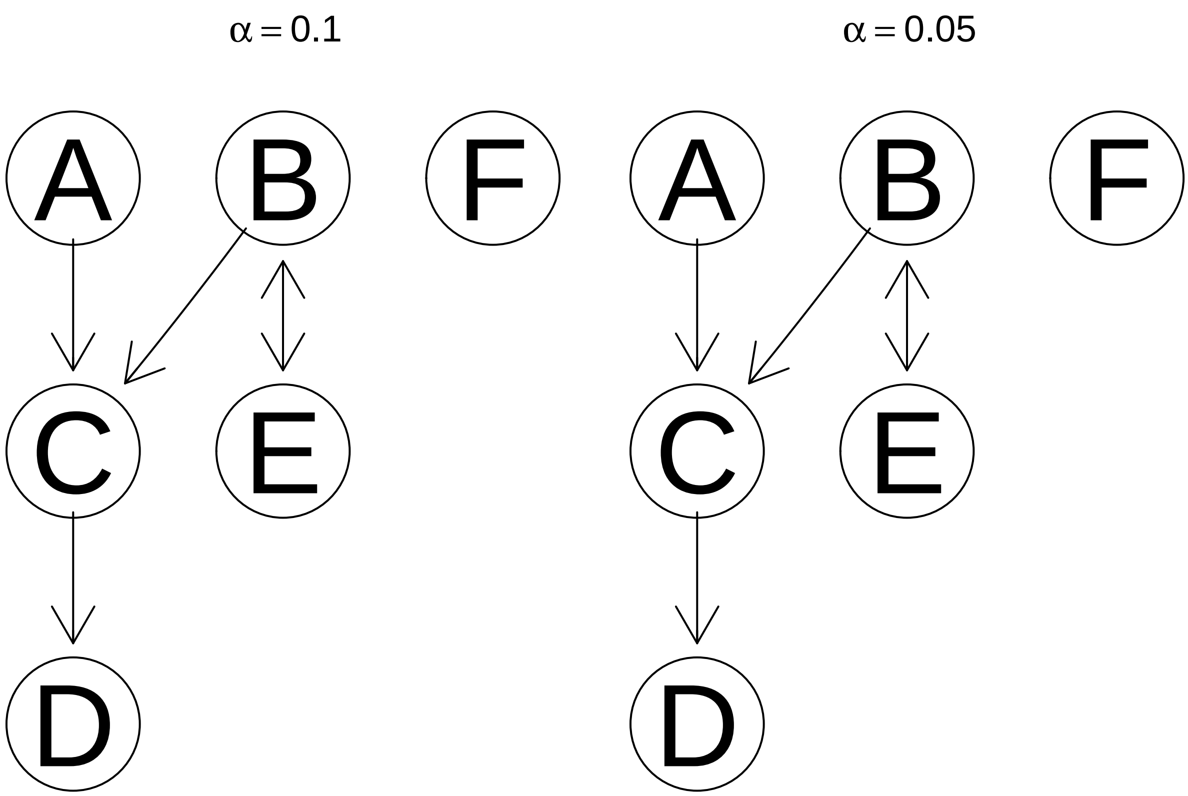
Install and load the `R` package `pcalg`. Use the function `pc()` to run the PC algorithm on the data in `MVN_DAG.rds`, and plot the result. Does the algorithm successfully learn the structure of the data-generating graph in Figure 2? How is the result affected by the significance level α for the conditional independence tests?

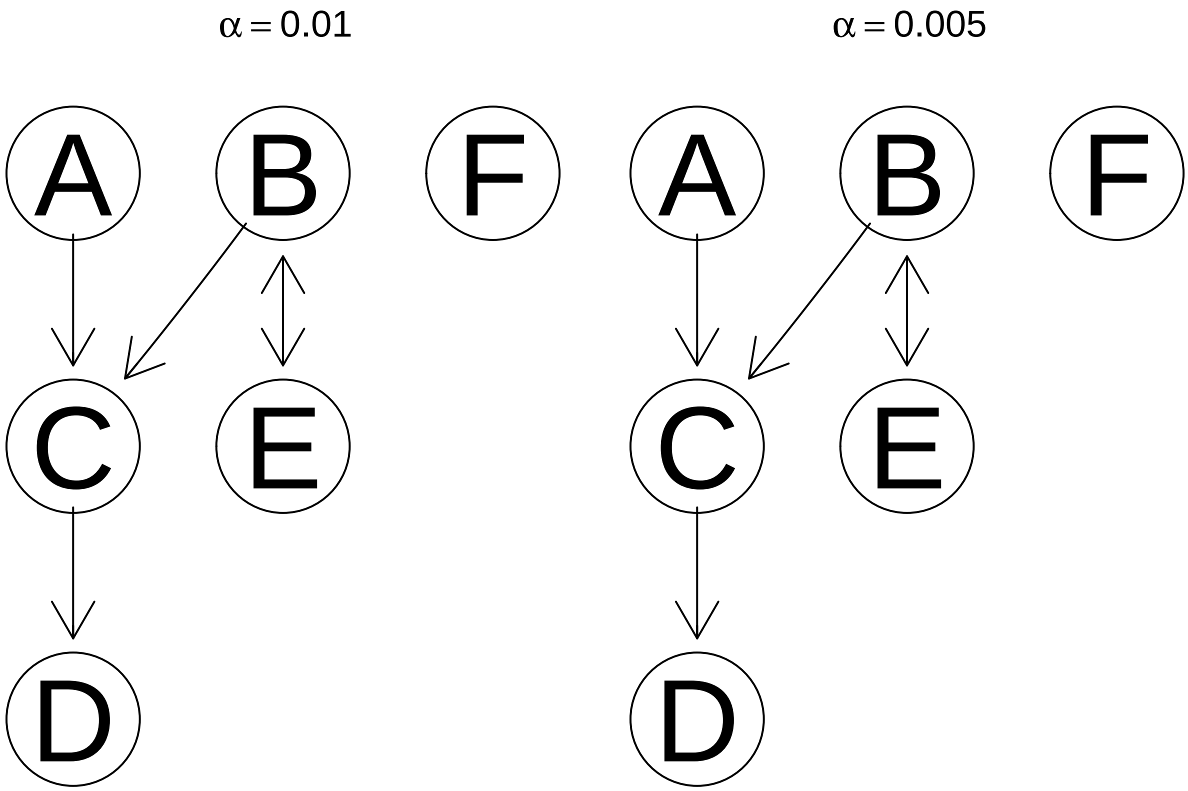
```
library(pcalg)
C = cor(data)
n = dim(data)[1]
pc.fit = pc(suffStat = list(C=C,n=n), indepTest = gaussCItest, alpha = 0.05,
            labels = colnames(data))

plot(pc.fit, main = "Estimated CPDAG")
```

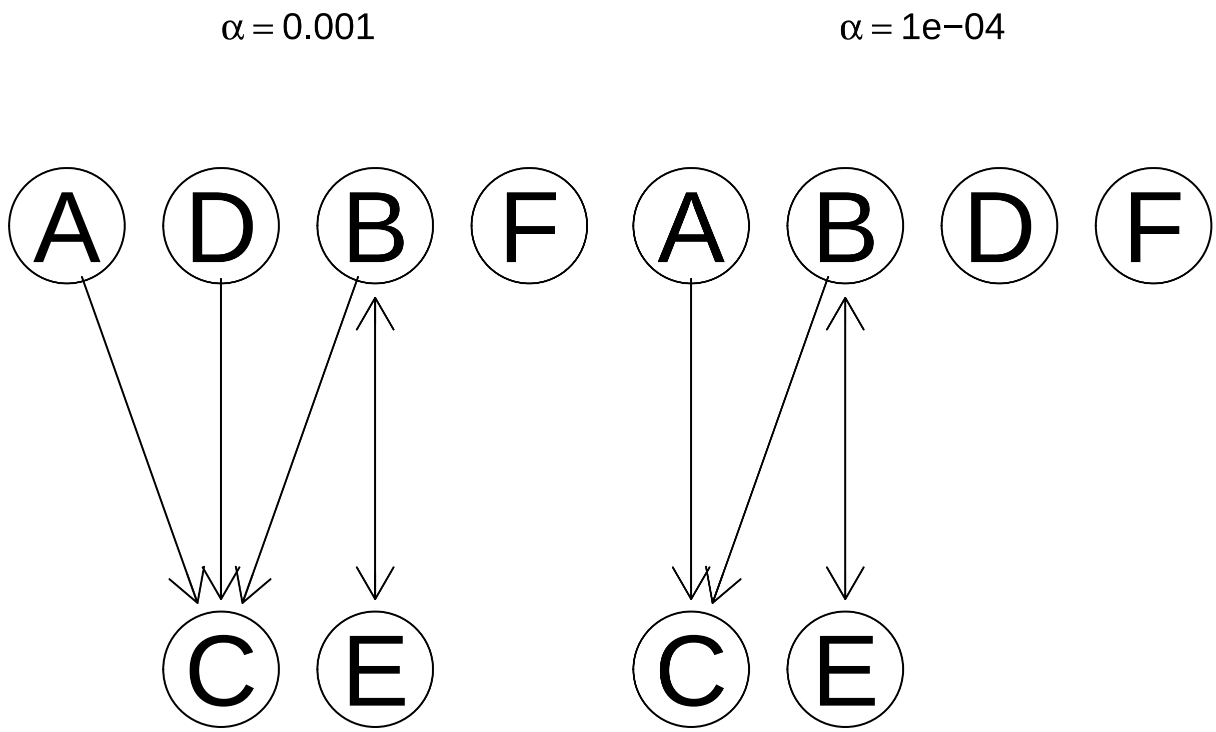


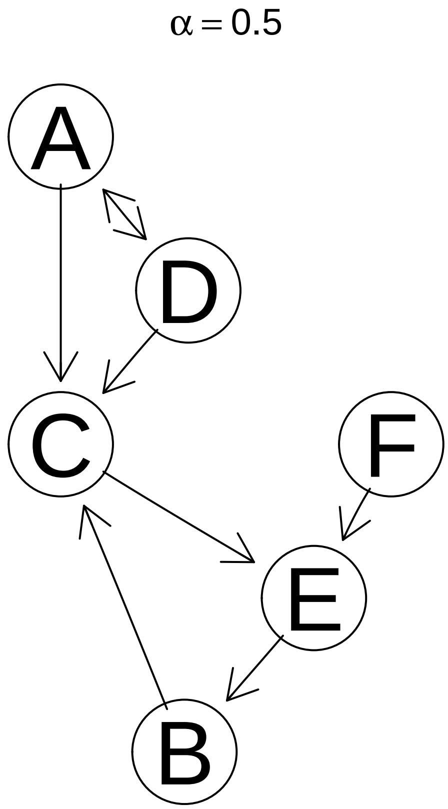
We can see that the algorithm successfully learns the structure of the data-generating graph in figure 2. The only discrepancy is that the edge between B and E is now undirected.

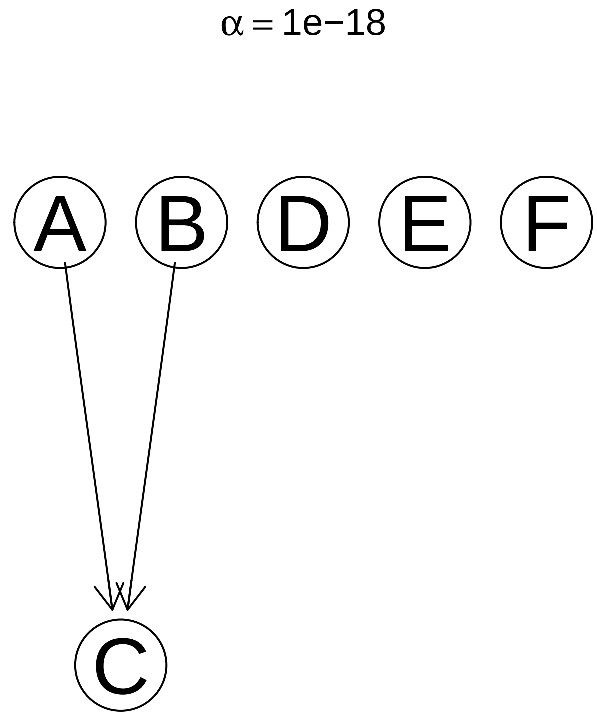
```r
# popular levels of significance and very high (0.5) and very low (10^-18)
alphas = c(0.1, 0.05, 0.01, 0.005, 0.001, 0.0001, 0.5, 1e-18)

plot_list=sapply(alphas, FUN=pc, suffStat = list(C=C,n=n),
                 indepTest = gaussCItest, labels = colnames(data))

plot_fun = function(x,y){
  plot(x, main=bquote(alpha==.(y)))
}
par(mfrow=c(1,2))

# invisible to supress the console message
invisible(mapply(plot_fun, x=plot_list, y=alphas))
```




α = 0.01
α = 0.005
A B F
C E
D
A B F
C E
D


α = 0.001
A
D
B
F
C
E
α = 1e−04
A
B
D
F
C
E





We see that for the popular significance levels α $(0.1 - 0.005)$ we get the same graphs. If we decrease α even further then the edge between node D and C gets unstable. It first flips direction and then gets lost. The relationship between the other nodes stays stable. If we take a very high α like 0.5 then we include false edges. If we take a very low α like 10^{-18} then we lose true edges. So in general we can conclude that there is a sweet spot of α where the estimated graph is very close to the true graph. Too high α risks including false positives, and too low α risks excluding true positives (creating false negatives).