PROJECT 1

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Problem 1:

(a) $P(A,B,C) = P(C)\,P(A|C)\,P(B|C)$ (*)

1) $P(A,B|C) = \frac{P(A,B,C)}{P(C)} = \frac{P(C)P(A|C)P(B|C)}{P(C)} = P(A|C)\,P(B|C) \Rightarrow$ $A \perp B \mid C$ holds

(by definition; (*))

2) $P(A,B) = \sum_C P(A,B|C)P(C)$ Law of total probability

$= \sum_C P(A|C)\,P(B|C)\,P(C)$ because of (*) (1)

compare it to $P(A)\,P(B) = \sum_C P(A|C)\,P(C)\,P(B)$ (2)

$P(B) \neq P(B|C) \Rightarrow (1) \neq (2) \rightarrow$ so $A \not\perp B$ (in general)

(b) $P(A,B,C) = P(A)\,P(B)\,P(C|A,B)$ (**)

1) $P(A,B) = \sum_C P(A,B,C)$

$= \sum_C P(A)P(B)P(C|A,B)$ from (**)

$= P(A)P(B)\underbrace{\sum_C P(C|A,B)}_{=1} = P(A)P(B) \Rightarrow$ $A \perp B$

2) $P(A,B|C) = \frac{P(A,B,C)}{P(C)} \overset{(**)}{=} \frac{P(A)P(B)P(C|A,B)}{P(C)} = \frac{P(C|A)P(A)}{P(C|A)} \cdot \frac{P(C|B)P(B)}{P(C|B)} \cdot \frac{P(C)P(C|A,B)}{P(C)^2}$

$= \frac{P(C|A)P(A)}{P(C)} \cdot \frac{P(C|B)P(B)}{P(C)} \cdot \frac{P(C)P(C|A,B)}{P(C|A)P(C|B)}$ (by definition)

$= P(A|C) \cdot P(B|C) \cdot \frac{P(C)P(C|A,B)}{P(C|A)P(C|B)}$

$\neq P(A|C)P(B|C) \Rightarrow$ $A \not\perp B \mid C$ (in general)

Problem 2: $MB(D)$ → set of parents, coparents and children: $MB(D) = \{B, F, E, G\}$

→ Show that $P(D|A,B,C,E,F,G) = P(D|MB(D)) = P(D|B,F,E,G)$

$P(A,B,C,D,E,F,G) = P(A)P(B)P(F)P(E|A)P(D|B,F)P(G|E,D)P(C|G)$

$P(D|A,B,C,E,F,G) = \frac{P(A,B,C,D,E,F,G)}{P(A,B,C,E,F,G)} = \frac{P(A)P(B)P(F)P(E|A)P(D|B,F)P(G|E,D)P(C|G)}{\sum_D P(A)P(B)P(F)P(E|A)P(D|B,F)P(G|E,D)P(C|G)}$

$= \frac{P(A)P(B)P(F)P(E|A)P(D|B,F)P(G|E,D)P(C|G)}{P(A)P(B)P(F)P(E|A)P(C|G)\sum_D P(D|B,F)P(G|E,D)}$

$= \frac{P(D|B,F)P(G|E,D)}{\sum_D P(D|B,F)P(G|E,D)}$

$P(D|MB(D)) = \frac{P(D,B,F,G,E)}{P(B,F,G,E)} = \frac{P(D,B,F,G,E)}{\sum_D P(D,B,F,G,E)}$ → $P(D,B,F,G,E) = P(B)P(F)P(D|B,F)P(E)P(G|D,E)$

$= \frac{P(B)P(F)P(D|B,F)P(E)P(G|D,E)}{P(B)P(F)P(E)\sum_D P(D|B,F)P(G|E,D)} = \frac{P(D|B,F)P(G|D,E)}{\sum_D P(D|B,F)P(G|E,D)}$

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Contents

Problem 3: Learning Bayesian networks from protein data

Preparation to run the code

Setting seed for reproducibility and loading packages. Some packages are additionally loaded inside the functions that are run in parallel.

```
library("GGally")
library("BiDAG")
library("igraph")
library("parallel")
library("doParallel")
```

Loading data

```
data <- read.table("2005_sachs_2_cd3cd28icam2_log_std.csv", sep=",", header=TRUE)
```

Variables and observations

```
num_variables <- ncol(data)
num_observations <- nrow(data)

print(paste("Number of variables:", num_variables))
```

```
## [1] "Number of variables: 11"
```

```
print(paste("Number of observations:", num_observations))
```

```
## [1] "Number of observations: 902"
```

Visualisation of transformed data

```
png(file="plot.png", width=650, height=1000)
ggpairs(data, progress=FALSE)
dev.off()
```

```
## pdf
##   2
```

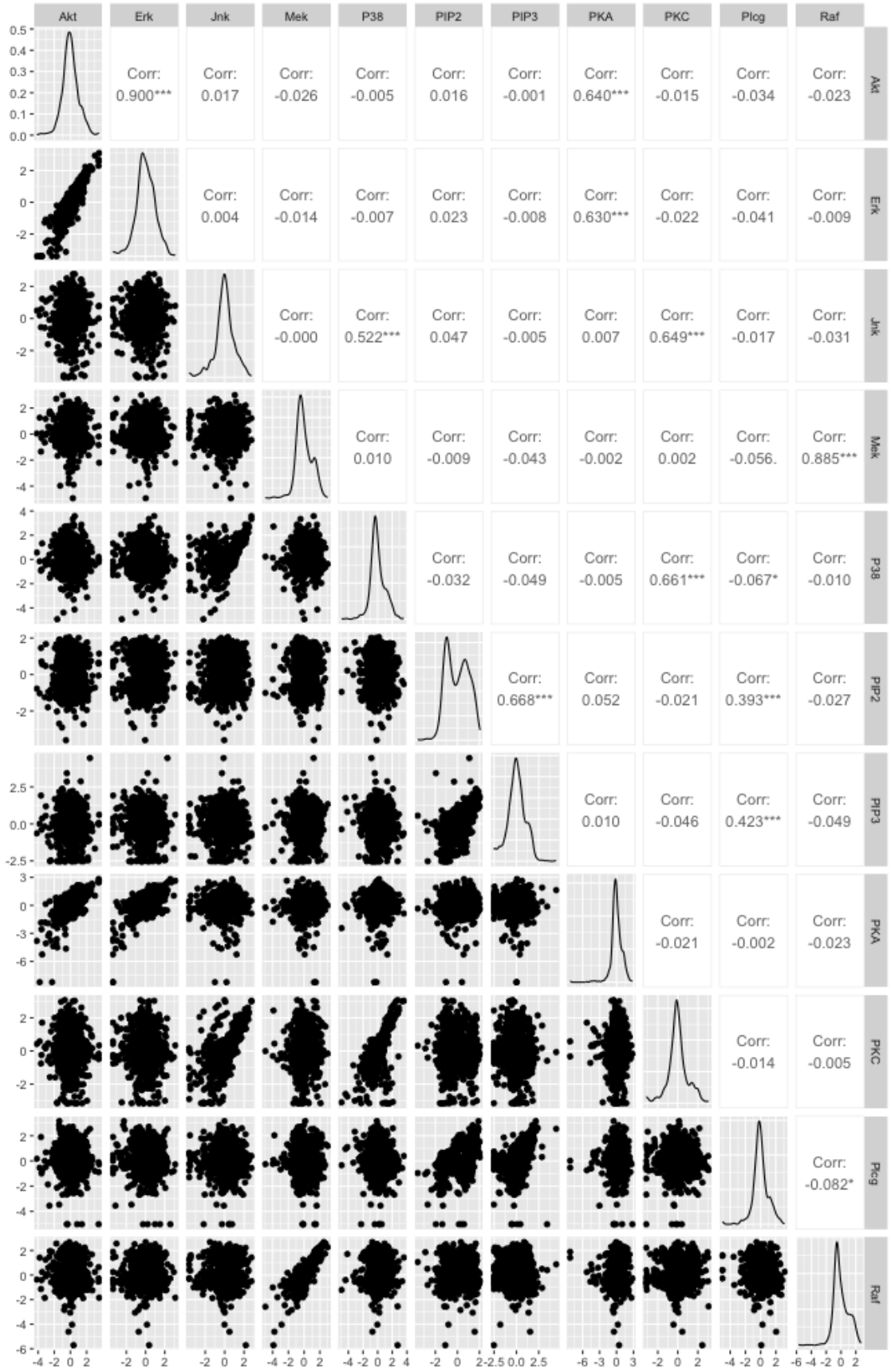


Figure 1: Plot of transformed data

Defining functions

```
splitting_data <- function(data) {
    # Shuffling data
    indices <- 1:nrow(data)
    indices <- sample(length(indices))

    # Splitting data
    train_size <- ceiling(nrow(data)*0.8)
    train_indices <- indices[1:train_size]
    test_indices <- indices[(train_size+1):(length(indices))]

    # Checking if there is no overlap
    if(length(unique(c(train_indices, test_indices))) != length(c(train_indices, test_indices))) {
        print("Overlap!")
    }

    train_data <- data[row.names(data) %in% train_indices, ]
    test_data <- data[row.names(data) %in% test_indices, ]

    split_data <- list("train_data"=train_data, "test_data"=test_data)

    return(split_data)
}

training_BN <- function(data, bgepar) {
    library("BiDAG")
    init_score_par <- scoreparameters("bge", data$train_data, bgepar)
    learnt_BN <- iterativeMCMC(init_score_par, verbose=FALSE)
    return(learnt_BN)
}

testing_BN <- function(data, BN, bgepar) {
    library("BiDAG")
    test_score_par <- scoreparameters("bge", data$test_data, bgepar)
    test_score <- scoreagainstDAG(test_score_par, BN$DAG)
    return(mean(test_score))
}

plot_DAG <- function(BN) {
    library("igraph")
    g <- graph_from_adjacency_matrix(BN$DAG)
    plot(g)
}

get_number_of_edges <- function(BN) {
    library("igraph")
    return(length(E(graph_from_adjacency_matrix(BN$DAG))))
}
```

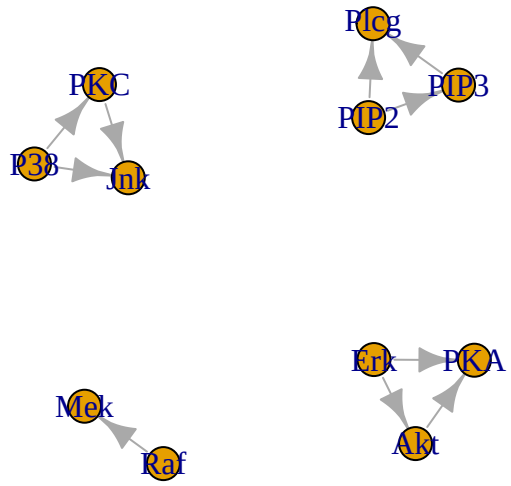
Default parameters

```
bgepar <- list(am=1, aw=NULL, edgepf=1)
split_data <- splitting_data(data)
learnt_BN <- training_BN(split_data, bgepar)

mean_test_score <- testing_BN(split_data, learnt_BN, bgepar)
print(paste0("Average BGe score on testing data: ", mean_test_score))
```

```
## [1] "Average BGe score on testing data: -12.4139751176187"
```

```
plot_DAG(learnt_BN)
```



Different parameters

```
# Set the number of cores to use
num_cores <- detectCores()

# Register parallel backend
cl <- makeCluster(num_cores)
registerDoParallel(cl)
```

```
ams <- c(10^(-5), 10^(-3), 10^(-1), 10, 10^2)

res <- foreach(am = ams, .combine=c) %dopar% {
    set.seed(42)
    bgepar <- list(am=am, aw=NULL, edgepf=1)
```

```
    numbers_of_edges <- c()
    mean_test_scores <- c()
    for(i in 1:10) {
        RNGkind("L'Ecuyer-CMRG")
        split_data <- splitting_data(data)
        learnt_BN <- training_BN(split_data, bgepar)
        number_of_edges <- get_number_of_edges(learnt_BN)
        numbers_of_edges <- append(numbers_of_edges, number_of_edges)
        mean_test_score <- testing_BN(split_data, learnt_BN, bgepar)
        mean_test_scores <- append(mean_test_scores, mean_test_score)
    }
    return(c(am, mean(numbers_of_edges), mean(mean_test_scores)))
}
```

```
stopCluster(cl)
```

```
res_m <- t(matrix(data=res, nrow=5, ncol=3, byrow=TRUE))
rownames(res_m) <- c("Parameter am", "Average number of edges", "Average BGe score of the test data")
print(res_m)
```

```
##                                        [,1]      [,2]      [,3]      [,4]      [,5]
## Parameter am                        0.00001   0.00100   0.10000  10.00000 100.00000
## Average number of edges             7.00000   7.00000   9.10000  13.40000  16.70000
## Average BGe score of the test data -12.73416 -12.73416 -12.70972 -12.80457 -13.58552
```

Retraining the best BN

The best BN (based on the highest BGe score) was the one with $\alpha_m = 10^{-1}$.

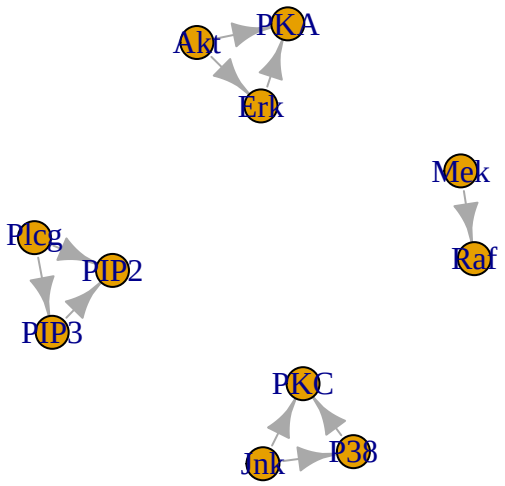
We observe that the average number of edges increases with increasing α_m.

```
set.seed(42)
bgepar <- list(am=10^(-1), aw=NULL, edgepf=1)
split_data <- splitting_data(data)
learnt_BN <- training_BN(split_data, bgepar)

mean_test_score <- testing_BN(split_data, learnt_BN, bgepar)
print(paste0("Average BGe score on testing data: ", mean_test_score))
```

```
## [1] "Average BGe score on testing data: -12.1209831813562"
```

```
plot_DAG(learnt_BN)
```



Render this .rmd into a pdf

```
library(rmarkdown)
render("1.Rmd", pdf_document(TRUE), "1.pdf")
```