Basic R tutorial

February 22, 2024

Contents

Problem 3: Learning Bayesian networks from protein data

Preparation to run the code

Setting seed for reproducibility and loading packages.

```
set.seed(42)
library("GGally")
library("BiDAG")
```

Loading data

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

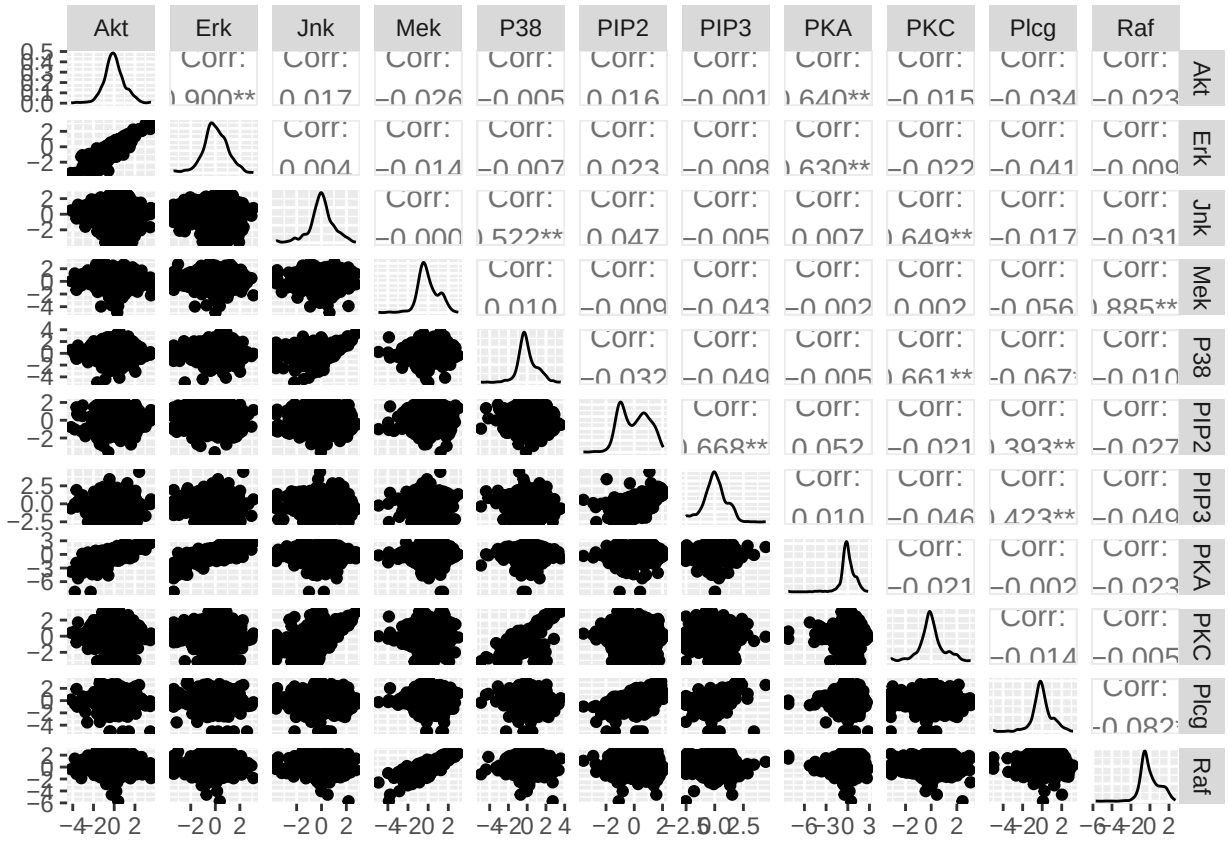
Variables and observations

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

Visualisation of transformed data

TODO: must resize the plot

```
pair_plot <- ggpairs(data, progress=FALSE)
pair_plot
```



TODO: execute the following routine with different parameters (10 times for each change of parameter)

TODO: include possibility of parallelization

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

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: -12.7214725878423"
```

Different parameters

```
library(parallel)
library(doParallel)
```

```
# 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)

foreach(am = ams) %dopar% {
    bgepar <- list(am=am, aw=NULL, edgepf=1)
    mean_test_scores <- c()
    for(i in 1:10) {
        RNGkind("L'Ecuyer-CMRG")
        library("BiDAG")
        split_data <- splitting_data(data)
        learnt_BN <- training_BN(split_data, bgepar)
        mean_test_score <- testing_BN(split_data, learnt_BN, bgepar)
        mean_test_scores <- append(mean_test_scores, mean_test_score)
    }
    print(paste(am, mean(mean_test_scores)))
}
```

```
## [[1]]
## [1] "1e-05 -12.7228948588341"
##
## [[2]]
## [1] "0.001 -12.6060223456489"
##
## [[3]]
## [1] "0.1 -12.7518385056867"
##
## [[4]]
## [1] "10 -12.6500697904181"
##
## [[5]]
## [1] "100 -13.5382678012819"
```

```
stopCluster(cl)
```

Render this .rmd into a pdf

```
library(rmarkdown)
render("1/1.Rmd", pdf_document(TRUE), "1.pdf") # TRUE adds table of content
```