Project 1: Learning Bayesian Networks from gene expression data

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(a) Install the packages and load and preprocess the data.

YeastCC data: This data package contains an ExpressionSet instance for the yeast cell cycle microarray experiment. The dataset contains gene expression measures (log-ratios, with Cy3-labeled common reference) for 6,178 yeast genes in 77 conditions.

```
# #Install deal and load yeastCC data
# install.packages("deal")
library(deal)
# source("https://bioconductor.org/biocLite.R")
# biocLite("yeastCC")
library(yeastCC)
# Load the Yeast cell cycle regulator dataset
yeastCC = yeastCC
# First 3 genes are: [1] "YAL001C" "YAL002W"
                                                "YALOO3W"
                   [1] "YPR202W" "YPR203W" "YPR204W"
# Last genes are:
# 77 conditions for each gene are measured in log-ratios:
          cln3.1 cln3.2 clb2.2 clb2.1 alpha0 alpha7 alpha14 alpha21 alpha28 alpha35
# YALOO1C
         0.15
                    NA -0.22 0.07 -0.15 -0.15 -0.21
# length(exprs(yeastCC[1]))
```

i) Turn data object yeastCC into an expression matrix (function exprs) with genes as columns and experiments as rows.

```
expr_df = as.data.frame(exprs(yeastCC))
expr_mt = t(as.matrix(expr_df))
expr_mt[1:5, 1:5]
         YALOO1C YALOO2W YALOO3W YALOO4W YALOO5C
## cln3.1
            0.15
                 -0.07
                          -1.22
                                   -0.09
                                         -0.60
## cln3.2
              NA
                   -0.76
                          -0.27
                                    1.20
                                           1.01
          -0.22
                          -0.10
                                           0.24
## clb2.2
                  -0.12
                                    0.16
## clb2.1
          0.07
                   -0.25
                          0.23
                                   -0.14
                                           0.65
           -0.15
                   -0.11
                           -0.14
                                   -0.02
                                           -0.05
## alpha0
```

ii) Restrict the genes to cell cycle regulators.

The ORF names for the 800 cell cycle regulated genes are stored in orf800.

```
# Create a mask with yeast gene indeces that correspond to 800 cell regulator genes
mask = which(colnames(expr_mt) %in% orf800)
# Subset cell regulators
expr_cc_mt = expr_mt[ , mask]
expr_cc_mt[1:5, 1:5]
          YALO22C YALO40C YALO53W YALO67C YAROO3W
##
## cln3.1
            -0.22
                     3.43
                             0.34
                                     -0.15
                                              0.41
                                     -1.25
## cln3.2
            -0.86
                     2.75
                                              0.25
                             0.90
## clb2.2
           -0.25
                     0.36
                            -0.58
                                             -0.62
                                        NA
                     0.72
## clb2.1
            0.89
                           -0.92
                                      0.07
                                             -0.29
## alpha0
           -0.36
                     1.04
                             0.21
                                      0.01
                                             -0.30
```

iii) Replace missing data (=NA) with each gene's median.

```
replace_na_with_col_medians = function(x) {
    x = replace(x, is.na(x), median(x, na.rm = T))
    return(x)
}

cat("Number of NA's before cleanup is:", length(which(is.na(expr_cc_mt) == TRUE)))

## Number of NA's before cleanup is: 2643

expr_cc_mt = apply(expr_cc_mt, 2, replace_na_with_col_medians)
cat("Number of NA's after cleanup is:", length(which(is.na(expr_cc_mt) == TRUE)))

## Number of NA's after cleanup is: 0

## Check if correct w/ 1st and 2nd genes
# which(is.na(expr_cc_mt[, 2]))  # cdc28.140 idx61; cdc28.110 idx58
# median(expr_cc_mt[, 2], na.rm = T)  # -0.5 -0.045
```

iv) Calculate the range between the 25th and 75th quantile for each gene and keep genes with a value > 1.6.

The interquartile range of an observation variable is the difference of its upper and lower quartiles. It is a measure of how far apart the middle portion of data spreads in value.

```
# Calculate IQRs for every gene/column, select IQRs with >1.6 and subset the data with them
iqrs = apply(expr_cc_mt, 2, IQR)
mask = which(iqrs > 1.6)
expr16 = as.data.frame(expr_cc_mt[, mask])
expr16[1:5,1:5]
##
          YBR054W YBR088C YER124C YGL028C YGR108W
## cln3.1
            -2.56
                            0.07
                                             0.21
                     2.05
                                    -0.31
## cln3.2
           -1.74
                     1.67
                            -1.29
                                     0.23
                                             0.87
## clb2.2
            2.76
                  -2.06
                                             2.28
                           -0.32
                                    -0.49
## clb2.1
            3.38
                   -1.43
                           -0.10
                                     0.16
                                             1.66
## alpha0
          -1.35
                   -1.15
                             0.92
                                     2.45
                                            -1.88
```

v) Add a dummy gene with expression 1 over all experiments (deal needs at least one discrete variable).

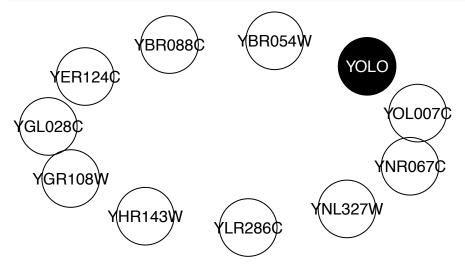
```
YOLO = as.factor(rep(1, length(expr16[, 1]))) # must be a factor because discrete variable expected in expr16 = cbind(expr16, YOLO) cat("Class of dummy discrete variable should be a factor:", class(expr16[1, 11]))
```

Class of dummy discrete variable should be a factor: factor

(b) Learn the optimal network

i) Create an empty network prior.

```
bn_expr16 = network(expr16) # to visually inspect local probs: inspectprob=TRUE
# nodes(bn_expr16) # YOLO node should be discrete!
plot(bn_expr16)
```



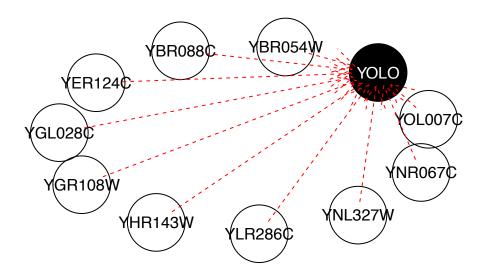
ii) What are the local probability distributions of the genes?

```
localprob(bn_expr16)
```

```
## $YBR054W
##
                   s2 Intercept:YBR054W
                             0.02649351
##
          1.42234485
##
## $YBR088C
                   s2 Intercept:YBR088C
##
                          -0.0005194805
##
        0.9768984314
##
## $YER124C
##
                   s2 Intercept:YER124C
##
          1.41456404
                            -0.02246753
##
## $YGL028C
```

```
s2 Intercept:YGL028C
##
        1.455174903 -0.009350649
##
##
## $YGR108W
                s2 Intercept:YGR108W
##
         0.92446915 0.06779221
##
## $YHR143W
##
                s2 Intercept:YHR143W
##
         1.04158249 -0.01097403
##
## $YLR286C
##
                s2 Intercept:YLR286C
       1.9945786136 -0.0007792208
##
##
## $YNL327W
##
                s2 Intercept:YNL327W
         1.41701617 -0.02616883
##
##
## $YNR067C
##
                s2 Intercept:YNRO67C
         1.60312299 -0.02415584
##
## $YOLOO7C
                s2 Intercept:YOL007C
##
         1.09477190 -0.01090909
##
## $YOLO
## 1
## 1
```

iii) Ban all outgoing edges for the dummy node (use function banlist).



iv) Create a joint prior with imaginary sample size 5, N=5

```
bn_expr16.prior = jointprior(bn_expr16, N=5)
## Imaginary sample size: 5
head(bn_expr16.prior)
## $jointalpha
## 1
## 5
##
## $jointnu
## 1
## 5
##
## $jointrho
## 1
## 5
##
## $jointmu
                                   YGL028C
##
      YBR054W
                YBR088C
                         YER124C
                                           YGR108W
  :1 0.02649351 -0.0005194805 -0.02246753 -0.009350649 0.06779221
##
##
       YHR143W
                 YLR286C
                          YNL327W
                                   YNR067C
                                           YOLOO7C
##
  :1 -0.01097403 -0.0007792208 -0.02616883 -0.02415584 -0.01090909
##
## $jointsigma
## $jointsigma$`:1`
##
        YBR054W
                YBR088C
                     YER124C YGL028C
                                    YGR108W
                                          YHR143W
## YER124C 0.000000 0.0000000 1.414564 0.000000 0.0000000 0.000000 0.000000
## YGL028C 0.000000 0.0000000 0.000000 1.455175 0.0000000 0.000000 0.000000
## YGR108W 0.000000 0.0000000 0.000000 0.000000 0.9244692 0.000000 0.000000
## YHR143W 0.000000 0.0000000 0.000000 0.000000 1.041582 0.000000
```

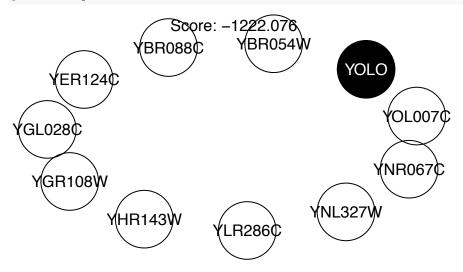
```
YNL327W YNR067C YOL007C
## YBR054W 0.000000 0.000000 0.000000
## YBR088C 0.000000 0.000000 0.000000
## YER124C 0.000000 0.000000 0.000000
## YGL028C 0.000000 0.000000 0.000000
## YGR108W 0.000000 0.000000 0.000000
## YHR143W 0.000000 0.000000 0.000000
## YLR286C 0.000000 0.000000 0.000000
## YNL327W 1.417016 0.000000 0.000000
## YNR067C 0.000000 1.603123 0.000000
## YOL007C 0.000000 0.000000 1.094772
##
##
## $jointphi
## $jointphi$\:1\
        YBR054W YBR088C YER124C YGL028C YGR108W YHR143W YLR286C
## YBR054W 5.689379 0.000000 0.000000 0.00000 0.000000 0.00000
## YER124C 0.000000 0.000000 5.658256 0.0000 0.000000 0.000000 0.000000
## YGL028C 0.000000 0.000000 0.000000 5.8207 0.000000 0.00000 0.000000
## YGR108W 0.000000 0.000000 0.000000 0.0000 3.697877 0.00000 0.000000
## YHR143W 0.000000 0.000000 0.000000 0.00000 4.16633 0.000000
## YLR286C 0.000000 0.000000 0.000000 0.0000 0.00000 0.00000 7.978314
YNL327W YNR067C YOL007C
## YBR054W 0.000000 0.000000 0.000000
## YBR088C 0.000000 0.000000 0.000000
## YER124C 0.000000 0.000000 0.000000
## YGL028C 0.000000 0.000000 0.000000
## YGR108W 0.000000 0.000000 0.000000
## YHR143W 0.000000 0.000000 0.000000
## YLR286C 0.000000 0.000000 0.000000
## YNL327W 5.668065 0.000000 0.000000
## YNR067C 0.000000 6.412492 0.000000
## YOL007C 0.000000 0.000000 4.379088
```

v) Learn the initial network (use getnetwork to turn the result into an actual network).

```
# master prior
bn_expr16.m_prior = learn(bn_expr16, expr16, bn_expr16.prior)
# initial network
bn_expr16.initial = getnetwork(bn_expr16.m_prior)
cat("Initial network score is:", bn_expr16.initial$score)
```

Initial network score is: -1222.076

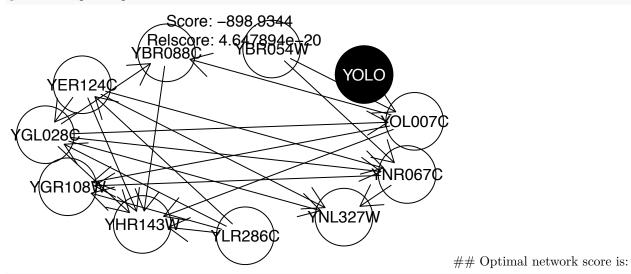
plot(bn_expr16.initial, showban = FALSE)



vi) Search for the optimal network and plot it

bn_expr16.optimal = autosearch(bn_expr16.initial, expr16, bn_expr16.prior, showban = F, trace = F, time ## (1) -1165.098 [YBR054W] [YBR088C] [YER124C] [YGL028C] [YGR108W] [YHR143W|YLR286C] [YLR286C] [YNL327W] [YNR06 ## (2) -1112.392 [YBR054W] [YBR088C] [YER124C|YHR143W] [YGL028C] [YGR108W] [YHR143W|YLR286C] [YLR286C] [YNL327 ## (3) -1065.071 [YBR054W][YBR088C|YOL007C][YER124C|YHR143W][YGL028C][YGR108W][YHR143W|YLR286C][YLR286C ## (4) -1023.883 [YBR054W] [YBR088C|Y0L007C] [YER124C|YHR143W] [YGL028C] [YGR108W] [YHR143W|YLR286C] [YLR286C ## (5) -985.7577 [YBR054W] [YBR088C|YOL007C] [YER124C|YHR143W] [YGL028C|YER124C] [YGR108W] [YHR143W|YLR286C] ## (6) -951.0645 [YBR054W] [YBR088C|Y0L007C] [YER124C|YHR143W] [YGL028C|YER124C] [YGR108W] [YHR143W|YLR286C] ## (7) -938.5766 [YBR054W] [YBR088C|Y0L007C] [YER124C|YHR143W] [YGL028C|YER124C] [YGR108W] [YHR143W|YLR286C] ## (8) -932.9585 [YBR054W][YBR088C|Y0L007C][YER124C|YHR143W][YGL028C|YER124C][YGR108W|YLR286C][YHR143W| ## (9) -927.7516 [YBR054W] [YBR088C|YOL007C] [YER124C|YHR143W] [YGL028C|YER124C:YLR286C] [YGR108W|YLR286C] [## (10) -922.9491 [YBR054W] [YBR088C|YOL007C] [YER124C|YHR143W] [YGL028C|YER124C:YLR286C] [YGR108W|YLR286C] ## (11) -918.3798 [YBR054W] [YBR088C|YOL007C] [YER124C|YHR143W:YLR286C] [YGL028C|YER124C:YLR286C] [YGR108W| ## (12) -915.6276 [YBR054W] [YBR088C|YOL007C] [YER124C|YHR143W:YLR286C] [YGL028C|YER124C:YLR286C] [YGR108W| ## (13) -913.0537 [YBR054W] [YBR088C|YGL028C:YOL007C] [YER124C|YHR143W:YLR286C] [YGL028C|YER124C:YLR286C] [## (14) -910.8 [YBR054W] [YBR088C|YGL028C:YOL007C] [YER124C|YHR143W:YLR286C] [YGL028C|YER124C:YLR286C] [YGR ## (15) -908.2162 [YBR054W] [YBR088C|YGL028C:YOL007C] [YER124C|YHR143W:YLR286C] [YGL028C|YER124C:YLR286C] [## (16) -907.1766 [YBR054W] [YBR088C|YGL028C:YOL007C] [YER124C|YHR143W:YLR286C] [YGL028C|YER124C:YHR143W:Y ## (17) -906.3018 [YBR054W] [YBR088C|YGL028C:YOL007C] [YER124C|YHR143W:YLR286C] [YGL028C|YER124C:YHR143W:Y ## (18) -905.355 [YBR054W][YBR088C|YGL028C:YOL007C][YER124C|YHR143W:YLR286C][YGL028C|YER124C:YHR143W:YL ## (19) -904.2094 [YBR054W] [YBR088C|YGL028C:YOL007C] [YER124C|YHR143W:YLR286C] [YGL028C|YER124C:YHR143W:Y ## (20) -903.7049 [YBR054W] [YBR088C|YGL028C:YHR143W:Y0L007C] [YER124C|YHR143W:YLR286C] [YGL028C|YER124C:Y ## (21) -903.2914 [YBR054W] [YBR088C|YGL028C:YHR143W:Y0L007C] [YER124C|YHR143W:YLR286C] [YGL028C|YER124C:Y ## (22) -902.0643 [YBR054W] [YBR088C|YGL028C:YHR143W:Y0L007C] [YER124C|YLR286C] [YGL028C|YER124C:YHR143W:Y ## (23) -901.318 [YBR054W] [YBR088C|YGL028C:YHR143W:YOL007C] [YER124C|YLR286C] [YGL028C|YER124C:YLR286C] [YGL028C|YER124C:YLR286C] ## (24) -900.5361 [YBR054W] [YBR088C|YGL028C:YHR143W:Y0L007C] [YER124C|YLR286C] [YGL028C|YER124C:YLR286C] [## (25) -900.0622 [YBR054W] [YBR088C|YGL028C:YOL007C] [YER124C|YLR286C] [YGL028C|YER124C:YLR286C] [YGR108W| ## (26) -899.878 [YBR054W] [YBR088C|YGL028C:YOL007C] [YER124C|YLR286C] [YGL028C|YER124C:YLR286C] [YGR108W|Y. ## (27) -898.9478 [YBR054W] [YBR088C|YGL028C:YOL007C] [YER124C|YLR286C] [YGL028C|YER124C:YLR286C] [YGR108W| ## (28) -898.9344 [YBR054W] [YBR088C|YGL028C:Y0L007C] [YER124C|YLR286C] [YGL028C|YER124C:YLR286C] [YGR108W|

```
bn_expr16.optimal = getnetwork(bn_expr16.optimal)
plot(bn_expr16.optimal, showban = F)
```



bn_expr16.optimal\$score

[1] -898.9344

Modes tas Filipanicins
Project |

Problem |

For reverse, apply chain
rule to recover full

Joint distro, P(x,y,z); and
then factorize it again into

Conditional probabilities: $P(X|Y,z) = \frac{P(X,Y,z)}{P(Y,z)} = \frac{P(X,Y,z)}{P(Y,z)} = \frac{P(X,Y,z)}{P(Y,z)} = \frac{P(X,Y,z)}{P(Y,z)} = \frac{P(X|Y,z)}{P(Y,z)} = \frac{P(X|Y,z)}{P(Y,z)} = \frac{P(X|Y,z)}{P(Y,z)} = \frac{P(X|Y,z)}{P(Y,z)} = \frac{P(X|Y,z)}{P(Y,z)}$

Roblem 2 For a graph w/ Knodes, joint (1) $P(\bar{x}) = \frac{\bar{x}}{|\bar{x}|} p + \frac{\bar{x}}{|\bar{x}|} P(x_k | parents_k)$ Using (1), define Markon blanket &; for a node Xi, conditioned on all remaining variables X jti, as entity that holds true regarding this the Alaring Cond. independence distillusion: $P(x_i|X_{j=i}) = \frac{P(x_1,x_2...X_K)}{} =$ = TIP (xk | parentsk) ≥ Np(xk printsk)

Thus, we can factor take all values factors P(+k/pak) that have no dipendance on X; allfaide of summation; thus carelling them out w/ corresponding nominator factors. We will be left w/ - P(xilpaxi) (Ponepts) - rodes Xe which are conditioned on Xi (Xi's children) - (0-parents of Xis children, For this graph the node C is conditionally indigendant of B, given parents (A), children (B) and G-parents (E), MB(C)={A,D,E} $P(C|ABDE) = \frac{P(D|C,E) \cdot P(E|B)}{P(C|A) \cdot P(D|C) \cdot P(E|B) \cdot P(B)}$ $P(C|ABDE) = \frac{P(C|A) \cdot P(D|C,E) \cdot P(E|B) \cdot P(B)}{\sum P(B) \cdot P(C|A) \cdot P(D|C,E) \cdot P(E|B) \cdot P(B)}$ $= \frac{p(A) \cdot p(C|A) \cdot p(D|C,E) \ P(E|B) \ p(B)}{p(A) \cdot P(E|B) \cdot P(B)} = \frac{p(C|A) \cdot p(D|C,E)}{\sum P(C|A) \cdot p(D|C,E)}$ The above proves that C depends on nodes { A, D, E},