Assignment 4

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Problem 1

Problem 2

```
# import file
data <- read.table("./data.txt", header = TRUE, sep = " ", stringsAsFactors = FALSE)
```

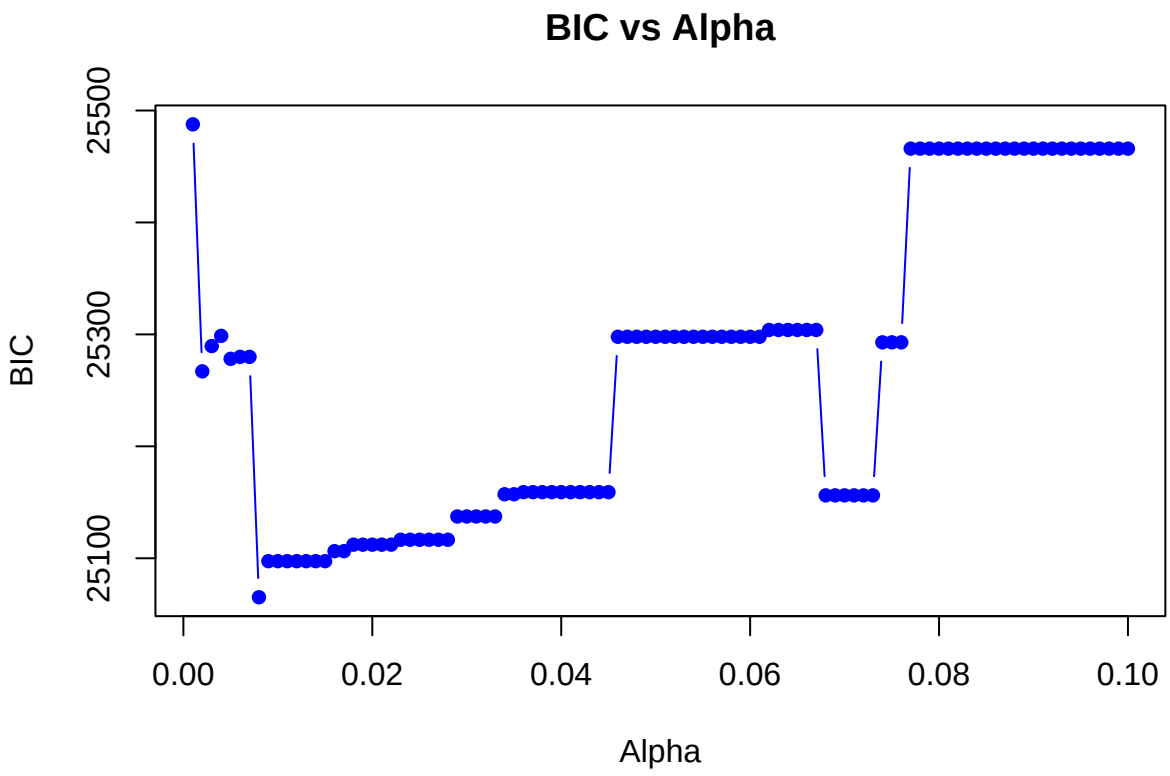
PC algorithm

```
# Function to calculate log likelihood
compute_log_likelihood <- function(data, adj_matrix) {
  sample_cov <- cov(data)  # Sample covariance matrix
  adj_cov <- sample_cov * adj_matrix  # Adjust covariance for graph

  # Regularization for numerical stability
  p <- ncol(data)
  regularization <- diag(10, p)
  adj_cov <- adj_cov + regularization

  # Log-likelihood calculation
  tryCatch({
    log_det <- log(det(adj_cov))  # Log determinant
    inv_cov <- solve(adj_cov)    # Inverse covariance
    log_likelihood <- -0.5 * nrow(data) * (log_det + sum(diag(inv_cov %*% sample_cov)))
    return(log_likelihood)
  }, error = function(e) {
    return(NA)  # Return NA if numerical issues occur
  })
}

# Function to calculate BIC
compute_bic <- function(pc_fit, data) {
  adj_matrix <- as(pc_fit@graph, "matrix")  # Adjacency matrix
```

```r
  num_params <- sum(adj_matrix)  # Number of edges (parameters)
  log_lik <- compute_log_likelihood(data, adj_matrix)

  if (is.na(log_lik)) return(Inf)  # Return infinite BIC for invalid graphs

  n <- nrow(data)  # Sample size
  p <- ncol(data)  # Number of variables
  bic <- -2 * log_lik + log(n) * (num_params + p)  # BIC formula
  return(bic)
}

# Generate a sequence of alpha values
alphas <- seq(0.001, 0.1, by = 0.001)

# Fit PC algorithm and compute BIC for each alpha
bic_values <- sapply(alphas, function(alpha) {
  pc_fit <- pc(
    suffStat = list(C = cor(data), n = nrow(data)),
    indepTest = gaussCItest,
    alpha = alpha,
    labels = colnames(data),
    verbose = FALSE
  )
  compute_bic(pc_fit, data)
})

# Find optimal alpha
optimal_alpha <- alphas[which.min(bic_values)]
cat("Optimal alpha based on BIC:", optimal_alpha, "\n")
```

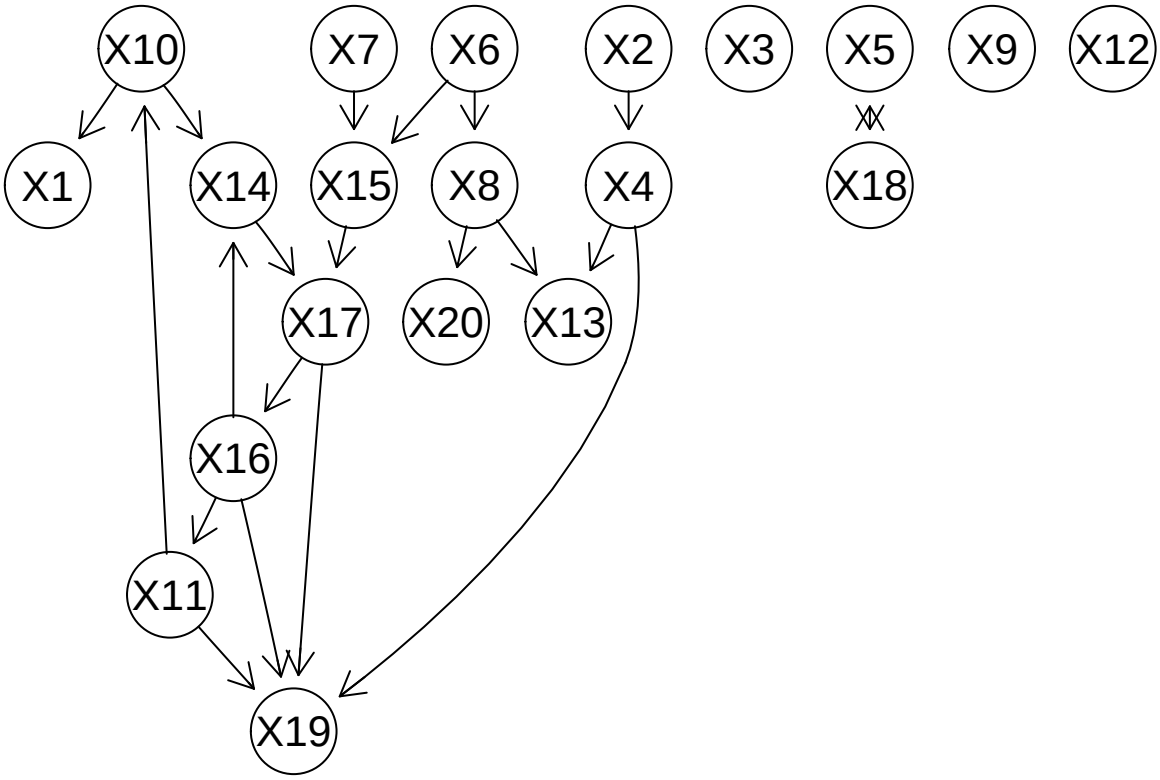
```
## Optimal alpha based on BIC: 0.008
```

```r
# Plot BIC vs Alpha
plot(
  alphas, bic_values, type = "b", pch = 16, col = "blue",
  xlab = "Alpha", ylab = "BIC",
  main = "BIC vs Alpha"
)
```

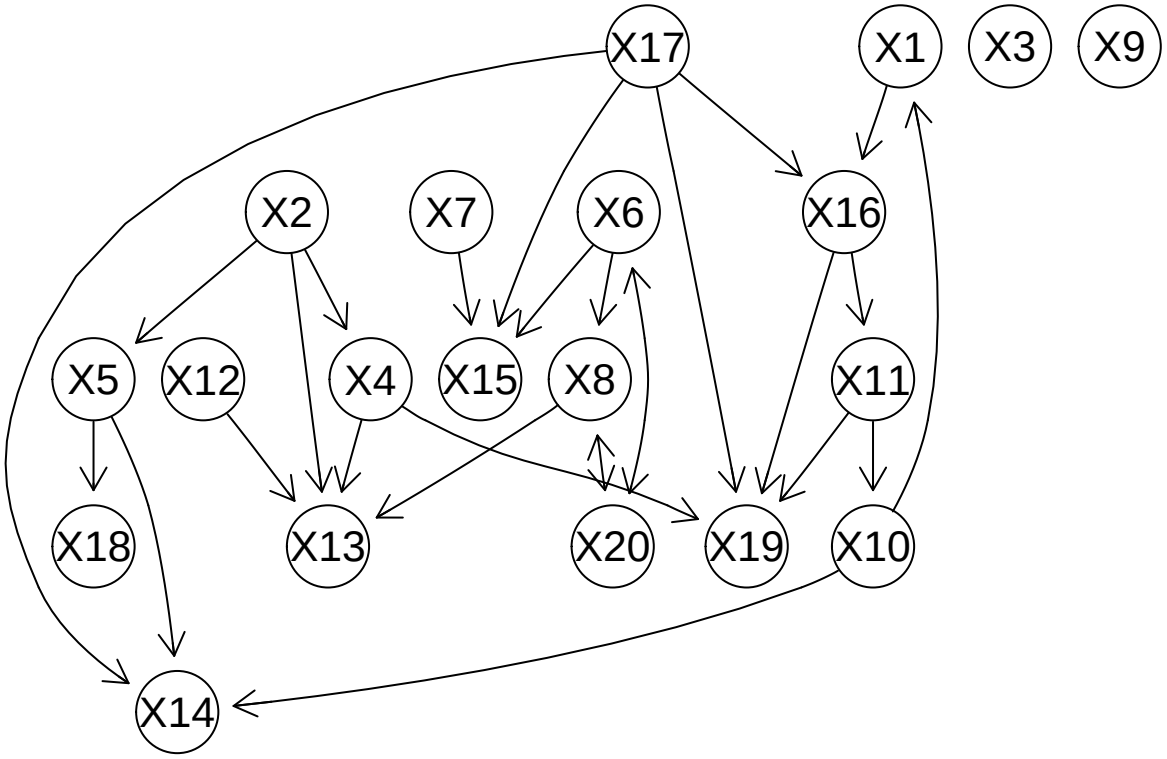



```
# Run pc algorithm with alpha = 0.001
pc.fit.001 <- pc(suffStat = list(C = cor(data), n = nrow(data)),
              indepTest = gaussCItest,
              alpha=0.001, labels = colnames(data), verbose = TRUE)

# alpha = 0.008
pc.fit.008 <- pc(suffStat = list(C = cor(data), n = nrow(data)),
              indepTest = gaussCItest,
              alpha=0.008, labels = colnames(data), verbose = TRUE)

# alpha = 0.1
pc.fit.1 <- pc(suffStat = list(C = cor(data), n = nrow(data)),
              indepTest = gaussCItest,
              alpha=0.1, labels = colnames(data), verbose = TRUE)
```

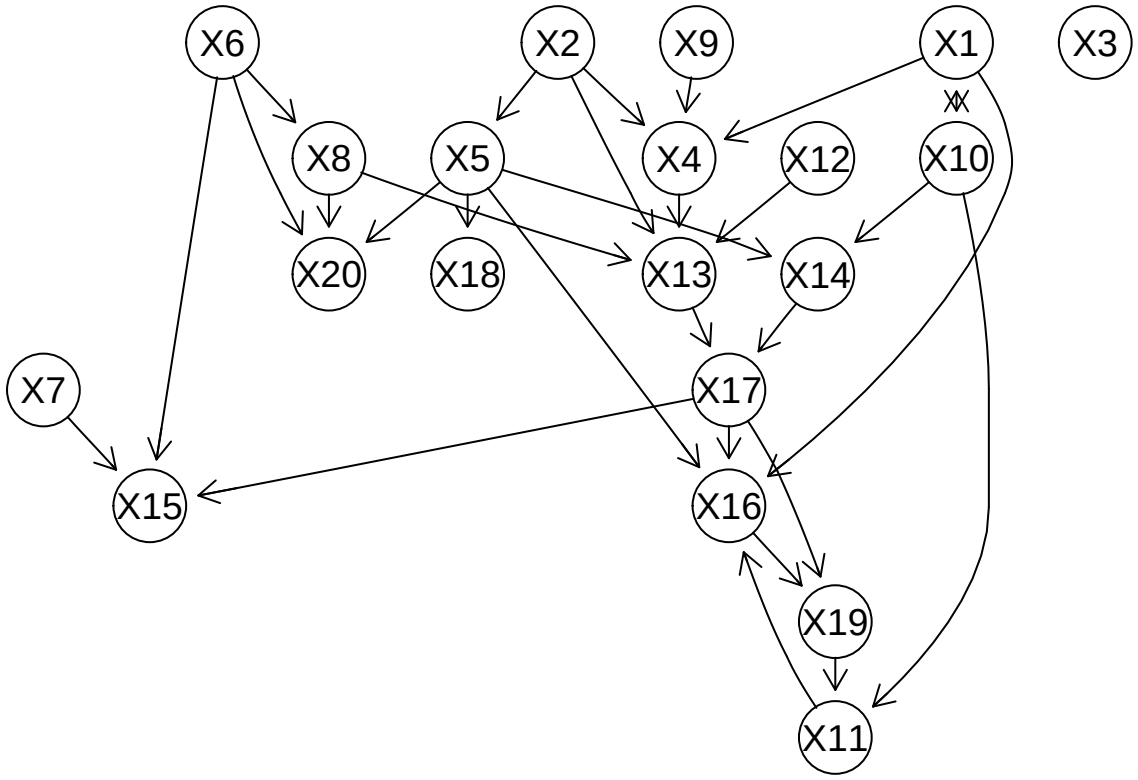
```
# Plot CPDAG
plot(pc.fit.001@graph)
```




```
plot(pc.fit.008@graph)
```




```
plot(pc.fit.1@graph)
```




```
# Check the number of edges
pc.fit.001
```

```
## Object of class 'pcAlgo', from Call:
## pc(suffStat = list(C = cor(data), n = nrow(data)), indepTest = gaussCItest,
##     alpha = 0.001, labels = colnames(data), verbose = TRUE)
## Number of undirected edges:  1
## Number of directed edges:    19
## Total number of edges:       20
```

```
pc.fit.008
```

```
## Object of class 'pcAlgo', from Call:
## pc(suffStat = list(C = cor(data), n = nrow(data)), indepTest = gaussCItest,
##     alpha = 0.008, labels = colnames(data), verbose = TRUE)
## Number of undirected edges:  2
## Number of directed edges:    23
## Total number of edges:       25
```

```
pc.fit.1
```

```
## Object of class 'pcAlgo', from Call:
## pc(suffStat = list(C = cor(data), n = nrow(data)), indepTest = gaussCItest,
##     alpha = 0.1, labels = colnames(data), verbose = TRUE)
## Number of undirected edges:  1
## Number of directed edges:    28
## Total number of edges:       29
```

I used the PC algorithm to estimate CPDAGs for a range of α values (0.001 to 0.1) to identify the optimal α that minimizes the Bayesian Information Criterion (BIC). For each α, the graph structure $G(\alpha)$ was used to compute the log-likelihood $-2\ell(\hat{\Sigma}_{G'}, \hat{\mu})$, where $\ell(\cdot)$ is the log-likelihood of a Gaussian model based on the graph-constrained covariance matrix. The BIC for each graph was computed as $-2\ell + \log(n)(k+p)$, with k representing the number of edges and p the number of variables.
The optimal $\alpha = 0.008$ was selected as the value minimizing BIC. This model is considered to have an optimal balance between complexity and fit.

Estimated CPDAGs were plotted for specific α values (0.001, 0.008, 0.1), and the number of edges was examined for each plot. We see that the smaller α value led to sparser graph with fewer edges, and the larger α value led to denser graphs with more edges.

Graphical lasso method

I will conduct model selection using EBIC, RIC and StARS.

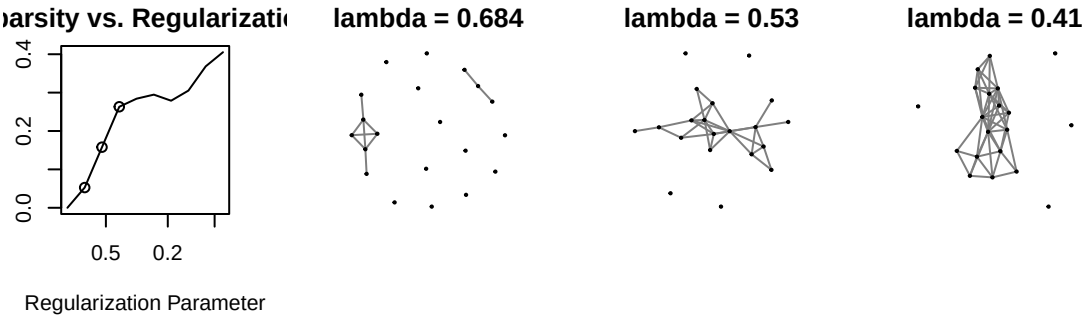
```
# Apply graphical lasso method
out.glasso <- huge(as.matrix(data), method = "glasso")
```

```
## Conducting the graphical lasso (glasso) wtih lossless screening....in progress: 9%Conducting the gra
## Conducting the graphical lasso (glasso)....done.
```

```
# Perform model selection using EBIC
out.select <- huge.select(out.glasso, criterion = "ebic")
```

```
## Conducting extended Bayesian information criterion (ebic) selection....done
```

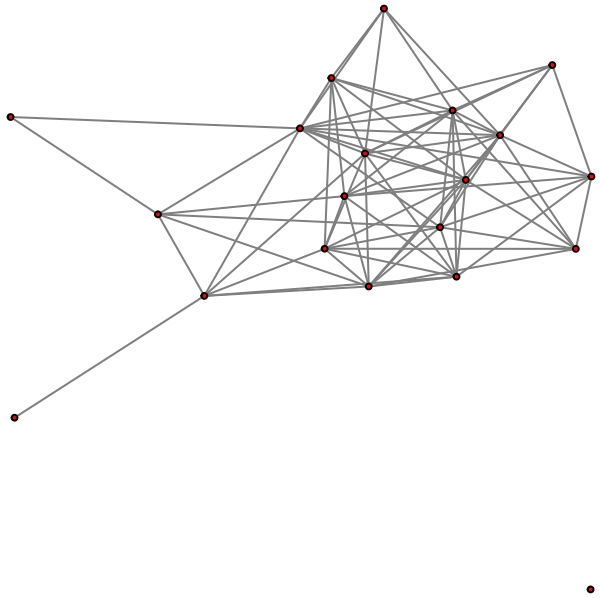
```
# Plot the selected graph
plot(out.glasso)
```




```
# Extract adjacency matrix of the selected graph
adj_matrix <- out.select$refit

# Check selected lambda
out.select$opt.lambda
```

```
## [1] 0.08835911
```

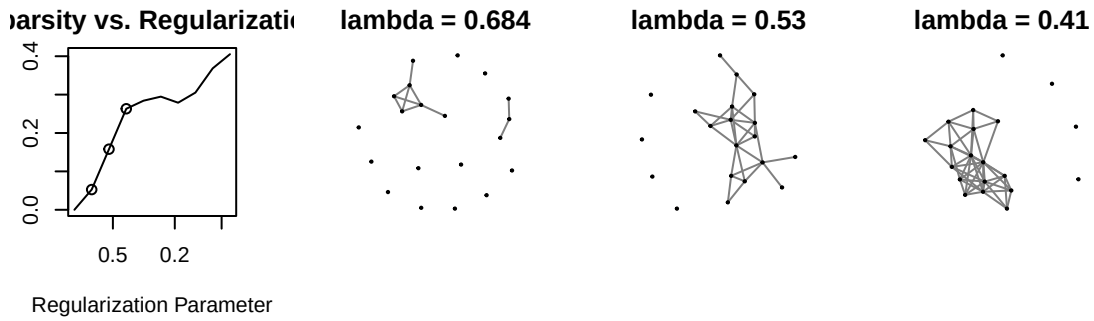
```
# Visualize the selected graph
huge.plot(adj_matrix)
```



```r
# Do the same using RIC
out.select <- huge.select(out.glasso, criterion = "ric")
```

```
## Conducting rotation information criterion (ric) selection....done
## Computing the optimal graph....done
```

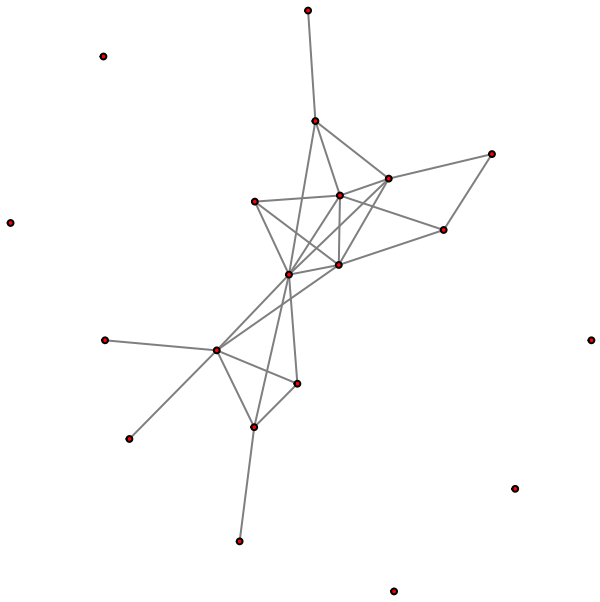
```r
plot(out.glasso)
```




```
adj_matrix <- out.select$refit
out.select$opt.lambda
```

```
## [1] 0.5574563
```

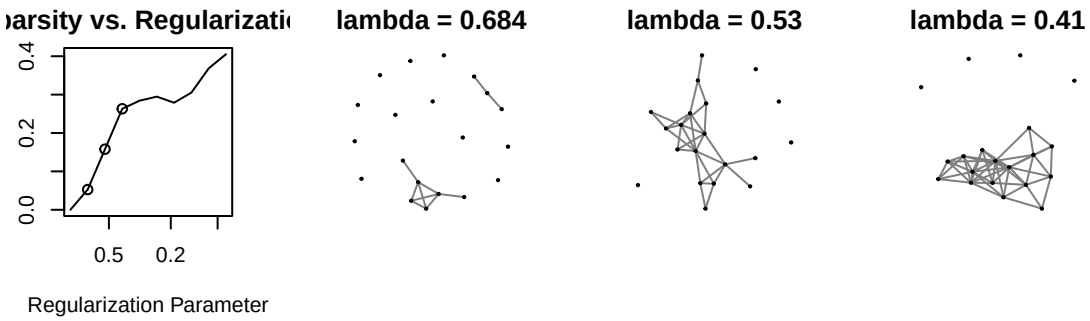
```
huge.plot(adj_matrix)
```



```
# Do the same using STARS
out.select <- huge.select(out.glasso, criterion = "stars")
```

```
## Conducting Subsampling....in progress:5% Conducting Subsampling....in progress:10% Conducting Subsamp
```

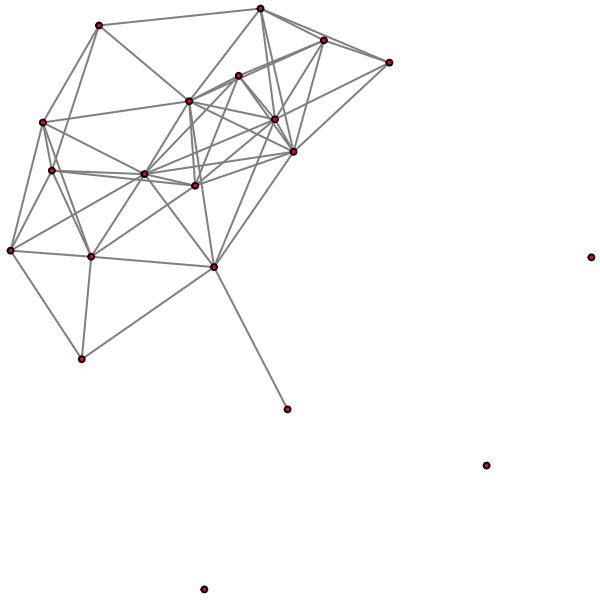
```
plot(out.glasso)
```




```
adj_matrix <- out.select$refit
out.select$opt.lambda
```

```
## [1] 0.1903639
```

```
huge.plot(adj_matrix)
```



First, I estimated a sequence of graphs corresponding to different regularization parameters (λ). Larger λ values produced sparser graphs with many isolated edges, while smaller λ values led to highly connected graphs. Subsequently, three model selection criteria were applied to identify the optimal graph that balances fit and sparsity. EBIC balances log-likelihood and penalizes model complexity in high-dimensional data ($\lambda = 0.0884$). RIC uses a simpler penalty that generally favors fewer edges, resulting in a moderate sparsity ($\lambda = 0.4997$). StARS prioritizes the stability of edges across subsampled data ($\lambda = 0.1904$). We need to choose the criteria based on the nature of data and underlying relationships in the data.