

Lab block 2

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Assignment 1

Assignment 2

Comparison of Mixture Model with Different Number of Clusters (M)

The EM algorithm was run for a Bernoulli Mixture Model with different values of M (number of clusters), specifically $M = 2$, $M = 3$, and $M = 4$. The objective was to analyze how the number of clusters influences the model's behavior, particularly its impact on the log-likelihood values and the convergence process.

Experimental Setup

- **Number of Data Points (n):** 1000
- **Number of Features (D):** 10
- **Maximum Iterations (max_it):** 100
- **Minimum Change in Log-Likelihood (min_change):** 0.1
- **True Mixture Components (true_pi):** $[1/3, 1/3, 1/3]$
- **True Conditional Distributions (true_mu):**
 - Cluster 1: $[0.5, 0.6, 0.4, 0.7, 0.3, 0.8, 0.2, 0.9, 0.1, 1]$
 - Cluster 2: $[0.5, 0.4, 0.6, 0.3, 0.7, 0.2, 0.8, 0.1, 0.9, 0]$
 - Cluster 3: $[0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5]$

Results

$M = 2$ (Too Few Clusters)

- **Final Log-Likelihood:** -6362.897
- **Number of Iterations for Convergence:** 12
- **Mixing Coefficients (π):**
 - Cluster 1: 0.4971
 - Cluster 2: 0.5029
- **Observed Behavior:** The log-likelihood converged quickly, but the two clusters attempted to merge three distinct distributions into two groups, leading to suboptimal modeling of the true data.

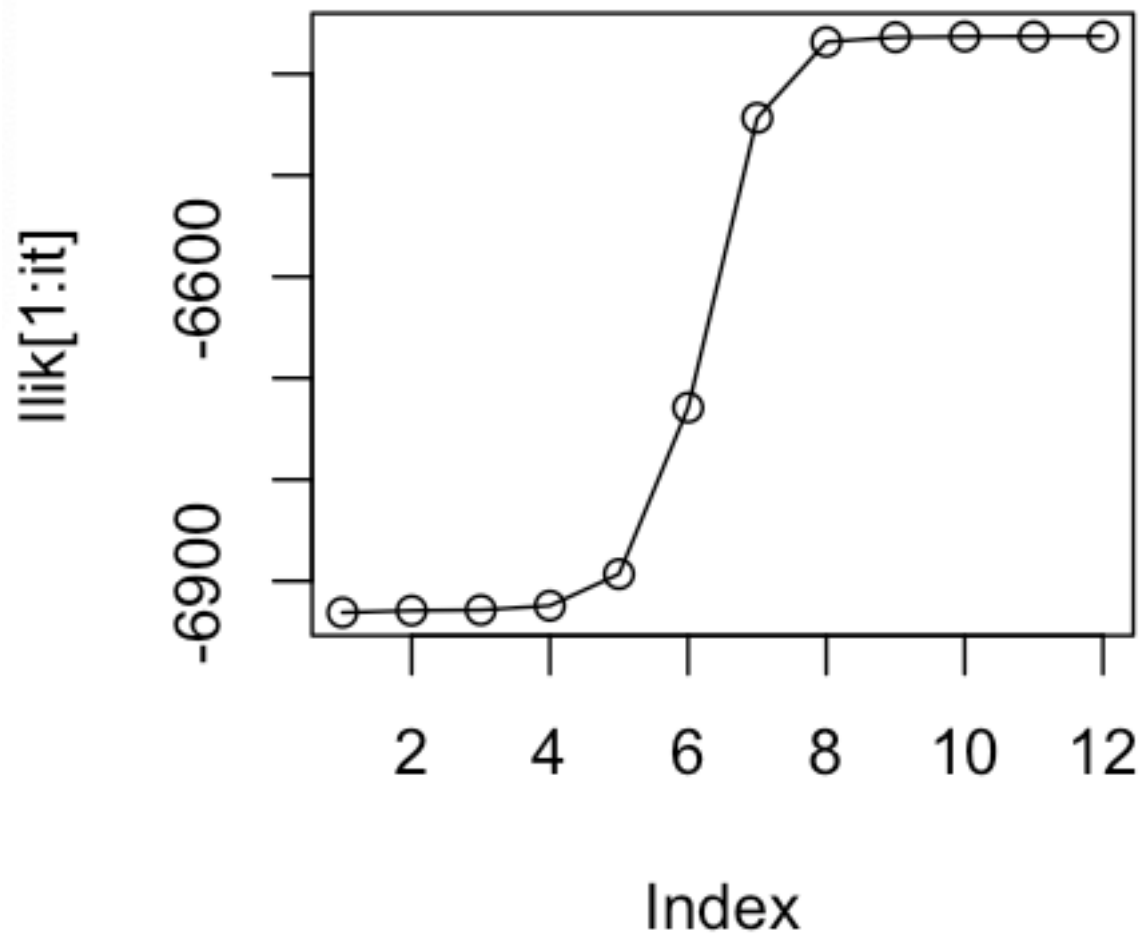


Figure 1: Log-Likelihood Plot for $M=2$

$M = 3$ (Ideal Number of Clusters)

- **Final Log-Likelihood:** -6344.57
- **Number of Iterations for Convergence:** 26
- **Mixing Coefficients (π):**
 - Cluster 1: 0.3417
 - Cluster 2: 0.2690
 - Cluster 3: 0.3893
- **Observed Behavior:** The log-likelihood achieved a higher value, indicating a better fit to the data. The three clusters accurately represented the true data distribution.

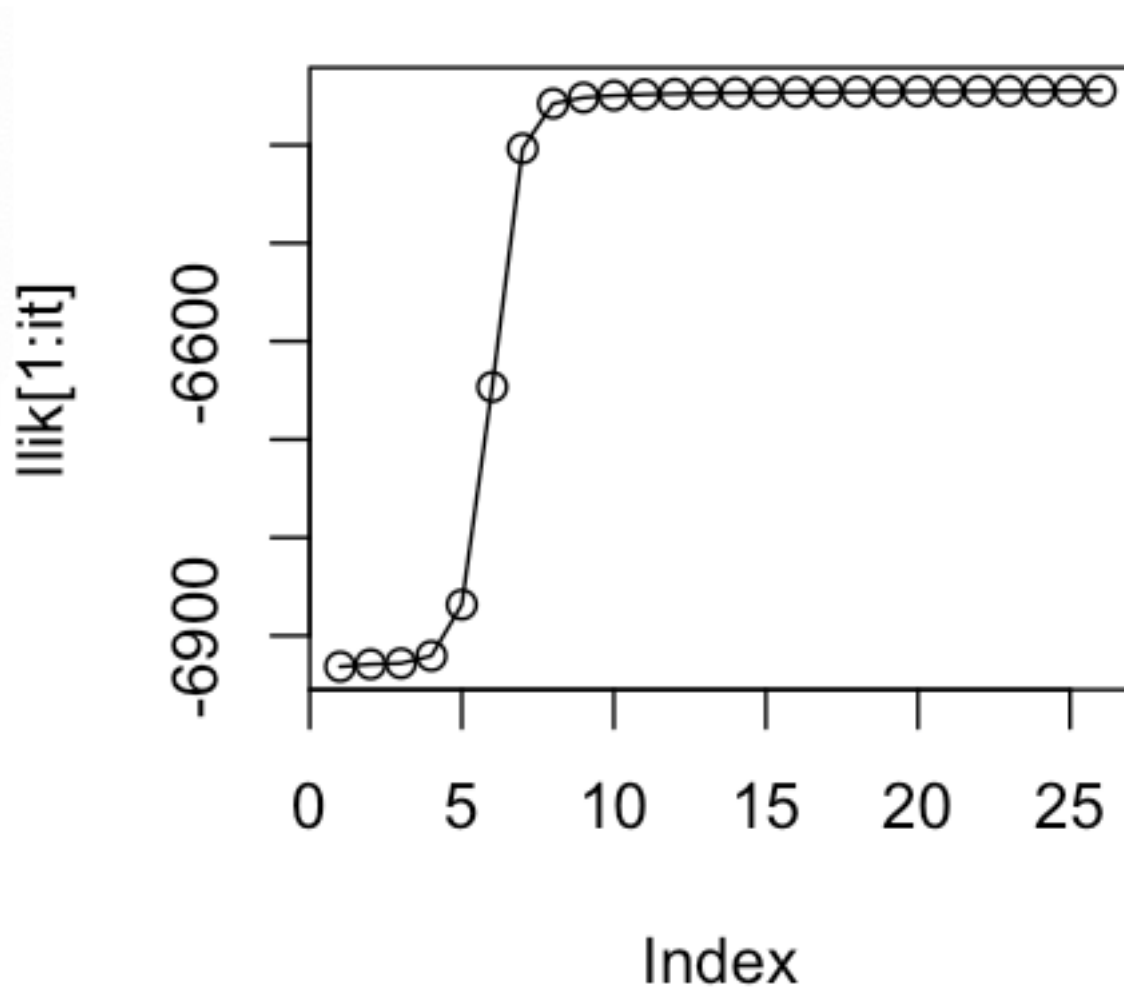


Figure 2: Log-Likelihood Plot for $M=3$

$M = 4$ (Too Many Clusters)

- **Final Log-Likelihood:** -6338.228
- **Number of Iterations for Convergence:** 44

- **Mixing Coefficients (π):**
 - Cluster 1: 0.1547
 - Cluster 2: 0.1419
 - Cluster 3: 0.3514
 - Cluster 4: 0.3520
- **Observed Behavior:** The model overfits the data by creating additional clusters that attempt to segment the data unnecessarily. This results in a marginal improvement in log-likelihood but at the cost of increased complexity.

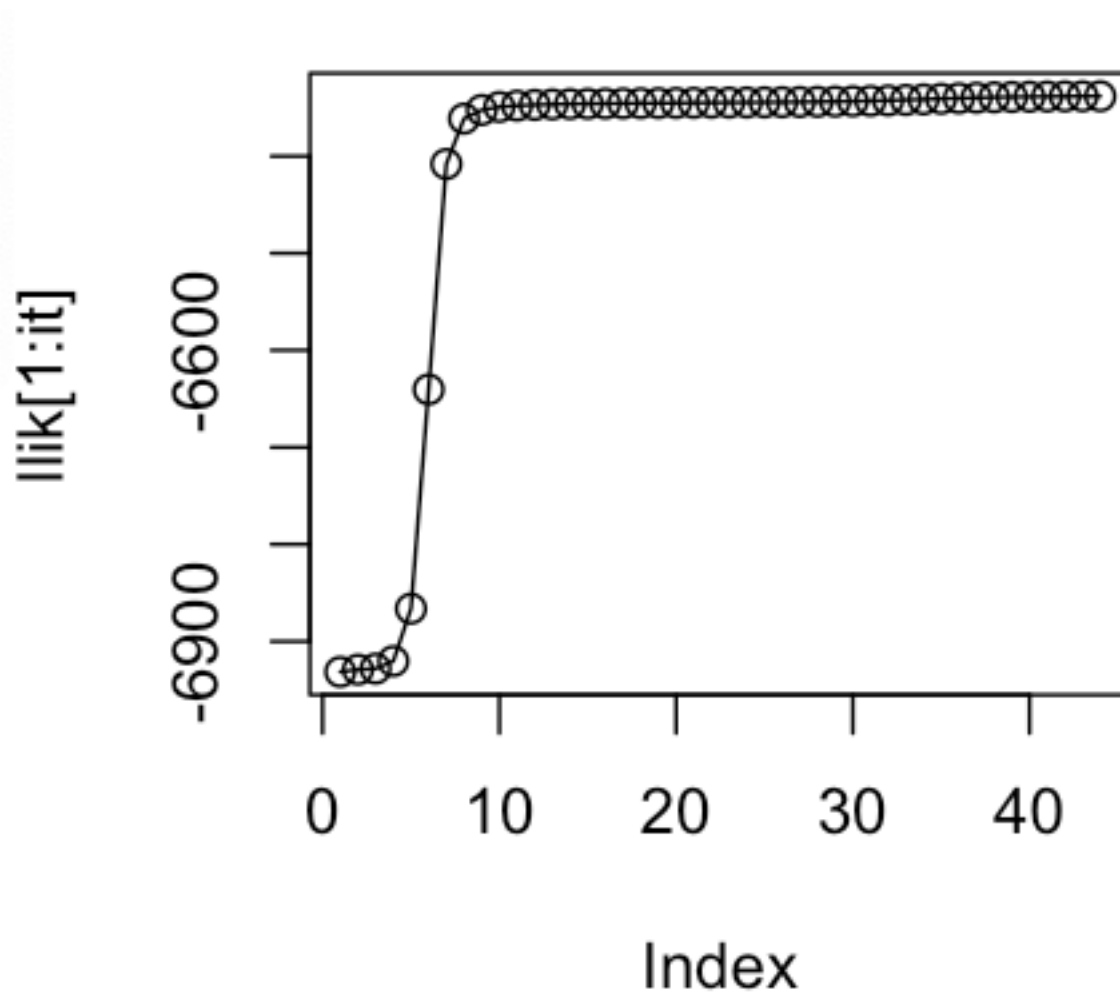


Figure 3: Log-Likelihood Plot for M=4

While the log-likelihood improves as the number of clusters increases, the additional clusters for $M = 4$ do not significantly enhance the fit, indicating overfitting. The ideal choice of $M = 3$ aligns with the true distribution and balances model complexity and fit quality.

Assignment 3

Appendix

Asssignment 1

Asssignment 2

```
set.seed(1234567890)
max_it <- 100 # max number of EM iterations
min_change <- 0.1 # min change in log likelihood between two consecutive iterations
n=1000 # number of training points
D=10 # number of dimensions
x <- matrix(nrow=n, ncol=D) # training data

true_pi <- vector(length = 3) # true mixing coefficients
true_mu <- matrix(nrow=3, ncol=D) # true conditional distributions
true_pi=c(1/3, 1/3, 1/3)
true_mu[1,]=c(0.5,0.6,0.4,0.7,0.3,0.8,0.2,0.9,0.1,1)
true_mu[2,]=c(0.5,0.4,0.6,0.3,0.7,0.2,0.8,0.1,0.9,0)
true_mu[3,]=c(0.5,0.5,0.5,0.5,0.5,0.5,0.5,0.5,0.5,0.5)
plot(true_mu[1,], type="o", col="blue", ylim=c(0,1))
points(true_mu[2,], type="o", col="red")
points(true_mu[3,], type="o", col="green")

# Producing the training data
for(i in 1:n) {
  m <- sample(1:3, 1, prob=true_pi)
  for(d in 1:D) {
    x[i, d] <- rbinom(1, 1, true_mu[m, d])
  }
}

M=3 # number of clusters
w <- matrix(nrow=n, ncol=M) # weights
pi <- vector(length = M) # mixing coefficients
mu <- matrix(nrow=M, ncol=D) # conditional distributions
llik <- vector(length = max_it) # log likelihood of the EM iterations

# Random initialization of the parameters
pi <- runif(M, 0.49, 0.51)
pi <- pi / sum(pi)
for(m in 1:M) {
  mu[m,] <- runif(D, 0.49, 0.51)
}
pi
mu

for(it in 1:max_it) {
  plot(mu[1,], type="o", col="blue", ylim=c(0,1))
  points(mu[2,], type="o", col="red")
}
```

```

points(mu[3,], type="o", col="green")
Sys.sleep(0.5)

# E-step: Computation of the weights
for(data_point in 1:n) {
  for(cluster in 1:M) {
    cluster_probability <- pi[cluster]
    for(feature in 1:D) {
      cluster_probability <- cluster_probability * (mu[cluster, feature]^x[data_point, feature]) *
        ((1 - mu[cluster, feature])^(1 - x[data_point, feature]))
    }
    w[data_point, cluster] <- cluster_probability
  }
  w[data_point, ] <- w[data_point, ] / sum(w[data_point, ])
}

# Log likelihood computation
llik[it] <- 0
for(data_point in 1:n) {
  total_probability <- 0
  for(cluster in 1:M) {
    cluster_probability <- pi[cluster]
    for(feature in 1:D) {
      cluster_probability <- cluster_probability * (mu[cluster, feature]^x[data_point, feature]) *
        ((1 - mu[cluster, feature])^(1 - x[data_point, feature]))
    }
    total_probability <- total_probability + cluster_probability
  }
  llik[it] <- llik[it] + log(total_probability)
}

cat("iteration: ", it, "log likelihood: ", llik[it], "\n")
flush.console()

# Stop if the log likelihood has not changed significantly
if(it > 1 && abs(llik[it] - llik[it-1]) < min_change) {
  break
}

# M-step: ML parameter estimation from the data and weights
for(cluster in 1:M) {
  pi[cluster] <- sum(w[, cluster]) / n
  for(feature in 1:D) {
    mu[cluster, feature] <- sum(w[, cluster] * x[, feature]) / sum(w[, cluster])
  }
}
}

pi
mu
plot(llik[1:it], type="o")

```