## Prob 1. Derive the formulae on p.31.

Gaussian Mixture Model EM

 $\theta = \{\mu_1, \dots, \mu_m, \sigma_1, \dots, \sigma_m, \alpha_1, \dots, \alpha_m\}$ , and so from the first section of this note, our likelihood is:

$$L\left( heta \mid X_{1}, \ldots, X_{n}
ight) = \prod_{i=1}^{n} \sum_{k=1}^{m} lpha_{k} N\left(x_{i}; \mu_{k}, \sigma_{k}^{2}
ight)$$

So our log-likelihood is:

$$\ell( heta) = \sum_{i=1}^{n} \log \left( \sum_{k=1}^{m} \alpha_k N\left(x_i; \mu_k, \sigma_k^2\right) \right)$$
 (1)

Take initial guesses for the parameters  $\widehat{\Theta}$ 

E step: compute the posterior distribution of  $z_i$  given the observations

$$\Lambda_{i,k} = P_{\hat{\theta}} (z_i = k \mid x_i) = \frac{\hat{\alpha}_k P_{\hat{\theta}_k} (x_i)}{P_{\hat{\theta}} (x_i)} = \frac{\hat{\alpha}_k P_{\hat{\theta}_k} (x_i)}{\sum_{j=1}^m \hat{\alpha}_j P_{\hat{\theta}_j} (x_i)}$$
(2)

$$Q(\Theta \mid \hat{ heta}) = \sum_{i=1}^{n} \sum_{k=1}^{m} \Lambda_{i,k} \log(lpha_k P_{ heta_k}\left(x_i
ight))$$

M step: update  $lpha_k, \mu_k, \sigma_k$  for each Gaussian  $k=1,\ldots,m$ 

$$\hat{lpha}_k = rac{1}{n} \sum_{i=1}^n \Lambda_{i,k}, \hat{\mu}_k = rac{\sum_{i=1}^n x_i \Lambda_{i,k}}{\sum_{i=1}^n \Lambda_{i,k}}, \hat{\sigma}_k^2 = rac{\sum_{i=1}^n \Lambda_{i,k} \|x_i - \hat{\mu}_k\|^2}{\sum_{i=1}^n \Lambda_{i,k}}$$

#### **Proof**

Let the partial derivative of (1) about  $\mu_k$  equal to

$$\sum_{i=1}^{n} \left\{ \frac{1}{\sum_{k=1}^{m} \alpha_k N\left(x_i; \mu_k, \sigma_k\right)} \alpha_k N\left(x_i; \mu_k, \sigma_k\right) \frac{\left(x_i - \mu_k\right)}{\sigma_k^2} \right\} = 0 \tag{3}$$

by (2) and (3)

$$egin{aligned} \sum_{i=1}^n \Lambda_{i,k} rac{(x_i - \mu_k)}{\sigma_k^2} &= 0 \ \Rightarrow \hat{\mu}_k &= rac{\sum_{i=1}^n x_i \Lambda_{i,k}}{\sum_{i=1}^n \Lambda_{i,k}} \end{aligned}$$

Similarly, let the partial derivative of (1) about  $\sigma_k^2$  , we have

$$\sum_{i=1}^{n} \left\{ \frac{1}{\sum_{k=1}^{m} \alpha_{k} N(x_{i}; \mu_{k}, \sigma_{k})} \alpha_{k} N(x_{i}; \mu_{k}, \sigma_{k}) \left( \frac{(x_{i} - \mu_{k})^{2}}{2\sigma_{k}^{4}} - \frac{1}{2\sigma_{k}^{2}} \right) \right\} = 0$$
 (4)

by (2) and (4)

$$\hat{\sigma}_k^2 = rac{\sum_{i=1}^n \Lambda_{i,k} \|x_i - \hat{\mu}_k\|^2}{\sum_{i=1}^n \Lambda_{i,k}}$$

According to the definition of  $\Lambda_{i,k}$  , the estimate of  $\alpha_k$  is obviously that

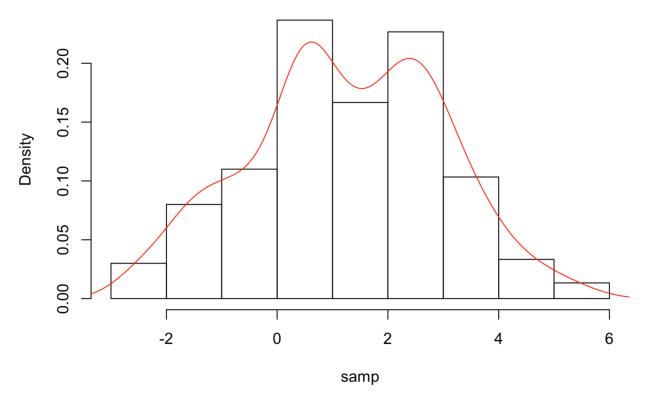
$$\hat{lpha}_k = rac{1}{n} \sum_{i=1}^n \Lambda_{i,k}$$

Q.E.D

# Prob 2 . For $k=3,\,{\rm simulate}$ 100 data points from such a GMM, and use the EM algorithm to estimate the parameters. Check how well the estimates are.

```
set.seed(1234)
   n <- 300
    alpha1 <- 0.4
    mu1 <- 3
    sigmal <- 1
    alpha2 <- 0.4
    mu2 <- -2
    sigma2 <- 2
    alpha3 <- 0.2
10
    mu3 <- 0
    sigma3 <- 2^0.5
11
    n1 <- floor(n*alpha1)</pre>
12
    n2 <- floor(n*(alpha2+alpha1))-n1</pre>
13
    n3 < - n-n2-n1
14
15
    samp <-numeric(n)</pre>
    samp[1:n1] <- rnorm(n1, mu1, sigma1)</pre>
16
17
    samp[(n1+1):n1+n2] \leftarrow rnorm(n2, mu2, sigma2)
    samp[(n2+1):n] \leftarrow rnorm(n3, mu3, sigma3)
    hist(samp, freq = FALSE)
19
20
    lines(density(samp), col = 'red')
21
    #EM
22
    library(mclust)
23
    em <- Mclust(samp)</pre>
    summary(em, parameters = T)
24
```

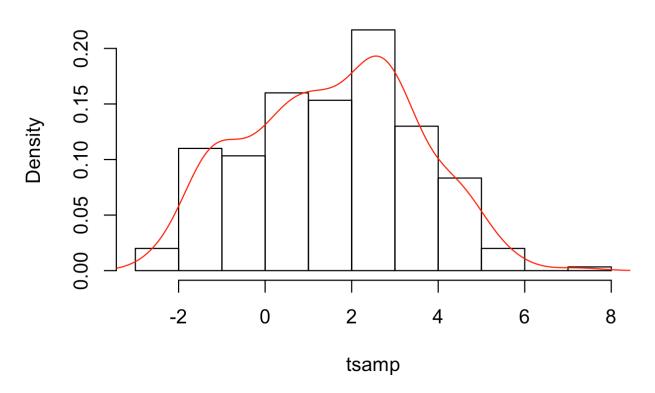
## Histogram of samp



```
Gaussian finite mixture model fitted by EM algorithm
2
3
4
   Mclust V (univariate, unequal variance) model with 3 components:
5
6
   log-likelihood n df
                          BIC
7
        -566.8767 300 8 -1179.384 -1242.349
9
   Clustering table:
10
    1 2 3
11
    63 52 185
12
13
   Mixing probabilities:
         1 2 3
14
15
   0.2089691 0.1350616 0.6559693
16
17
   Means:
18
         1
               2
   19
20
21
   Variances:
22
   0.60241205 0.01478454 1.57299074
```

The result is quite different from the initial set parameters. This is because the three distributions are dense and coupled together, and the estimated value may not be unique. If the distribution is sparse and n is larger, the effect is better. The following figure is a histogram drawn according to the estimated value, and you can see that the fit is well.

## Histogram of tsamp



Prob 3. Finish all the exercises on pages entitled "Exercise".

The law school data set law in the bootstrap package contains average LSAT and average GPA for 15 law schools. This data set is a random sample from the universe of 82 law schools in law 82.

- 1. Estimate the correlation between LSAT and GPA scores, and compute the bootstrap estimate of the standard error of the sample correlation.
- 2. Use the boot function from package boot.

```
> print(cor(law$LSAT, law$GPA)) # sample correlation coef
2
   [1] 0.7763745
   > print(cor(law82$LSAT, law82$GPA)) # population correlation coef
   [1] 0.7599979
4
   # bootstrap estimate of standard error of
   B <- 200 #number of replicates
6
7
   n <- nrow(law) #sample size</pre>
   R <- numeric(B) #storage for replicates</pre>
   #bootstrap estimate of standard error of R
9
10
   for (b in 1:B) {
```

```
#randomly select the indices
i <- sample(1:n, size = n, replace = TRUE)

LSAT <- law$LSAT[i] # i -- vector of indices

GPA <- law$GPA[i]

R[b] <- cor(LSAT, GPA)

#output

print(se.R <- sd(R))

[1] 0.1297349</pre>
```

### Compute the bootstrap estimation of bias for the law school sample correlation problem

```
library(bootstrap)
 2
   data(law)
   theta.hat <- cor(law$LSAT, law$GPA)
   # bootstrap estimate of bias
   B <- 2000 # number of bootstrap replicates
 6
   n <- nrow(law) # sample size</pre>
 7
   theta.b <- numeric(B)</pre>
   for (b in 1:B) { # randomly select the indices
    i <- sample(1:n, size = n, replace = TRUE) # i is a vector of indices</pre>
9
10
   LSAT <- law$LSAT[i]
   GPA <- law$GPA[i]</pre>
11
    theta.b[b] <- cor(LSAT, GPA)</pre>
12
13
   bias <- mean(theta.b) - theta.hat</pre>
14
15
   bias
16 > bias
17 [1] 0.007822616
```

The patch (bootstrap) data contains measurements of a certain hormone in the bloodstream of eight subjects after wearing a medical patch. The parameter of interest is

$$heta = rac{E(new) - E(old)}{E(old) - E(placebo)}$$

If  $|\theta| \leq 0.2$ , this indicates bioequivalence of the old and new patches. The statistic is  $\bar{Y}/\bar{Z}$ . Compute a bootstrap estimate of bias in the bioequivalence ratio statistic.

```
data(patch, package = "bootstrap")
n <- nrow(patch)
y <- patch$y
z <- patch$z
theta.hat <- mean(y) / mean(z)</pre>
```

```
6  > print (theta.hat)
7  [1] -0.0713061
8  theta.jack <- numeric(n)
9  for (i in 1:n){
10  theta.jack[i] <- mean(y[-i]) / mean(z[-i])
11  }
12  bias <- (n - 1) * (mean(theta.jack) - theta.hat)
13  > print(bias)
14  [1] 0.008002488
```

### Compute the confidence intervals for the patch ratio statistic.

```
#for boot and boot.ci
 1
    library(boot)
         data(patch, package = "bootstrap")
 2
 3
         theta.boot <- function(dat, ind) {</pre>
 4
             #function to compute the statistic
 5
             y <- dat[ind, 1]</pre>
             z <- dat[ind, 2]</pre>
 6
 7
             mean(y) / mean(z)
 8
        }
 9
        y <- patch$y
10
        z <- patch$z
        dat <- cbind(y, z)</pre>
11
12
        boot.obj <- boot(dat, statistic = theta.boot, R = 2000)</pre>
13
        print(boot.obj)
        print(boot.ci(boot.obj,
14
15
                        type = c("basic", "norm", "perc")))
16
        #calculations for bootstrap confidence intervals
        alpha <- c(.025, .975)
17
18
        #normal
19
        print(boot.obj$t0 + qnorm(alpha) * sd(boot.obj$t))
20
         #basic
21
        print(2*boot.obj$t0 - quantile(boot.obj$t, rev(alpha), type=1))
22
         #percentile
         print(quantile(boot.obj$t, alpha, type=6))
23
```

```
ORDINARY NONPARAMETRIC BOOTSTRAP

Call:
boot(data = dat, statistic = theta.boot, R = 2000)

Bootstrap Statistics:
original bias std. error
```

```
10 t1* -0.0713061 0.007706594 0.1009925
11
   BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
12
13
   Based on 2000 bootstrap replicates
14
   CALL:
15
   boot.ci(boot.out = boot.obj, type = c("basic", "norm", "perc"))
16
17
   Intervals :
18
   Level Normal
19
                                 Basic
                                                   Percentile
20
   95% (-0.2770, 0.1189) (-0.3126, 0.0863) (-0.2289, 0.1700)
   Calculations and Intervals on Original Scale
21
22
23
24
   > #calculations for bootstrap confidence intervals
25
   > alpha <- c(.025, .975)
26
27
   > #normal
   > print(boot.obj$t0 + qnorm(alpha) * sd(boot.obj$t))
28
   [1] -0.2692477 0.1266355
29
30
   > #basic
31
32
   > print(2*boot.obj$t0 -
33 +
              quantile(boot.obj$t, rev(alpha), type=1))
        97.5%
34
   -0.31247046 0.08631008
35
36
   >
37
   > #percentile
   > print(quantile(boot.obj$t, alpha, type=6))
38
39
         2.5%
                   97.5%
   -0.2288723 0.1700097
40
41
```

## Compute the confidence intervals using the boot. ci function.

```
BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
2
   Based on 2000 bootstrap replicates
3
4
   CALL:
5
   boot.ci(boot.out = boot.obj, type = c("basic", "norm", "perc"))
6
7
   Intervals :
   Level Normal
8
                               Basic
                                                 Percentile
   95% (0.5223, 1.0388) (0.5902, 1.0886) (0.4641, 0.9625)
9
   Calculations and Intervals on Original Scale
10
```

Use linear regression model to predict cat heart weights with cat body weights. Compute the confidence intervals of the regression coefficients with bootstrap resampling.

```
1
    library(MASS)
 2
    data(cats)
    resample <- function(x) {</pre>
 3
    sample(x,size=length(x),replace=TRUE)
5
 6
    coefs.cats.lm <- function(subset) {</pre>
7
    fit <- lm(Hwt~Bwt,data=cats,subset=subset)</pre>
8
    return(coefficients(fit))
9
    cats.lm.sampling.dist <- replicate(1000,</pre>
10
    coefs.cats.lm(resample(1:nrow(cats))))
    (limits <- apply(cats.lm.sampling.dist,1,quantile,c(0.025,0.975)))
```

```
1 (Intercept) Bwt
2 2.5% -1.948358 3.442391
3 97.5% 1.210477 4.636989
```