Homework7

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9/21/2020

Dirichlet Process Mixture Models The goal of this homework is to use the R package dirichletprocess to implement an infinite dimensional Gaussian mixture model, then compare it to finite Gaussian mixtures with model selection via cross-validation (mclust).

1.First use rnorm to generate random data from 5 cluster centers, as we did in class last week (use 20 data points per cluster center). Scale the data set.

```
library(ggplot2)
library(data.table)
library(mclust)
library(dirichletprocess)
N.true.clusters <- 5
true.means <- 1:N.true.clusters
N.simulated.data <- 20*N.true.clusters
means.simulated.data <- rep(true.means, each=N.simulated.data/N.true.clusters
)

# set.seed(1)
true.sd <- 0.2
sim.data.vec <- rnorm(N.simulated.data, means.simulated.data, sd=true.sd)

## linear transformation on each column so that mean=0 and sd=1.
df <- scale(sim.data.vec)
```

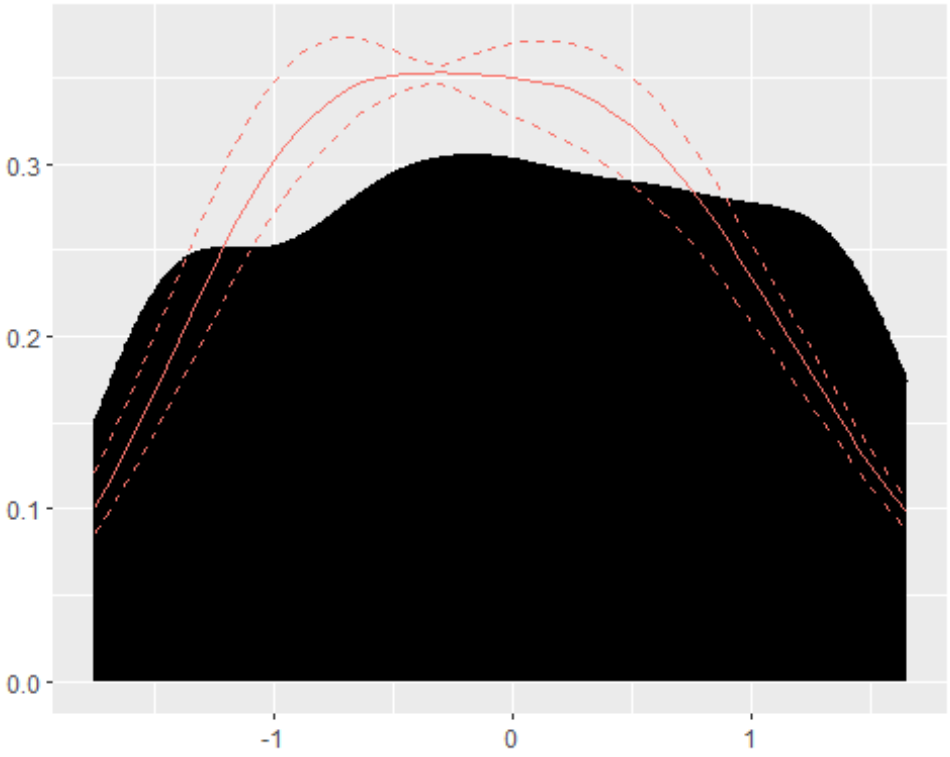
Then use dirichletprocess::DirichletProcessGaussian to fit the mixture model, Use system.time on the model fitting process – how long does it take?

```
dp <- DirichletProcessGaussian(df)

system.time(dp<- Fit(dp, its=500))#iterations of sampling algorithm.

##    user  system elapsed
##     3.3     0.0     3.3
```

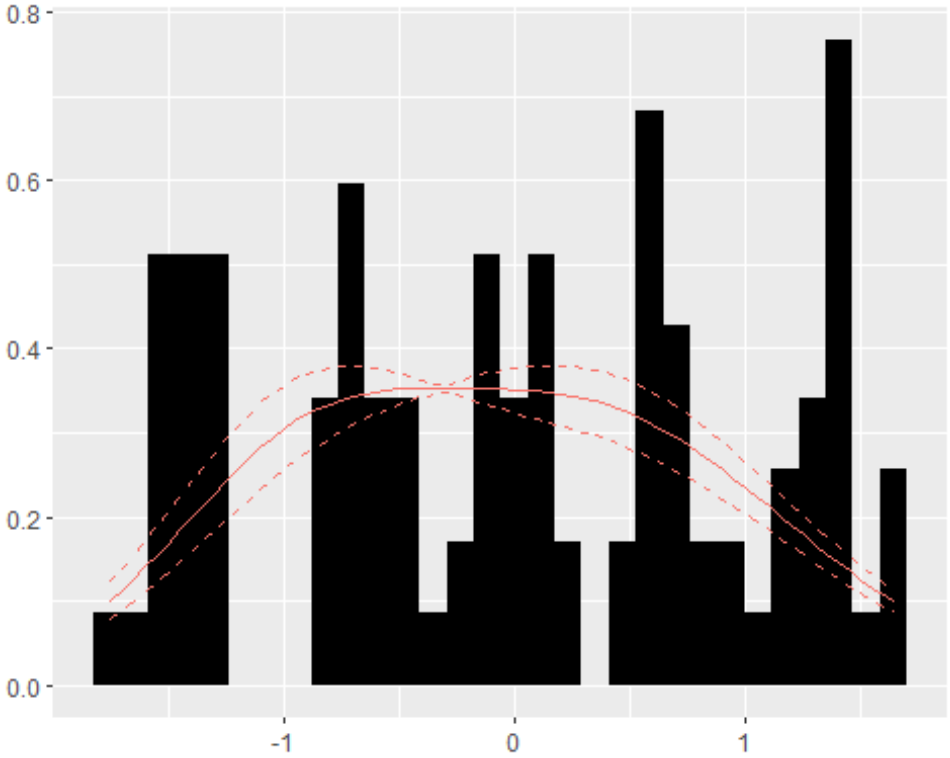
It takes 3.3seconds

then use the plot function to make a figure similar to Figure 1 (right) in vignette ("dirichletprocess", package="dirichletprocess") (histogram for data, solid/dashed lines for the model).

```
plot(dp)
```

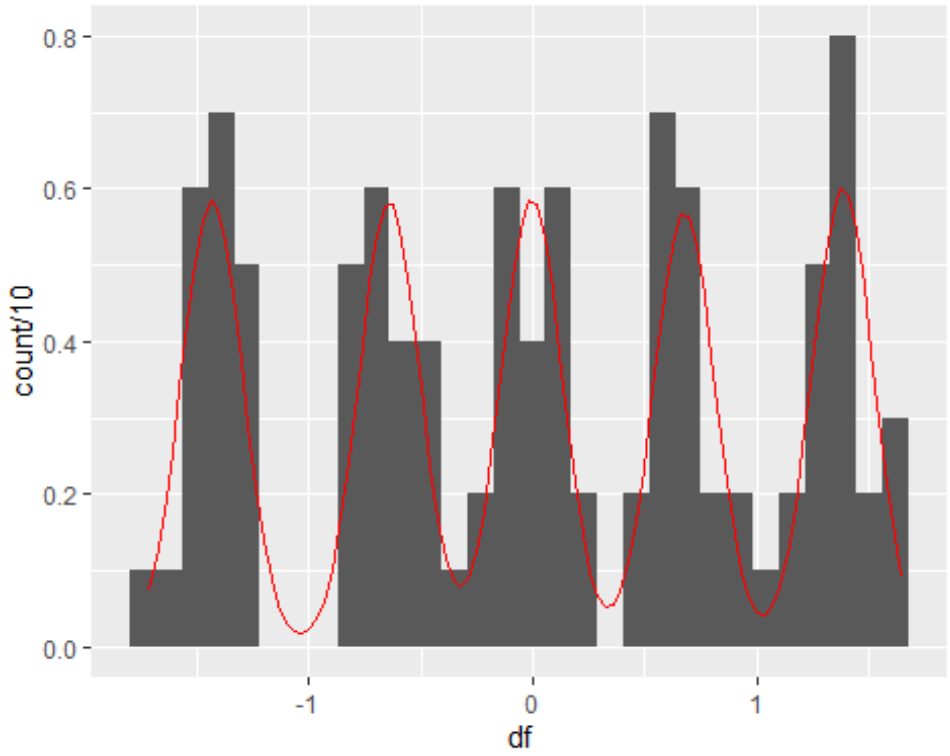



```r
plot(dp, data_method="hist")
```



2.Now use mclust to fit a model with 5 clusters to the scaled data. Make a plot similar to the previous one. Use geom_bar or geom_histogram to plot the data. Use the mclust::dens function to compute the mixture density to plot with geom_line. Do the two models look similar?

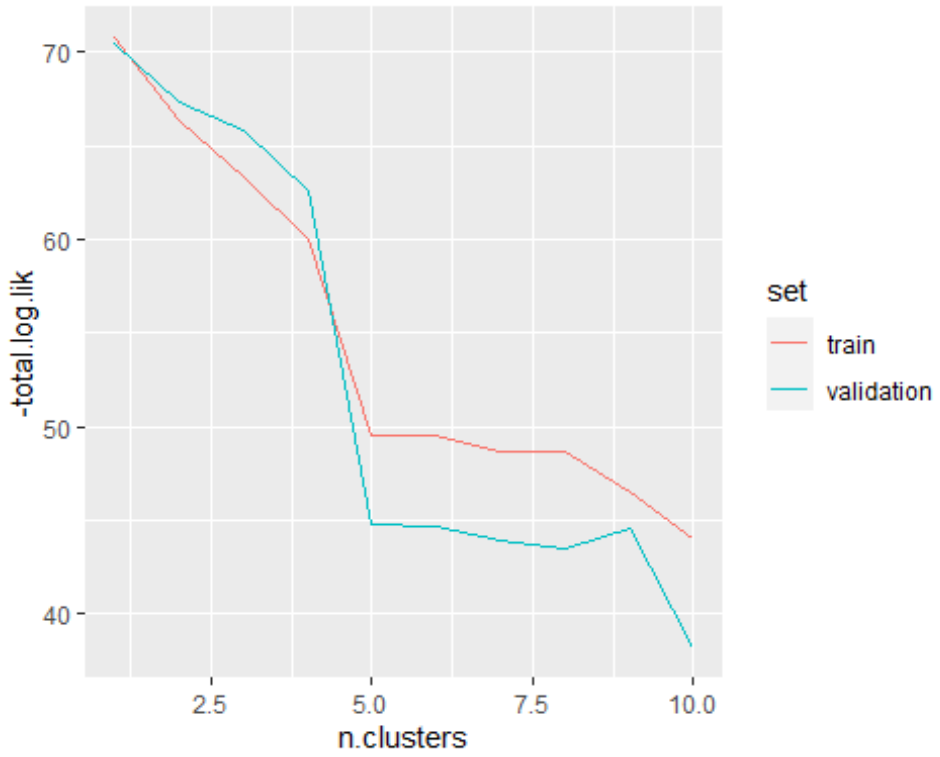
```
#Now use mclust to fit a model with 5 clusters to the scaled data.
fit <- Mclust(df,5)
conc.vec <- seq(min(df),max(df),l=100)

#Use the mclust::dens function to compute the mixture density
Dens <- dens(modelName = fit$modelName,data = conc.vec,parameters = fit$param
eters)

density <- data.table(concentration = conc.vec,den = Dens)

ggplot() + geom_histogram(aes(x=df, y =stat(count) /10)) + geom_line(aes(conc
entration,den),data=density,color='red')

## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



These two models don't simlier to each other

3.Divide the data into 50% train, 50% validation. Use mclust to fit a mixture model with K=1 to 10 components on the train set, then compute and plot y=validation negative log likelihood as a function of x=number of components. Use system.time on the whole process (excluding the plot) – how much time does it take to do model selection yourself? Is that faster or slower than the Dirichlet Process mixture model from question?

```
set.prop.vec <- c(validation=0.5, train=0.5)
N <- length(df)
rounded.counts <- floor(set.prop.vec*(N))
not.shuffled.sets <- rep(names(set.prop.vec), rounded.counts)

set.seed(1)
shuffled.sets <- sample(not.shuffled.sets)
clusters <- 10

lik.dt.list <- list()



system.time(
  for(n.clusters in 1:clusters){
    for (set in names(set.prop.vec)) {
        data.set <- df[shuffled.sets == set,]
        mclust <- Mclust(data.set, n.clusters, modelNames="E")
        log.lik.vec <- dens(
                            modelName = mclust[["modelName"]],
                            data = data.set,
                            parameters = mclust[["parameters"]],
                            logarithm=TRUE)
       total.log.lik <- sum(log.lik.vec)
       rbind(my=total.log.lik, mclust=mclust[["loglik"]])
       lik.dt.list[[paste(n.clusters, set)]] <- data.table(n.clusters, set, t
otal.log.lik)
    }

}
)

##    user  system elapsed
##    0.11    0.00    0.11

lik.dt <- do.call(rbind, lik.dt.list)

ggplot()+
  geom_line(aes(
    n.clusters, -total.log.lik, color=set),
    data=lik.dt)
```



It takes 0.11seconds. It is much faster than the Dirichlet Process mixture model