```r
#irisClassificationPre.r, (C) 2014 Shojiro Tanaka
#getwd()
#objects()
#list.files()
#help(foo)

rm(list=ls(all=TRUE))

#区分別のデータにする（cm単位；Rに予め組み込まれている）
data1 <- subset(iris, iris[,5]=='setosa');
data2 <- subset(iris, iris[,5]=='versicolor');
data3 <- subset(iris, iris[,5]=='virginica');

#平均，分散・共分散などの計算
mean1   <- mean(data1[,1:4])
mean1   <- matrix(mean1,1,4)
cov1    <- cov (data1[,1:4])
invCov1 <- solve(cov1);
denom1  <- (2*pi)^(2/2)*sqrt(det(cov1));

mean2   <- mean(data2[,1:4])
mean2   <- matrix(mean2,1,4)
cov2    <- cov (data2[,1:4])
invCov2 <- solve(cov2);
denom2  <- (2*pi)^(2/2)*sqrt(det(cov2));

mean3   <- mean(data3[,1:4])
mean3   <- matrix(mean3,1,4)
cov3    <- cov (data3[,1:4])
invCov3 <- solve(cov3);
denom3  <- (2*pi)^(2/2)*sqrt(det(cov3));

#大小の計算
r       <- matrix(0,1,4)
c       <- matrix(0,1,3)
t       <- c(0)
class   <- c(0)
z       <- matrix(0,150,2)
for(i in 1:150) {
  r <- as.matrix(iris[i,1:4])
  c[1,1] <- log(denom1)+(r-mean1) %*% invCov1 %*% t(r-mean1)
  c[1,2] <- log(denom2)+(r-mean2) %*% invCov2 %*% t(r-mean2)
  c[1,3] <- log(denom3)+(r-mean3) %*% invCov3 %*% t(r-mean3)
  t  <- min(c)
  if(t == c[1,1]) class <- 1
  if(t == c[1,2]) class <- 2
  if(t == c[1,3]) class <- 3
  z[i,1] <- iris[i,5]
  z[i,2] <- class
}
```