```r
#irisClassifDisp-allVar-MuchTIME.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])
cov1    <- cov (data1[,1:4])
invCov1 <- solve(cov1);
denom1  <- (2*pi)^(2/2)*sqrt(det(cov1));

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

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

#大小の計算（0cm～10cm，1mm毎）
r  <- array(0, dim=c(101,51,61,31))
c  <- matrix(0,1,3)
t  <- c(0)
z  <- array(0, dim=c(101,51,61,31))
for(l in 0:101){
  x4 <- l/10
  for(k in 0:51){
    x3 <- k/10
    for(j in 0:61){
      x2 <- j/10
      for(i in 0:31){
        x1 <- i/10
        r <- cbind(x4, x3, x2, x1)
        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[l,k,j,i] <- class
      }
    }
  }
}

#3D表示
x3 <- seq(0,3,length=61)
```

```
x4 <- seq(0,6,length=31)

persp(x3,x4,z[59,31,,], theta =10, phi=20, expand=0.5,col="grey")

dev.new()
#par(new=T)
#x,y軸の表示に改善が必要
image(x3,x4,z[59,31,,])
```