

```

#irisClassificationDisplay-x3x4.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[,3:4])
cov1 <- cov (data1[,3:4])
invCov1 <- solve(cov1)
denom1 <- (2*pi)^(2/2)*sqrt(det(cov1))

mean2 <- mean(data2[,3:4])
cov2 <- cov (data2[,3:4])
invCov2 <- solve(cov2)
denom2 <- (2*pi)^(2/2)*sqrt(det(cov2))

mean3 <- mean(data3[,3:4])
cov3 <- cov (data3[,3:4])
invCov3 <- solve(cov3);
denom3 <- (2*pi)^(2/2)*sqrt(det(cov3))

#各区分共通の分散を求める
#cov <- (n1*cov1+n2*cov2+n3*cov3)/N
cov <- (cov1+cov2+cov3)/3
invCov <- solve(cov)

#大小の計算 (0cm~10cm, 1mm毎)
r <- matrix(0, nrow=1, ncol=2)
c <- matrix(0, 1, 3)
t <- c(0)
z <- array(0, dim=c(101, 101))
for(l in 0:101) {
  x4 <- l/10
  for(k in 0:101) {
    x3 <- k/10
    r <- cbind(x4, x3)
    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)
#    c[1,1] <- (r-mean1) %*% invCov %*% t(r-mean1)
#    c[1,2] <- (r-mean2) %*% invCov %*% t(r-mean2)
#    c[1,3] <- (r-mean3) %*% invCov %*% 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] <- class
  }
}
}

```

#x, y軸の表示に改善が必要
image(z)

dev.new()
#par(new=T)
#x, y軸の表示に改善が必要
contour(z)