

```

#irisBivariateDistributionDisplays-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));

#2変量正規分布の計算 (0cm~10cm, 1mm毎)
r1 <- matrix(0, nrow=101, ncol=101)
z1 <- matrix(0, nrow=101, ncol=101)
for(j in 0:100) {
  y <- j/10
  for(i in 0:100) {
    x <- i/10
    r1 <- cbind(y, x)
    z1[j, i] <- (1.0/denom1)*exp( -(1.0/2.0) *(r1-mean1) %*% invCov1 %*%
t(r1-mean1) )
  }
}
r2 <- matrix(0, nrow=101, ncol=101)
z2 <- matrix(0, nrow=101, ncol=101)
for(j in 0:100) {
  y <- j/10
  for(i in 0:100) {
    x <- i/10
    r2 <- cbind(y, x)
    z2[j, i] <- (1.0/denom2)*exp( -(1.0/2.0) *(r2-mean2) %*% invCov2 %*%
t(r2-mean2) )
  }
}
r3 <- matrix(0, nrow=101, ncol=101)
z3 <- matrix(0, nrow=101, ncol=101)
for(j in 0:100) {
  y <- j/10
  for(i in 0:100) {
    x <- i/10

```

```
    r3 <- cbind(y, x)
    z3[j, i] <- (1.0/denom3)*exp( -(1.0/2.0) *(r3-mean3) %*% invCov3 %*%
t(r3-mean3) )
  }
}
```

#3D表示

```
x3 <- seq(0, 10, length=101)
x4 <- x3
```

```
persp(x3, x4, z1, theta =10, phi=20, expand=0.5, col="red")
```

```
dev.new() #par(new=T)
persp(x3, x4, z2, theta =10, phi=20, expand=0.5, col="blue")
```

```
dev.new() #par(new=T)
persp(x3, x4, z3, theta =10, phi=20, expand=0.5, col="green")
```