Modern Applyed Statistics(Chap 11)

Library Package

```
library(MASS)
# install.packages("../package/xgobi_1.2-15.tar.gz", repos = NULL, type = "source")
# https://cran.r-project.org/src/contrib/Archive/xgobi/
library(xgobi)
library(class)
```

Data input

```
# 1. Iris data
data(iris3)
head(iris)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa
## 3          4.7         3.2          1.3         0.2  setosa
## 4          4.6         3.1          1.5         0.2  setosa
## 5          5.0         3.6          1.4         0.2  setosa
## 6          5.4         3.9          1.7         0.4  setosa
```

```
# 2. Leptograpsus variegatus crabs data
data("crabs")
head(crabs)
```

```
##   sp sex index   FL  RW   CL   CW  BD
## 1  B   M     1  8.1 6.7 16.1 19.0 7.0
## 2  B   M     2  8.8 7.7 18.1 20.8 7.4
## 3  B   M     3  9.2 7.8 19.0 22.4 7.7
## 4  B   M     4  9.6 7.9 20.1 23.1 8.2
## 5  B   M     5  9.8 8.0 20.3 23.0 8.2
## 6  B   M     6 10.8 9.0 23.0 26.5 9.8
```

1. Visualization Methods

1-1) Principal component analysis

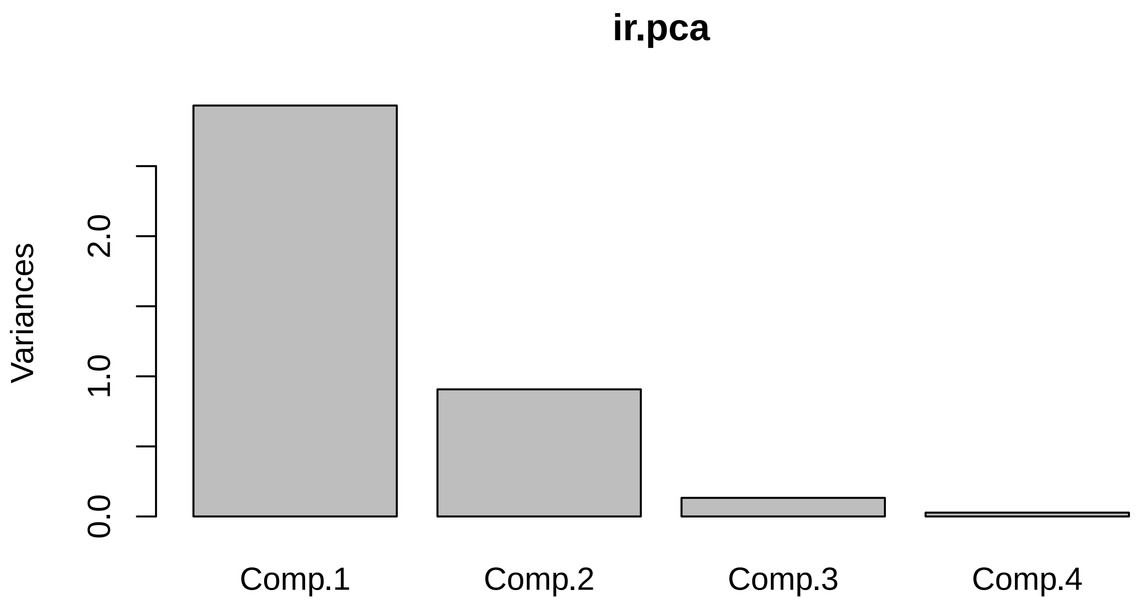
```
# Iris Data
ir <- rbind(iris3[,,1], iris3[,,2], iris3[,,3])
ir.species <- factor(c(rep("s", 50), rep("c", 50), rep("v", 50)))
(ir.pca <- princomp(log(ir), cor = T))
```

```
## Call:
## princomp(x = log(ir), cor = T)
##
## Standard deviations:
##    Comp.1    Comp.2    Comp.3    Comp.4
## 1.7124583 0.9523797 0.3647029 0.1656840
##
##  4  variables and  150 observations.
```

```
summary(ir.pca)
```

```
## Importance of components:
##                           Comp.1    Comp.2     Comp.3    Comp.4
## Standard deviation     1.7124583 0.9523797 0.36470294 0.1656840
## Proportion of Variance 0.7331284 0.2267568 0.03325206 0.0068628
## Cumulative Proportion  0.7331284 0.9598851 0.99313720 1.0000000
```

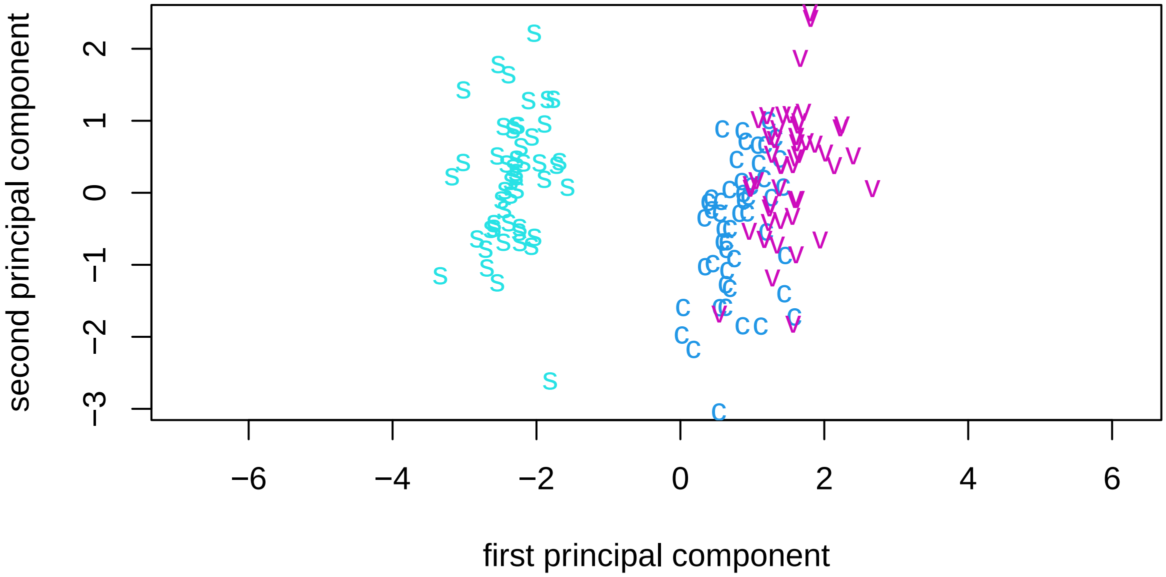
```
plot(ir.pca)
```



```
loadings(ir.pca)
```

```
##
## Loadings:
##          Comp.1 Comp.2 Comp.3 Comp.4
## Sepal L.  0.504  0.455  0.709  0.191
## Sepal W. -0.302  0.889 -0.331
## Petal L.  0.577        -0.219 -0.786
## Petal W.  0.567        -0.583  0.580
##
##                Comp.1 Comp.2 Comp.3 Comp.4
## SS loadings      1.00   1.00   1.00   1.00
## Proportion Var   0.25   0.25   0.25   0.25
## Cumulative Var   0.25   0.50   0.75   1.00
```

```
ir.pc <- predict(ir.pca)
eqscplot(ir.pc[, 1:2], type = "n",
         xlab = "first principal component",
         ylab = "second principal component")
text(ir.pc[, 1:2], labels = as.character(ir.species),
     col = 3 + as.integer(ir.species))
```



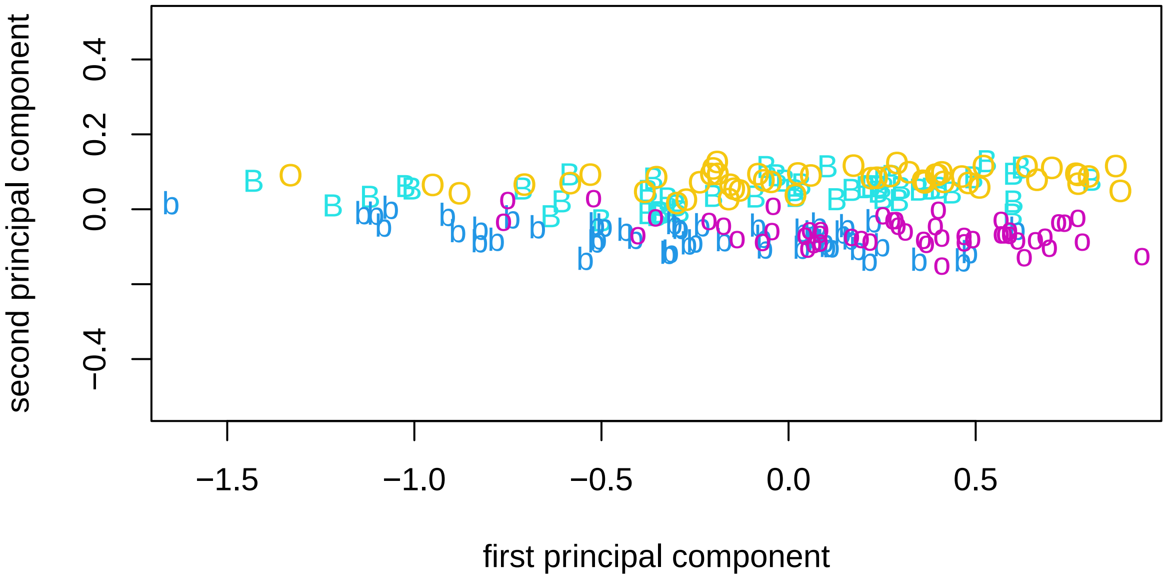
```
# Leptograpsus variegatus crabs dat
lcrabs <- log(crabs[,4:8])
crabs.grp <- factor(c("B", "b", "O", "o")[rep(1:4, each = 50)])
(lcrabs.pca <- princomp(lcrabs))
```

```
## Call:
## princomp(x = lcrabs)
##
## Standard deviations:
##      Comp.1      Comp.2      Comp.3      Comp.4      Comp.5
## 0.516640451 0.074653581 0.047914392 0.024804021 0.009052189
##
##  5  variables and  200 observations.
```

```
loadings(lcrabs.pca)
```

```
##
## Loadings:
##    Comp.1 Comp.2 Comp.3 Comp.4 Comp.5
## FL  0.452  0.157  0.438  0.752  0.114
## RW  0.387 -0.911
## CL  0.453  0.204 -0.371        -0.784
## CW  0.440        -0.672         0.591
## BD  0.497  0.315  0.458 -0.652  0.136
##
##                 Comp.1 Comp.2 Comp.3 Comp.4 Comp.5
## SS loadings        1.0    1.0    1.0    1.0    1.0
## Proportion Var     0.2    0.2    0.2    0.2    0.2
## Cumulative Var     0.2    0.4    0.6    0.8    1.0
```

```
lcrabs.pc <- predict(lcrabs.pca)
dimnames(lcrabs.pc) <- list(NULL, paste("PC", 1:5, sep = ""))
eqscplot(lcrabs.pc[, 1:2], type = "n",
         xlab = "first principal component",
         ylab = "second principal component")
text(lcrabs.pc[, 1:2], labels = as.character(crabs.grp),
     col = 3 + as.integer(crabs.grp))
```



1-2) Exploratory projection pursuit

```
xgobi(lcrabs, colors = c("SkyBlue", "SlateBlue", "Orange", "Red")[rep(1:4, each = 50)])
```

```
## C:/Users/ParkSeHyun/AppData/Local/R/win-library/4.2/xgobi/scripts/xgobi.bat -vtitle 'lcrabs' -std mm
```

```
xgobi(lcrabs, glyphs = 12 + 5*rep(0:3, each = 50))
```

```
## C:/Users/ParkSeHyun/AppData/Local/R/win-library/4.2/xgobi/scripts/xgobi.bat -vtitle 'lcrabs' -std mm
```

1-3) Distance methods

```
par(mfrow = c(2,2))

ir.scal <- cmdscale(dist(ir) , k = 2, eig = T)
ir.scal$points[, 2] <- -ir.scal$points[, 2]
eqscplot(ir.scal$points, type = "n", main = "Metric scaling")
text(ir.scal$points, labels = as.character(ir.species), col = 3 + as.integer(ir.species), cex = 0.8)

distp <- dist(ir)
dist2 <- dist(ir.scal$points)
sum((distp - dist2)^2)/sum(distp^2)
```

```
## [1] 0.001746943
```

```
ir.sam <- sammon(dist(ir[-143,]))
```

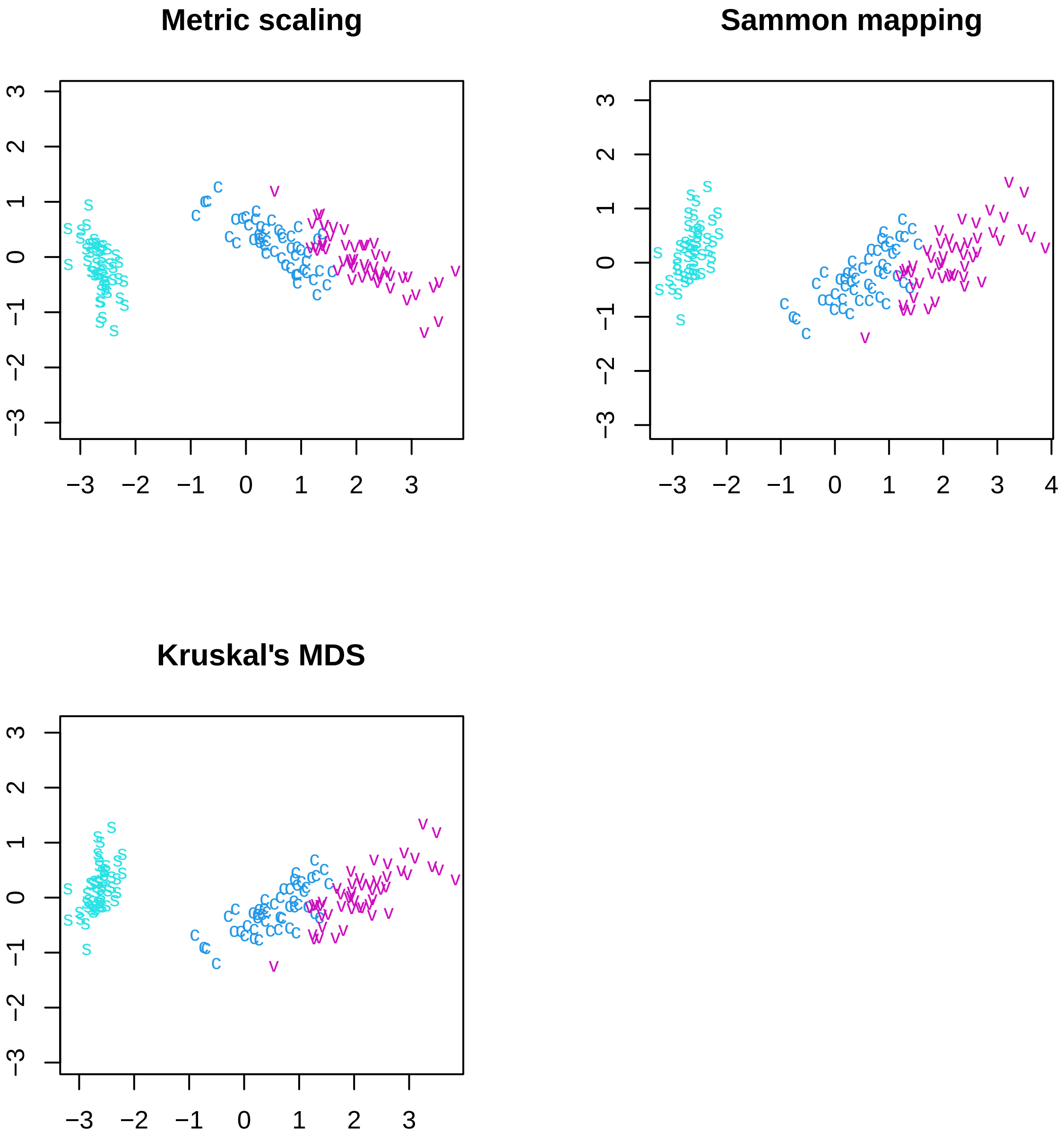
```
## Initial stress        : 0.00678
## stress after  10 iters: 0.00404, magic = 0.500
## stress after  12 iters: 0.00402
```

```
eqscplot(ir.sam$points, type = "n", main = "Sammon mapping")
text(ir.sam$points, labels = as.character(ir.species[-143]), col = 3 + as.integer(ir.species), cex = 0.8

ir.iso <- isoMDS(dist(ir[-143,]))
```

```
## initial  value 3.024856
## iter   5 value 2.638471
## final  value 2.579979
## converged
```

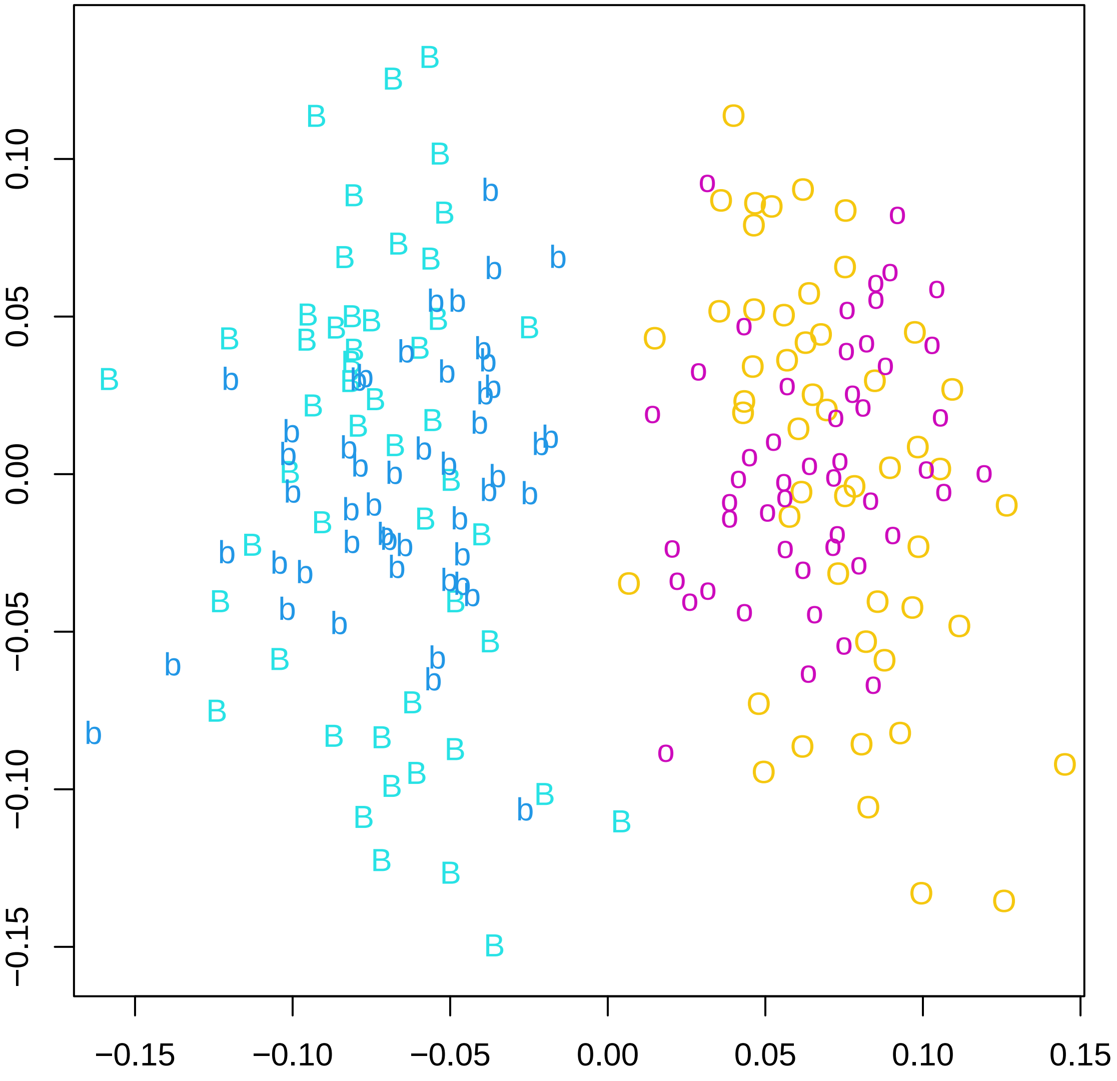
```
eqscplot(ir.iso$points, type = "n", main = "Kruskal's MDS")
text(ir.iso$points, labels = as.character(ir.species[-143]), col = 3 + as.integer(ir.species), cex = 0.8
```



```
cr.scale <- 0.5 * log(crabs$CL * crabs$CW)
slcrabs <- lcrabs - cr.scale
cr.means <- matrix(0, 2, 5)
cr.means[1,] <- colMeans(slcrabs[crabs$sex == "F", ])
cr.means[2,] <- colMeans(slcrabs [crabs$sex == "M", ])
dslcrabs <- slcrabs - cr.means[as.numeric(crabs$sex),]
lcrabs.sam <- sammon(dist(dslcrabs))
```

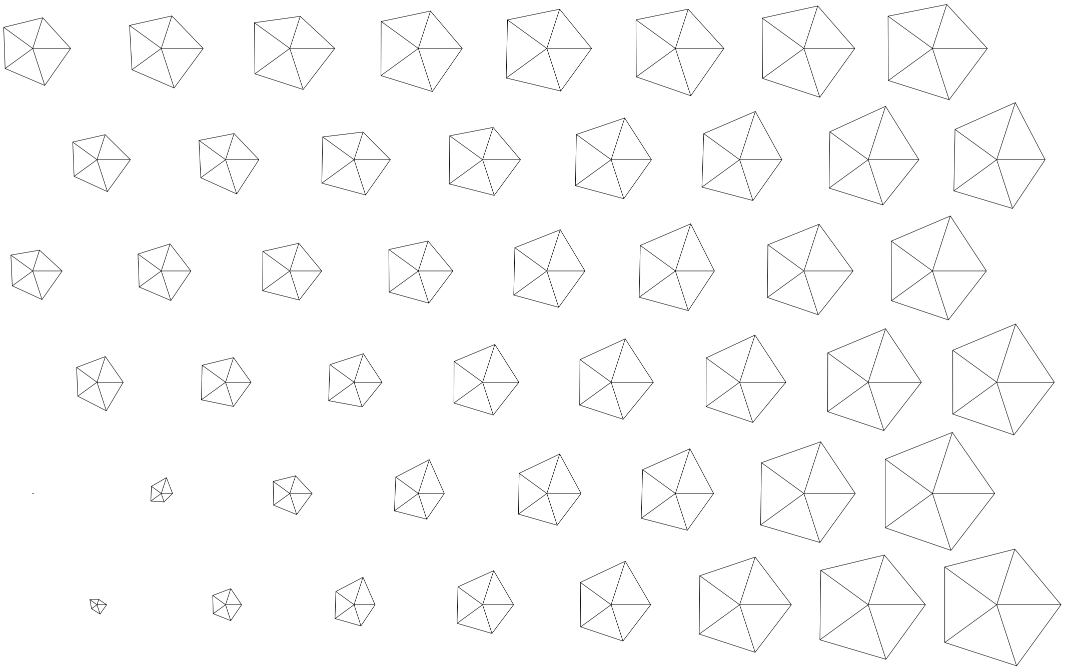
```
## Initial stress        : 0.01902
## stress after  10 iters: 0.01321, magic = 0.500
## stress after  20 iters: 0.01318, magic = 0.500
```

```
eqscplot(lcrabs.sam$points, type = "n", xlab = "", ylab = "")
text(lcrabs.sam$points , labels = as.character(crabs.grp), col = 3 + as.integer(crabs.grp))
```



1-4) Self-organizing maps

```
gr <- somgrid(topo = "hexagonal")
crabs.som <- batchSOM(lcrabs, gr, c(4, 4, 2, 2, 1, 1, 1, 0, 0))
plot(crabs.som)
```



```
bins <- as.numeric(knn1 (crabs.som$code, lcrabs, 0:47))
plot(crabs.som$grid, type = "n")
symbols(crabs.som$grid$pts[, 1], crabs.som$grid$pts[, 2], circles = rep(0.4, 48), inches = FALSE, add =
text (crabs.som$grid$pts[bins, ] + rnorm(400, 0, 0.1), as.character(crabs.grp))
```