Modern Applyed Statistics(Chap 11)

```
library(MASS)
library(class)
library(fastICA)
library(cluster)
options(width=65, digits=5)

# install.packages("../package/xgobi_1.2-15.tar.gz", repos = NULL, type = "source")
# install.packages("../package/RGtk2_2.20.36.tar.gz", repos = NULL, type = "source")
# install.packages("../package/rggobi_2.1.22.tar.gz", repos = NULL, type = "source")
```

11.1 Visualization methods

1) Principal Component analysis

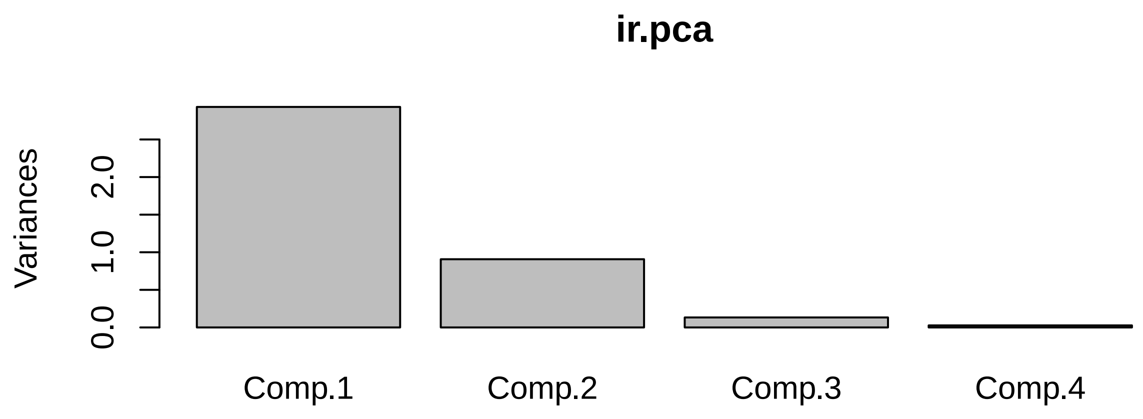
```
# Iris data
ir <- rbind(iris3[,,1], iris3[,,2], iris3[,,3])
ir.species <- factor(c(rep("s", 50), rep("c", 50), rep("v", 50)))

# Principal Component for the log-transforrned iris data.
(ir.pca <- princomp(log(ir), cor = TRUE))
```

```
## Call:
## princomp(x = log(ir), cor = TRUE)
##
## Standard deviations:
##  Comp.1  Comp.2  Comp.3  Comp.4
## 1.71246 0.95238 0.36470 0.16568
##
##  4  variables and  150 observations.
```

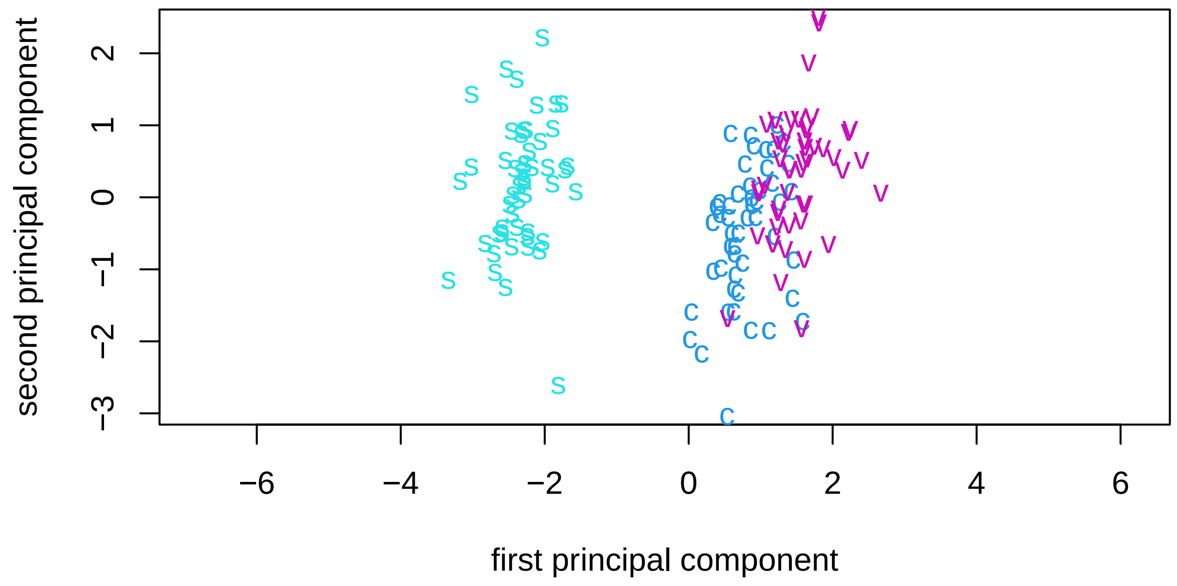
```
summary(ir.pca)
```

```
## Importance of components:
##                         Comp.1  Comp.2   Comp.3    Comp.4
## Standard deviation     1.71246 0.95238 0.364703 0.1656840
## Proportion of Variance 0.73313 0.22676 0.033252 0.0068628
## Cumulative Proportion  0.73313 0.95989 0.993137 1.0000000
```

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



```r
# First two principal components for the log-transforrned iris data.
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 + unclass(ir.species))
```



```r
# Crabs data
lcrabs <- log(crabs[, 4:8])
crabs.grp <- factor(c("B", "b", "O", "o")[rep(1:4, each = 50)])

# Principal Component for the crabs data.
(lcrabs.pca <- princomp(lcrabs))
```

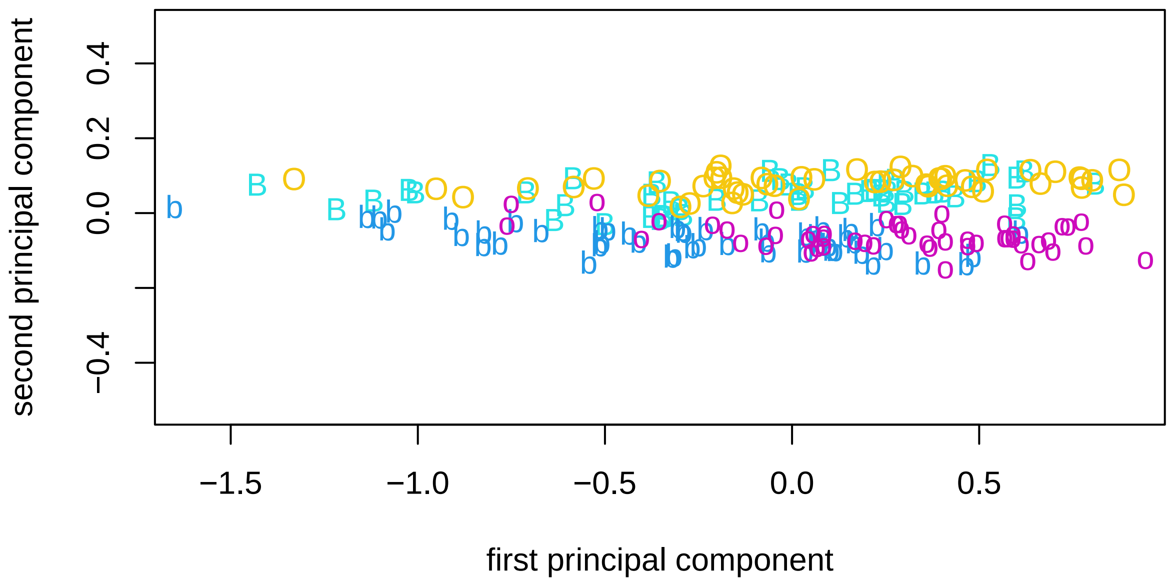
```
## Call:
## princomp(x = lcrabs)
##
## Standard deviations:
##    Comp.1    Comp.2    Comp.3    Comp.4    Comp.5
## 0.5166405 0.0746536 0.0479144 0.0248040 0.0090522
##
##  5  variables and  200 observations.
```

```r
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
```

```r
lcrabs.pc <- predict(lcrabs.pca)
dimnames(lcrabs.pc) <- list(NULL, paste("PC", 1:5, sep = ""))
```

```r
# First two principal components for the crabs data.
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))
```



2) Exploratory projection pursuit

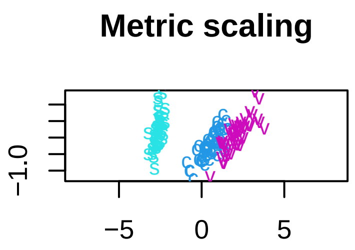
```
if(FALSE) { ## needs interaction with XGobi, or, better, rggobi
  library(xgobi)
  xgobi(lcrabs, colors = c("SkyBlue", "SlateBlue", "Orange",
                         "Red")[rep(1:4, each = 50)])
  xgobi(lcrabs, glyphs = 12 + 5*rep(0:3, each = 50, 4))

  library(rggobi)
  g <- ggobi(lcrabs)
  d <- displays(g)[[1]]
  pmode(d) <- "2D Tour"
  crabs.grp <- factor(c("B", "b", "O", "o")[rep(1:4, each = 50)])
  glyph_colour(g$lcrabs) <- crabs.grp
  colorscheme(g) <- "Paired 4"
}
```

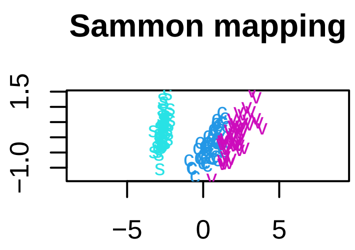
3) Distance methods

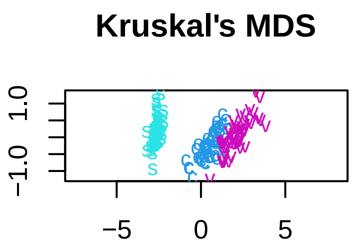
```
# Distance-based representations of the iris data
ir.scal <- cmdscale(dist(ir) , k = 2, eig = T)

distp <- dist(ir); dist2 <- dist(ir.scal$points)
sum((distp - dist2)^2)/sum(distp^2) # calculating a measure of 'stress'
```

```
## [1] 0.0017469
```

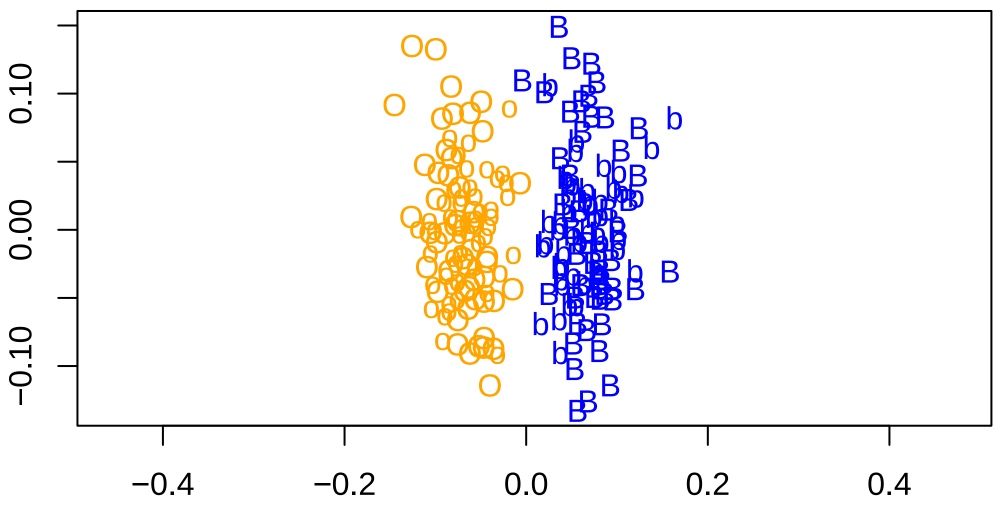
```
par(mfrow = c(2,2))

eqscplot(ir.scal$points, type = "n", main = "Metric scaling", ratio = 2)
text(ir.scal$points, labels = as.character(ir.species),
     col = 3 + as.integer(ir.species), cex = 0.8)
ir.sam <- sammon(dist(ir[-143,]))
eqscplot(ir.sam$points, type = "n", main = "Sammon mapping", ratio = 2)
text(ir.sam$points, labels = as.character(ir.species[-143]),
     col = 3 + as.integer(ir.species), cex = 0.8)
ir.iso <- isoMDS(dist(ir[-143,]))
eqscplot(ir.iso$points, type = "n", main = "Kruskal's MDS", ratio = 2)
text(ir.iso$points, labels = as.character(ir.species[-143]),
     col = 3 + as.integer(ir.species), cex = 0.8)
```



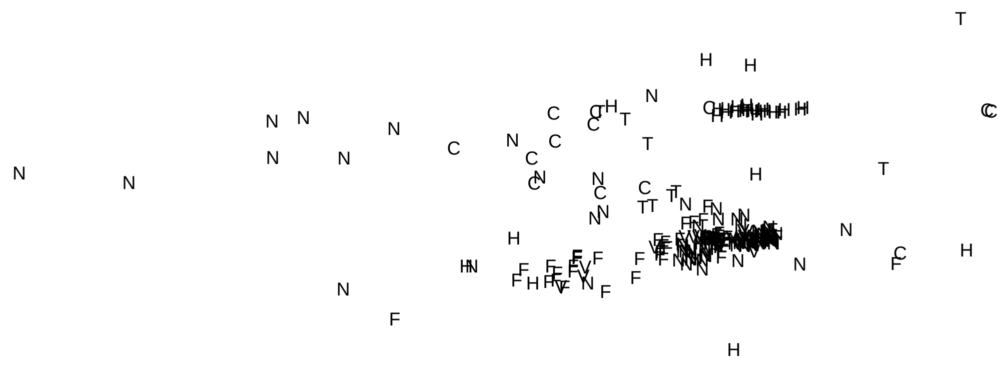




```r
# Sammon mapping of crabs data
cr.scale <- 0.5 * log(crabs$CL * crabs$CW)
slcrabs <- lcrabs - cr.scale
cr.means <- matrix(0, 2, 5)
cr.means[1,] <- colMeans(slcrabs[crabs$sex == "F", ])
cr.means[2,] <- colMeans(slcrabs [crabs$sex == "M", ])
dslcrabs <- slcrabs - cr.means[as.numeric(crabs$sex),]
lcrabs.sam <- sammon(dist(dslcrabs))
eqscplot(-lcrabs.sam$points, type = "n", xlab = "", ylab = "", tol = 0.08, ratio = 1.5)
text(-lcrabs.sam$points , labels = as.character(crabs.grp),
     col = rep(c("blue", "orange"), each = 100))
```



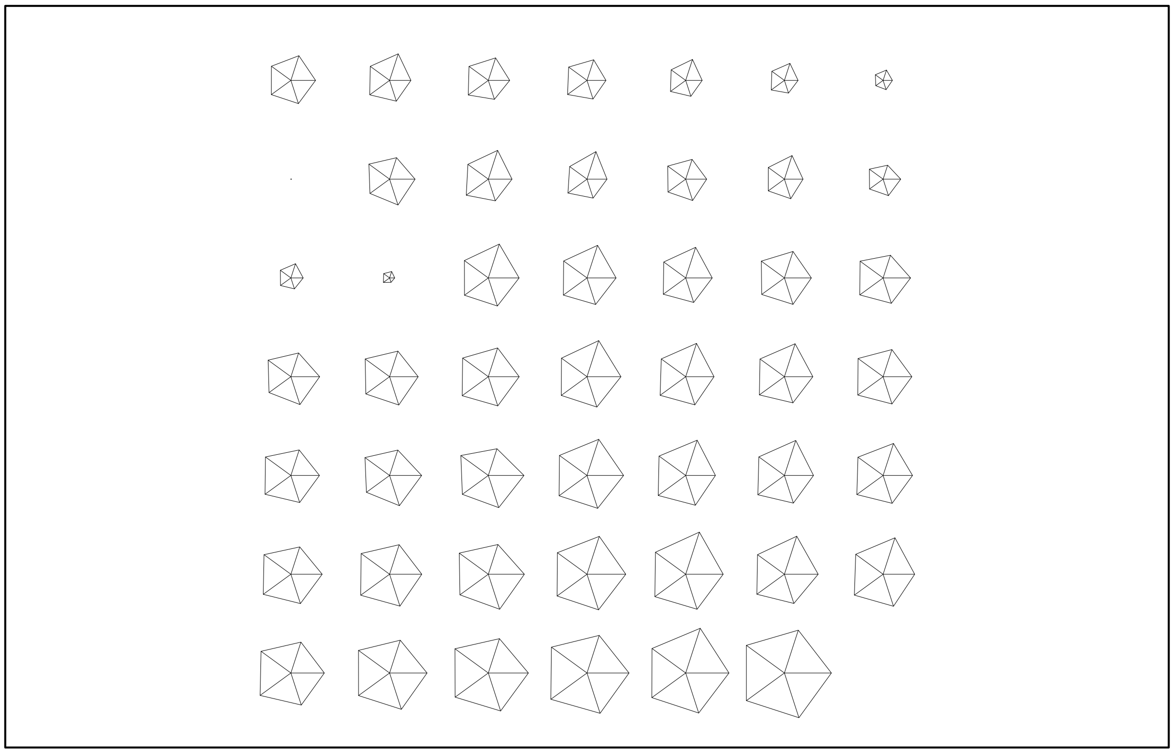
```r
# Isotonic multidimensional scaling representation of the fgl data.
fgl.iso <- isoMDS(dist(as.matrix(fgl[-40, -10])))
eqscplot(fgl.iso$points, type = "n", xlab = "", ylab = "", axes = FALSE)
# either
# for(i in seq(along = levels(fgl$type))) {
#   set <- fgl$type[-40] == levels(fgl$type)[i]
#   points(fgl.iso$points[set,], pch = 18, cex = 0.6, col = 2 + i)}
# key(text = list(levels(fgl$type), col = 3:8))
# or
text(fgl.iso$points, labels = c("F", "N", "V", "C", "T", "H")[fgl$type[-40]], cex = 0.6)
```



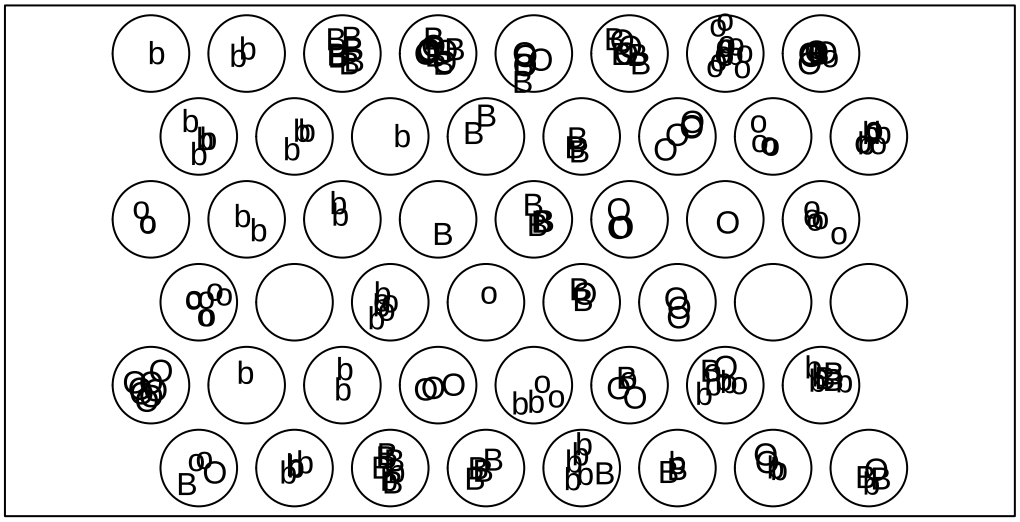
```
fgl.iso3 <- isoMDS(dist(as.matrix(fgl[-40, -10])), k = 3)
# S: brush(fgl.iso3$points)
fgl.col <- c("SkyBlue", "SlateBlue", "Orange", "Orchid", "Green", "HotPink")[fgl$type]
# xgobi(fgl.iso3$points, colors = fgl.col)
```

4) Self-organizing maps

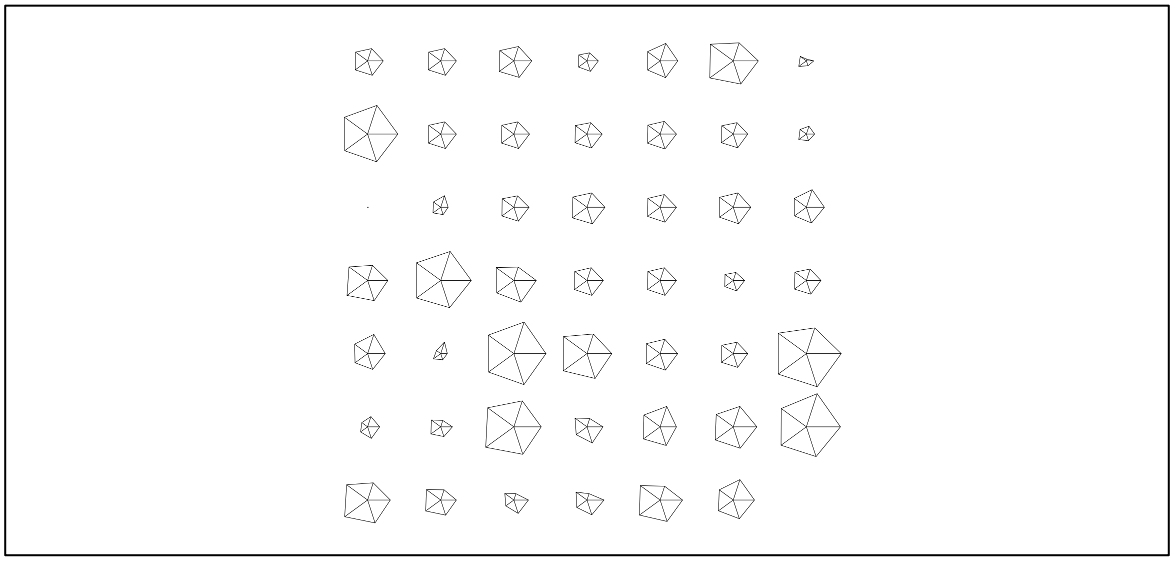
```r
# Batch SOM applied to the crabs dataset.
set.seed(0)
gr <- somgrid(topo = "hexagonal")
crabs.som <- batchSOM(lcrabs, gr, c(4, 4, 2, 2, 1, 1, 1, 0, 0))

# stars plot of the representatives
stars(crabs.som$codes, labels = NULL, frame.plot = T)
```



```r
set.seed(0)

# Plot that shows the assignments of the original points
bins <- as.numeric(knn1(crabs.som$code, lcrabs, 0:47))
plot(crabs.som$grid, type = "n", frame.plot = T,
     xlim = c(min(crabs.som$grid$pts[,1])-0.4, max(crabs.som$grid$pts[,1])+0.4),
     ylim = c(min(crabs.som$grid$pts[,2])-0.4, max(crabs.som$grid$pts[,2])+0.4))
symbols(crabs.som$grid$pts[, 1], crabs.som$grid$pts[, 2],
        circles = rep(0.4, 48), inches = FALSE, add = TRUE)
text(crabs.som$grid$pts[bins, ] + rnorm(400, 0, 0.1), as.character(crabs.grp))
```

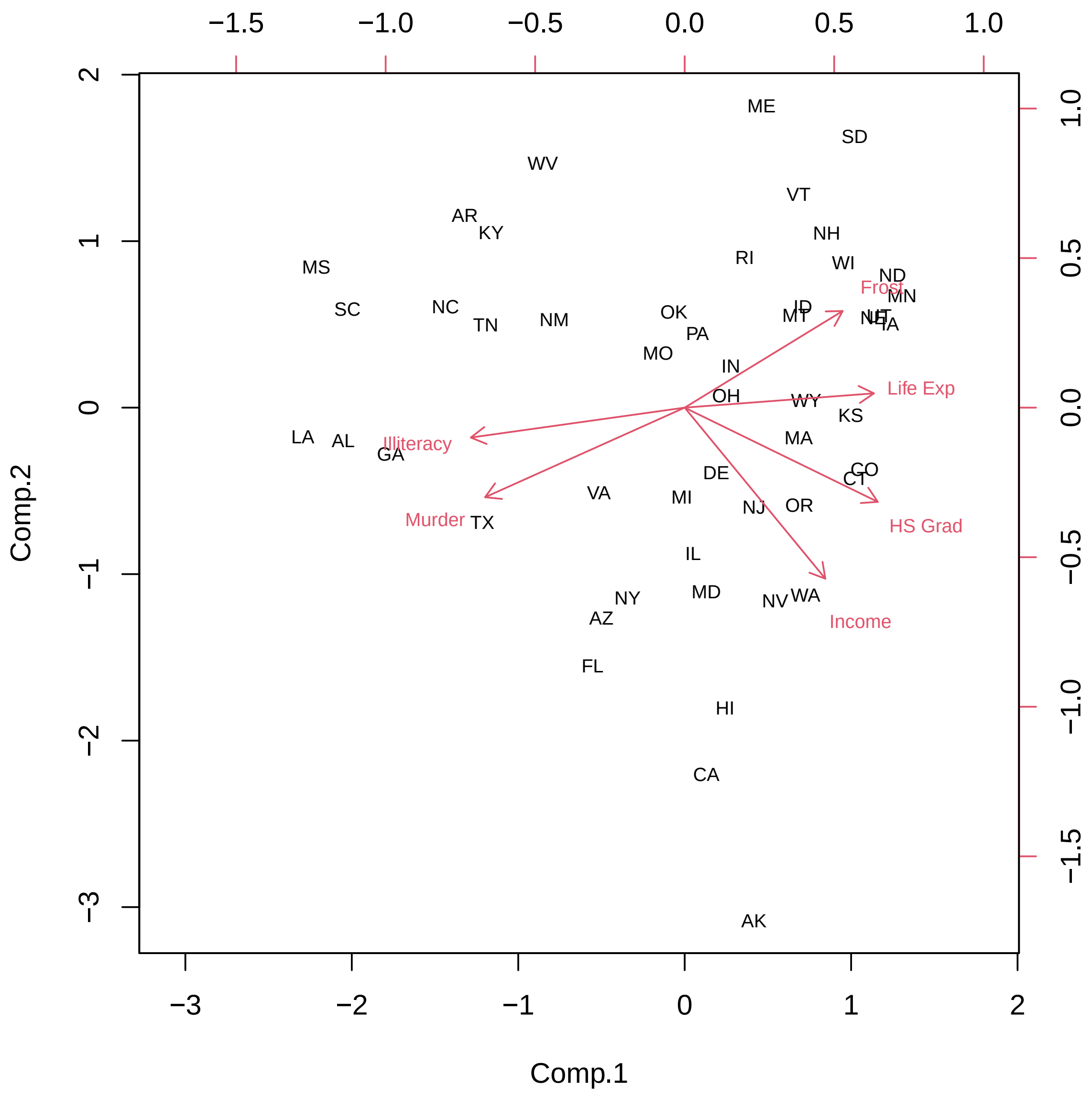


```
set.seed(0)

# Traditional SOM applied to the crabs dataset.
crabs.som2 <- SOM(lcrabs, gr); stars(crabs.som2$codes, frame.plot = T)
```



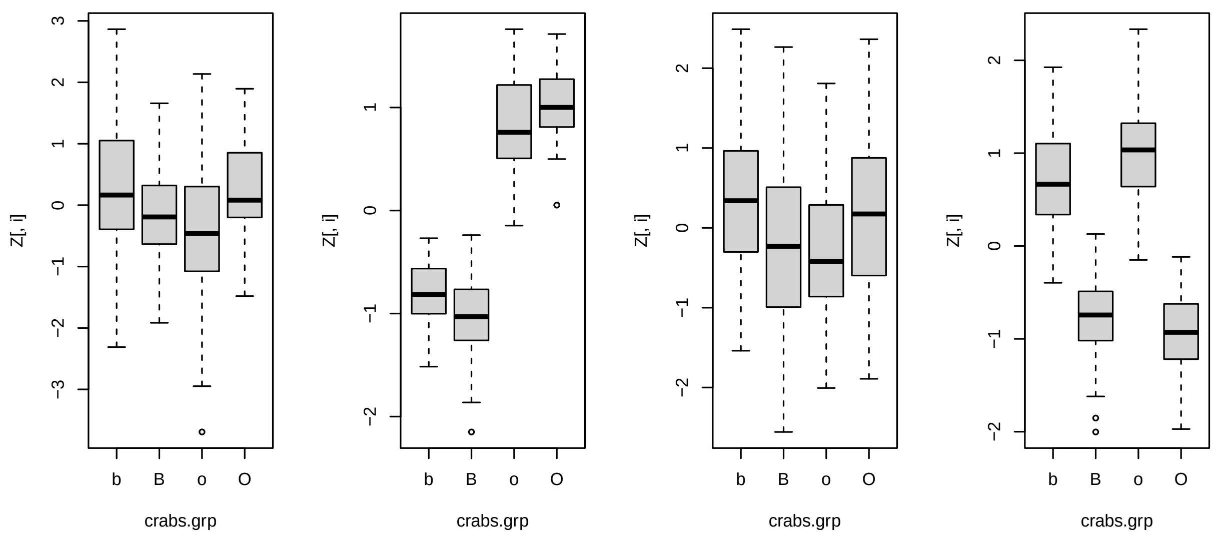
5) Biplots

```
# Principal component biplot of the part of the state.x77 data.
state <- state.x77[, 2:7]; row.names(state) <- state.abb
state.pca <- princomp(state, cor = TRUE)
state.pca$loadings[,2] <- -state.pca$loadings[,2]
state.pca$scores[,2] <- -state.pca$scores[,2]
biplot(state.pca, pc.biplot = TRUE, cex = 0.7, expand = 0.8)
```



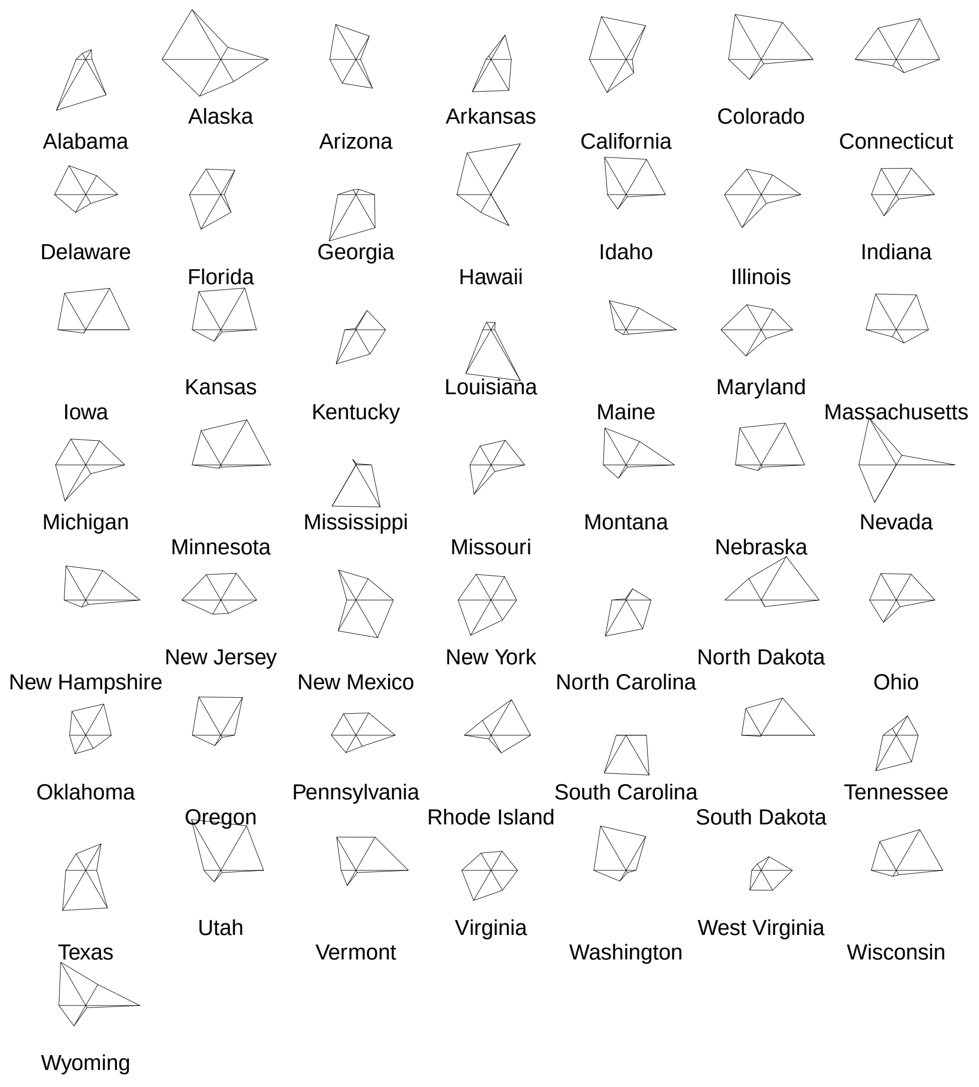
6) Independent component analysis

```r
set.seed(0)

# Boxplots of four 'signals' recovered by ICA from the crabs data.
nICA <- 4
crabs.ica <- fastICA(crabs[, 4:8], nICA)
Z <- crabs.ica$S
par(mfrow = c(1, nICA))
for(i in 1:nICA) boxplot(Z[, i] ~ crabs.grp)
```



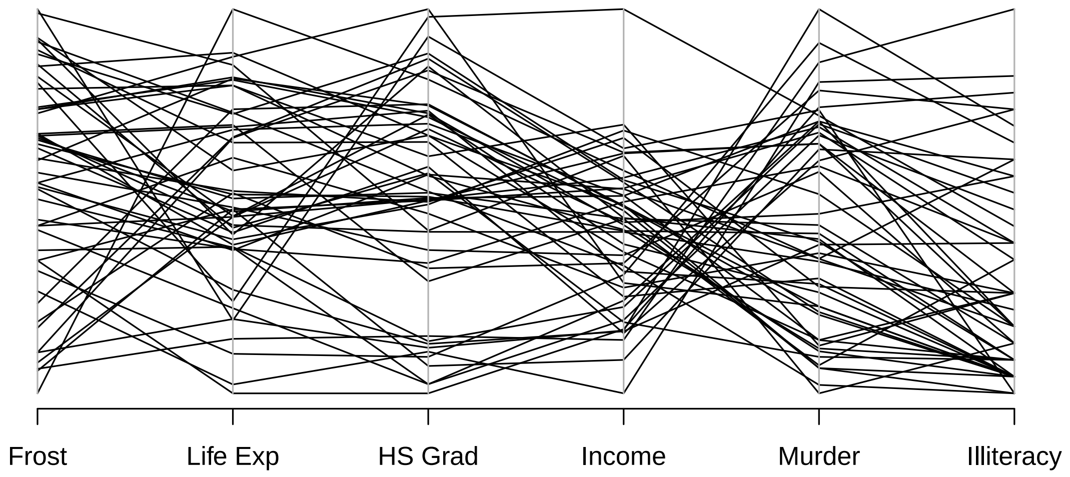
7) Glyph representations

```r
# stars plot of the state.x77 dataset.
stars(state.x77[, c(7, 4, 6, 2, 5, 3)])
```

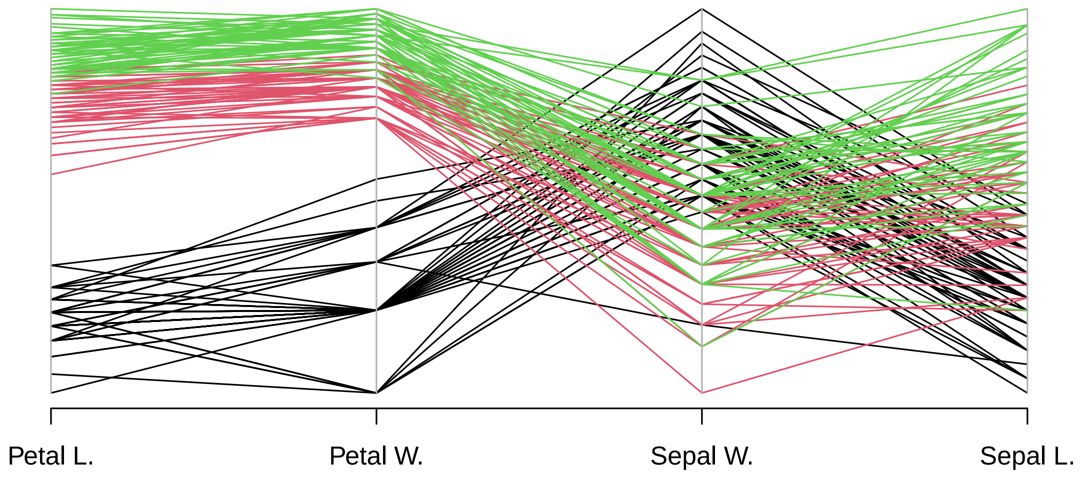


8) Parallel coordinate plots

```
# Parallel coordinates plots of the state.x77 dataset.
parcoord(state.x77[, c(7, 4, 6, 2, 5, 3)])
```

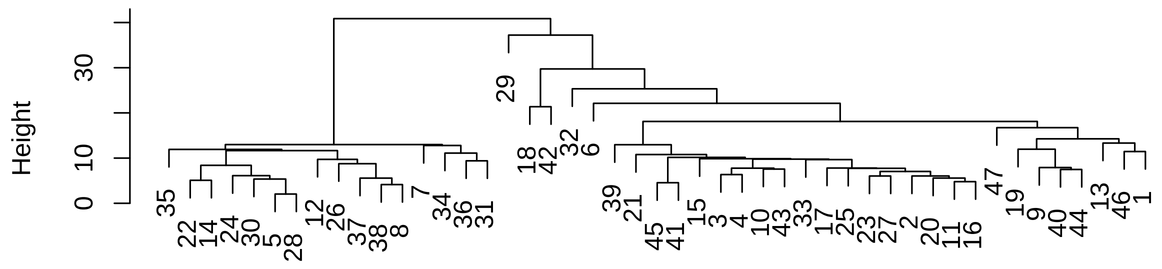


```
# Parallel coordinates plots of the log-transforrned iris data
parcoord(log(ir)[, c(3, 4, 2, 1)], col = 1 + (0:149)%/%50)
```

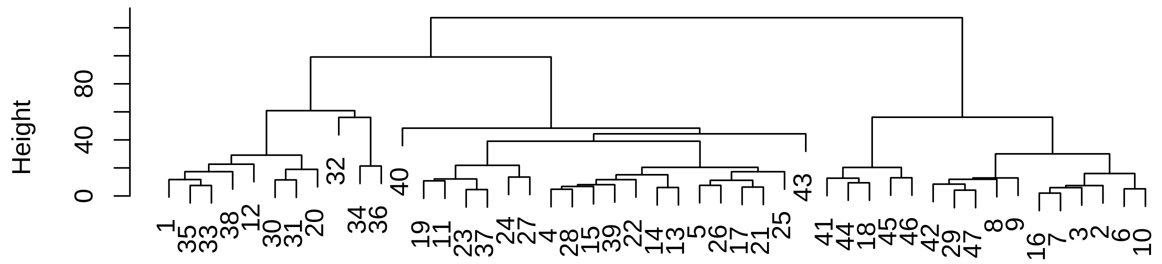


11.2 Cluster Analysis

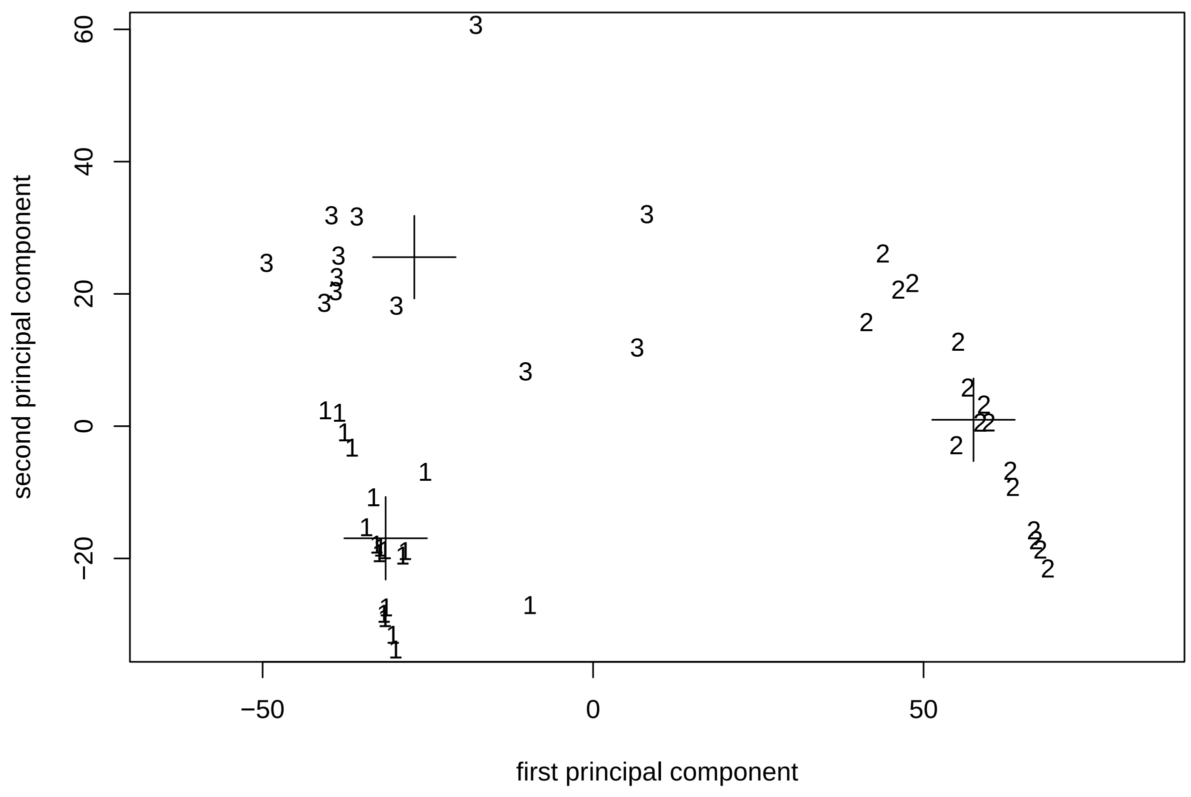
```
# Dendograms for the socio-economic data on Swiss provinces by single-link clustering
swiss.x <- as.matrix(swiss[,-1])
h <- hclust(dist(swiss.x), method = "single")
plot(h, labels = h$order, main = "", xlab = "", sub = "")
```



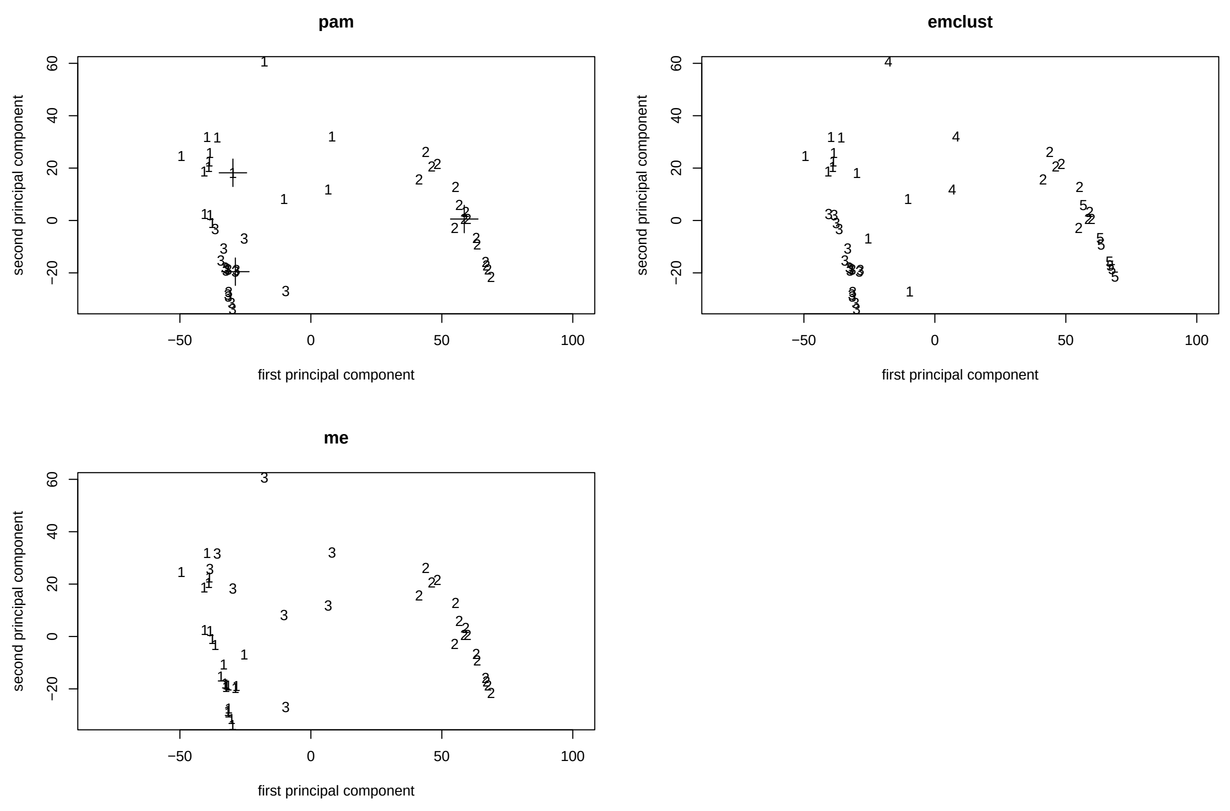
```
# Dendograms for the socio-economic data on Swiss provinces by divisive clustering
d <- diana(swiss.x, )
pltree(d, labels = d$order, main = "", xlab = "", sub = "")
```



```
# First two principal components for the swiss data
# and labeling by the groups assigned by K-means
h <- hclust(dist(swiss.x), method = "average")
initial <- tapply(swiss.x, list(rep(cutree(h, 3), ncol(swiss.x)), col(swiss.x)), mean)
dimnames(initial) <- list(NULL, dimnames(swiss.x)[[2]])
km <- kmeans(swiss.x, initial)
(swiss.pca <- princomp(swiss.x))
swiss.px <- predict(swiss.pca); swiss.px[,2] <- -swiss.px[,2]
dimnames(km$centers)[[2]] <- dimnames(swiss.x)[[2]]
swiss.centers <- predict(swiss.pca, km$centers); swiss.centers[,2] <- -swiss.centers[,2]
eqscplot(swiss.px[, 1:2], type = "n",
         xlab = "first principal component" , ylab = "second principal component")
text(swiss.px[, 1:2], labels = km$cluster)
points(swiss.centers[,1:2], pch = 3, cex = 5)
identify(swiss.px[, 1:2], cex = 0.5)
```



```r
# Clusterings of the Swiss provinces data by pam, me, emclust
par(mfrow = c(2,2))

swiss.pam <- pam(swiss.px, 3)
eqscplot(swiss.px[, 1:2], type = "n",
         xlab = "first principal component", ylab = "second principal component",
         main = "pam")
text(swiss.px[,1:2], labels = swiss.pam$clustering)
points(swiss.pam$medoid[,1:2], pch = 3, cex = 3)

library(mclust)
vals <- mclustBIC(swiss.x)
sm <- summary(vals, swiss.x)
eqscplot (swiss.px [, 1: 2], type = "n",
          xlab = "first principal component" , ylab = "second principal component",
          main = "emclust")
text(swiss.px[, 1:2], labels = sm$classification)

h <- hc(modelName = "VVV", swiss.x)
mh <- as.vector(hclass(h, 3))
z <- me(modelName = "VVV", swiss.x, z = 0.5*(unmap(mh)+1/3))
eqscplot(swiss.px[, 1:2], type = "n",
         xlab = "first principal component", ylab = "second principal component",
         main = "me")
text(swiss.px[, 1:2], labels = max.col(z$z))
```



11.3 Factor analysis

```
ability.FA <- factanal(covmat = ability.cov, factors = 1)
ability.FA
```

```
##
## Call:
## factanal(factors = 1, covmat = ability.cov)
##
## Uniquenesses:
## general picture  blocks    maze reading   vocab
##   0.535   0.853   0.748   0.910   0.232   0.280
##
## Loadings:
##         Factor1
## general 0.682
## picture 0.384
## blocks  0.502
## maze    0.300
## reading 0.877
## vocab   0.849
##
##                Factor1
## SS loadings      2.443
## Proportion Var   0.407
##
## Test of the hypothesis that 1 factor is sufficient.
## The chi square statistic is 75.18 on 9 degrees of freedom.
## The p-value is 1.46e-12
```

```
(ability.FA <- update(ability.FA, factors = 2))
```

```
##
## Call:
## factanal(factors = 2, covmat = ability.cov)
##
## Uniquenesses:
## general picture  blocks    maze reading   vocab
##   0.455   0.589   0.218   0.769   0.052   0.334
##
## Loadings:
##         Factor1 Factor2
## general 0.499   0.543
## picture 0.156   0.622
## blocks  0.206   0.860
## maze    0.109   0.468
## reading 0.956   0.182
## vocab   0.785   0.225
##
##                Factor1 Factor2
## SS loadings      1.858   1.724
## Proportion Var   0.310   0.287
## Cumulative Var   0.310   0.597
##
## Test of the hypothesis that 2 factors are sufficient.
## The chi square statistic is 6.11 on 4 degrees of freedom.
## The p-value is 0.191
```

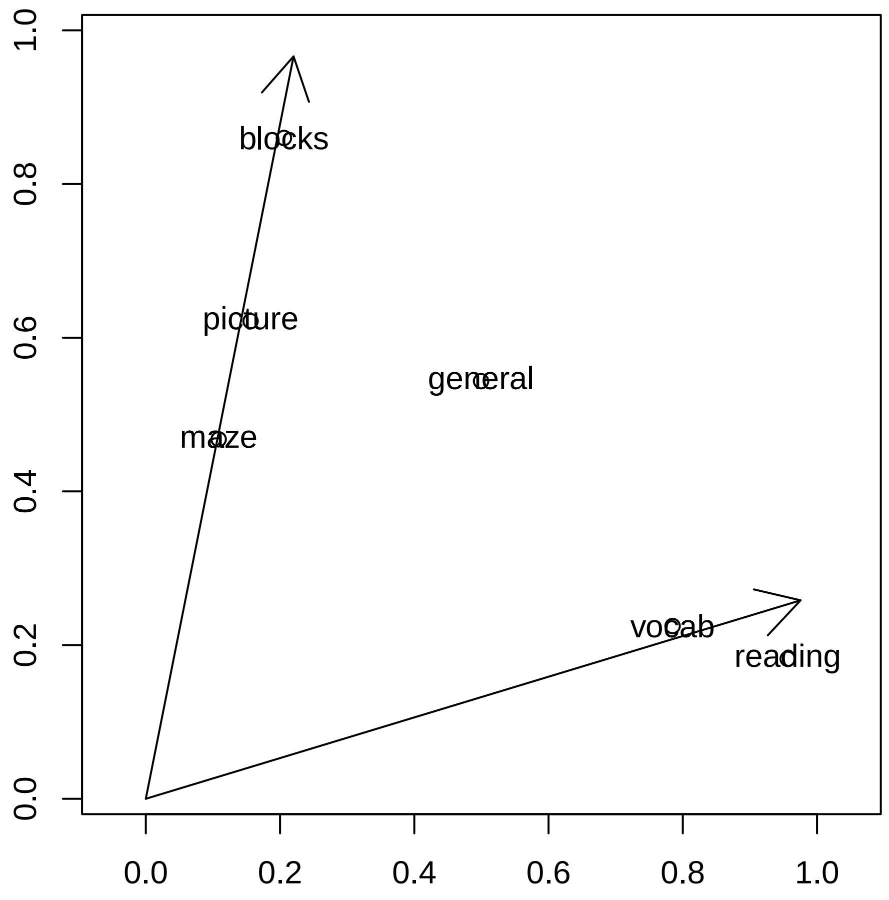
```
#summary(ability.FA)
round(loadings(ability.FA) %*% t(loadings(ability.FA)) +
        diag(ability.FA$uniq), 3)
```

```
##         general picture blocks  maze reading vocab
## general   1.000   0.416  0.570 0.308   0.577 0.514
## picture   0.416   1.000  0.567 0.308   0.262 0.262
## blocks    0.570   0.567  1.000 0.425   0.353 0.355
## maze      0.308   0.308  0.425 1.000   0.189 0.190
## reading   0.577   0.262  0.353 0.189   1.000 0.791
## vocab     0.514   0.262  0.355 0.190   0.791 1.000
```

```
# Factor rotations
library(GPArotation)
L <- loadings(ability.FA)
print(oblirot <- oblimin(L))
```

```
## Oblique rotation method Oblimin Quartimin converged.
## Loadings:
##         Factor1 Factor2
## general  0.3864  0.4745
## picture -0.0110  0.6459
## blocks  -0.0263  0.8961
## maze    -0.0180  0.4883
## reading  0.9901 -0.0371
## vocab    0.7906  0.0526
##
## Rotating matrix:
##        [,1]   [,2]
## [1,]  1.091 -0.249
## [2,] -0.292  1.102
##
## Phi:
##       [,1]  [,2]
## [1,] 1.000 0.465
## [2,] 0.465 1.000
```

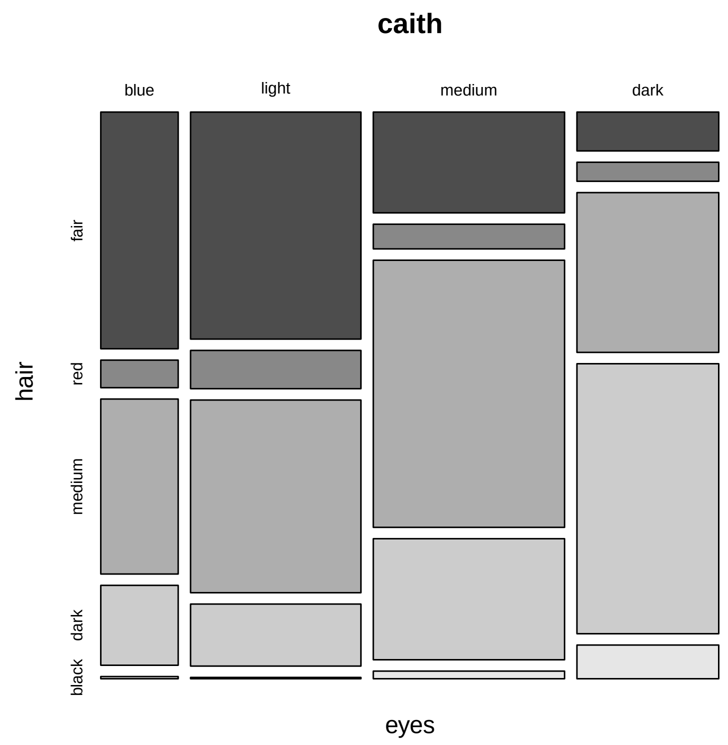
```
par(pty = "s")
eqscplot(L, xlim = c(0,1), ylim = c(0,1))
if(interactive()) identify(L[1:6,1], dimnames(L)[[1]])
naxes <- oblirot$Th
arrows(rep(0, 2), rep(0, 2), naxes[,1], naxes[,2])
text(L[1:6,1:2], dimnames(L)[[1]])
```

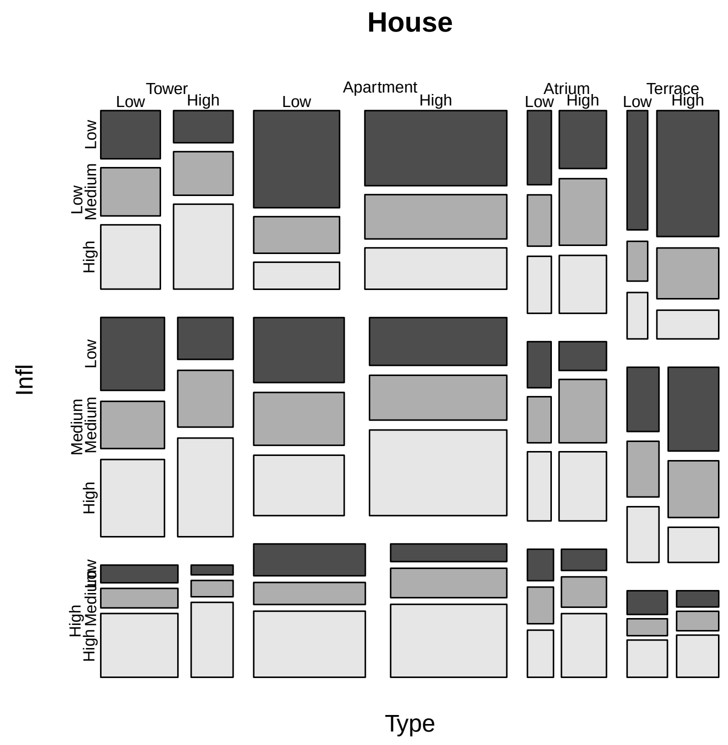


11.4 Discrete multivariate analysis

mosaic plot

```
par(mfrow = c(2,1))
# Mosaic plots for Fisher's data on people from Caithness
caith <- as.matrix(caith)
names(dimnames(caith)) <- c("eyes", "hair")
mosaicplot(caith, color = TRUE)
# Mosaic plots for Copenhagen housing satisfaction data
House <- xtabs(Freq ~ Type + Infl + Cont + Sat, housing)
mosaicplot(House, color = TRUE)
```

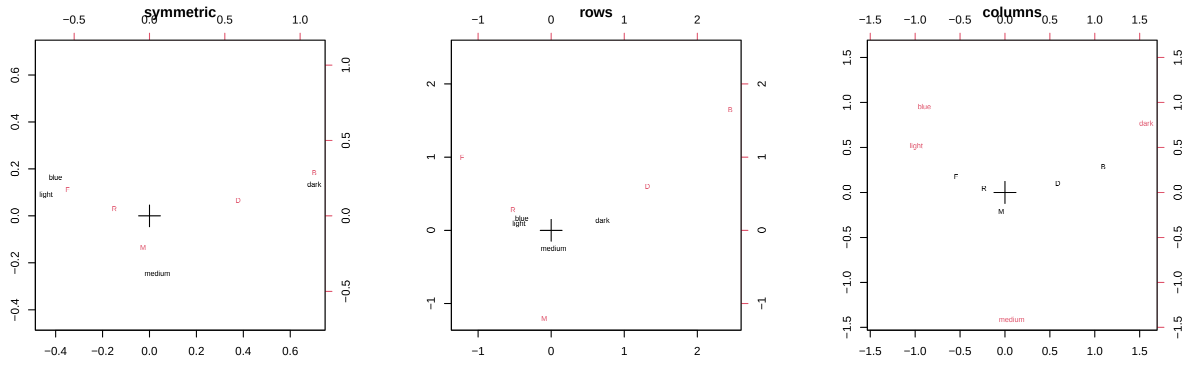

caith
blue
light
medium
dark
fair
red
medium
dark
black
hair
eyes


House
Tower
Low
High
Apartment
Low
High
Atrium
Low
High
Terrace
Low
High
Low
Medium
High
Low
Low
Medium
High
Medium
Low
Medium
High
High
Infl
Type

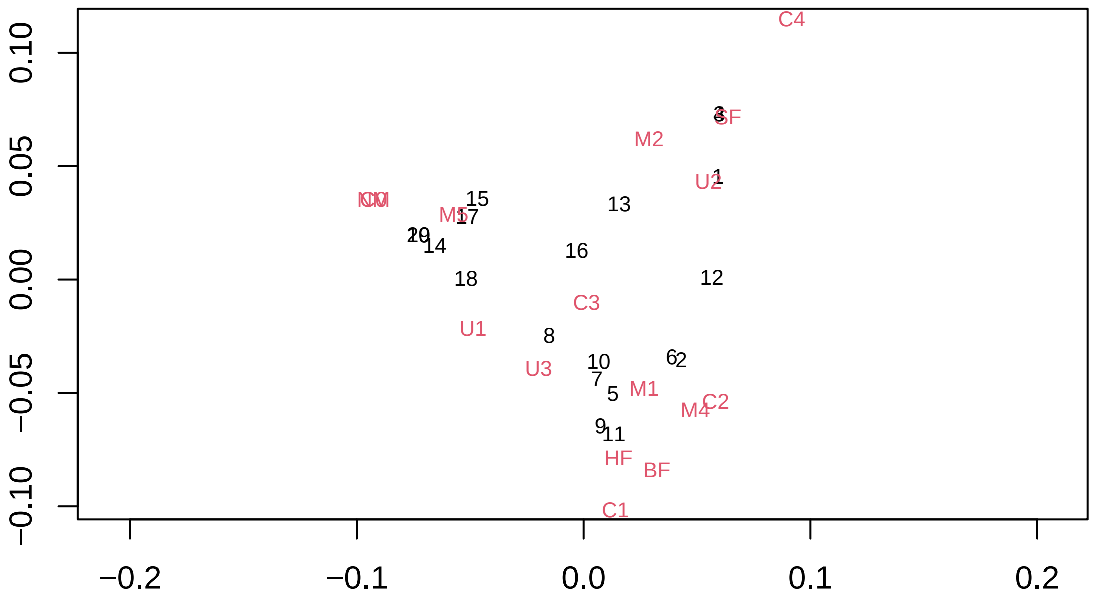
```
corresp(caith)
```

```
## First canonical correlation(s): 0.44637
##
##  eyes scores:
##      blue     light    medium      dark
## -0.896793 -0.987318  0.075306  1.574347
##
##  hair scores:
##      fair       red    medium      dark     black
## -1.218714 -0.522575 -0.094147  1.318885  2.451760
```

```r
# Three variants of correspondence analysis plots from Fisher's data
caith2 <- caith
dimnames(caith2)[[2]] <- c("F", "R", "M", "D", "B")
par(mfcol = c(1, 3))
plot(corresp(caith2, nf = 2)); title("symmetric")
plot(corresp(caith2, nf = 2), type = "rows"); title("rows")
plot(corresp(caith2, nf = 2), type = "col"); title("columns")
```



```r
# Multiple correspondence analysis plot of dataset farms
farms.mca <- mca(farms, abbrev = TRUE)  # Use levels as names
plot(farms.mca, cex = rep(0.7, 2))
```


C4
SF
M2
U2
NM
M5
C3
U1
U3
M1
M4
C2
HF
BF
C1