

# Principle component analysis

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## 1 class command :

The class of the iris dataset is a `data.frame`, a “tightly coupled collections of variables which share many of the properties of matrices and of lists, used as the fundamental data structure by most of R’s modeling software.”

```
pf4d@citadel: ~/Insync - exmortis223/pattern_recognition/hw/hw2/src
R version 3.1.2 (2014-10-31) -- "Pumpkin Helmet"
Copyright (C) 2014 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

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Natural language support but running in an English locale

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Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> class
function(x) .Primitive("class")
> class(iris)
[1] "data.frame"
```

## 2 summary command :

The `summary` command applied to the iris dataset, is a “generic function used to produce result summaries of the results of various model fitting functions. The function invokes particular methods which depend on the ‘class’ of the first argument.”

```
pf4d@citadel: ~/Insync - exmortis223/pattern_recognition/hw/hw2/src
> summary(iris)
      Sepal.Length      Sepal.Width      Petal.Length      Petal.Width
Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100
1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300
Median :5.800   Median :3.000   Median :4.350   Median :1.300
Mean   :5.843   Mean   :3.057   Mean   :3.758   Mean   :1.199
3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800
Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500
      Species
setosa   :50
versicolor:50
virginica :50
```

## 3 labels command :

The `labels` command: “Find[s] a suitable set of labels from an object for use in printing or plotting. For example, a generic function.”

```
pf4d@citadel: ~/Insync - exmortis223/pattern_recognition/hw/hw2/src
> labels(iris)
[1]
[11] "1" "2" "3" "4" "5" "6" "7" "8" "9" "10" "11" "12"
[13] "13" "14" "15" "16" "17" "18" "19" "20" "21" "22" "23" "24"
[25] "25" "26" "27" "28" "29" "30" "31" "32" "33" "34" "35" "36"
[37] "37" "38" "39" "40" "41" "42" "43" "44" "45" "46" "47" "48"
[49] "49" "50" "51" "52" "53" "54" "55" "56" "57" "58" "59" "60"
[61] "61" "62" "63" "64" "65" "66" "67" "68" "69" "70" "71" "72"
[73] "73" "74" "75" "76" "77" "78" "79" "80" "81" "82" "83" "84"
[85] "85" "86" "87" "88" "89" "90" "91" "92" "93" "94" "95" "96"
[97] "97" "98" "99" "100" "101" "102" "103" "104" "105" "106" "107" "108"
[109] "109" "110" "111" "112" "113" "114" "115" "116" "117" "118" "119" "120"
[121] "121" "122" "123" "124" "125" "126" "127" "128" "129" "130" "131" "132"
[133] "133" "134" "135" "136" "137" "138" "139" "140" "141" "142" "143" "144"
[145] "145" "146" "147" "148" "149" "150"

[21]
[1] "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width" "Species"
```

## 4 colnames command :

The `colnames` command: “Retrieve[s] or set[s] the row or column names of a matrix-like object.”

```
pf4d@citadel: ~/Insync - exmortis223/pattern_recognition/hw/hw2/src
> colnames(iris)
[1] "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width" "Species"
```

## 5 tab-completion :

Pressing `tab` after a `data.frame` object with accessor-operator `$` will provide variable names.

```
pf4d@citadel: ~/Insync - exmortis223/pattern_recognition/hw/hw2/src
> iris$
iris$Sepal.Length iris$Petal.Length iris$Species
iris$Sepal.Width  iris$Petal.Width
> iris$Species
```

## 6 Iris data PCA plotting :

```
pf4d@citadel: ~/lnsync - exmortis223/pattern_recognition/hw/hw2/src
> p = prcomp(d)
> p
> p$dev      p$rotation p$center p$scale p$x
> p$
```

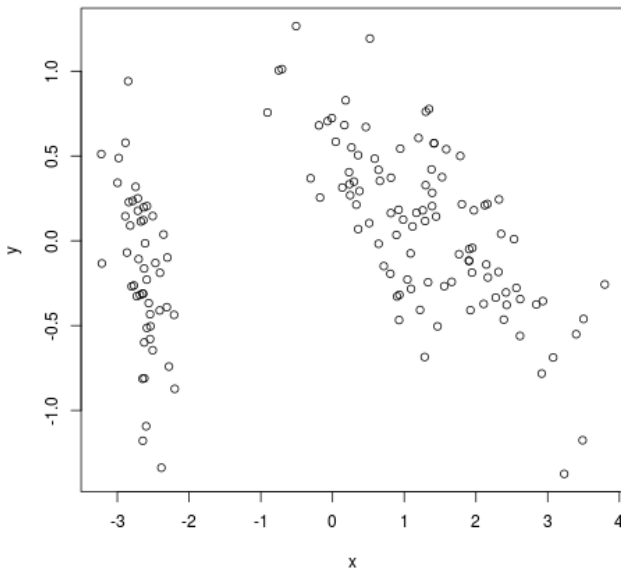
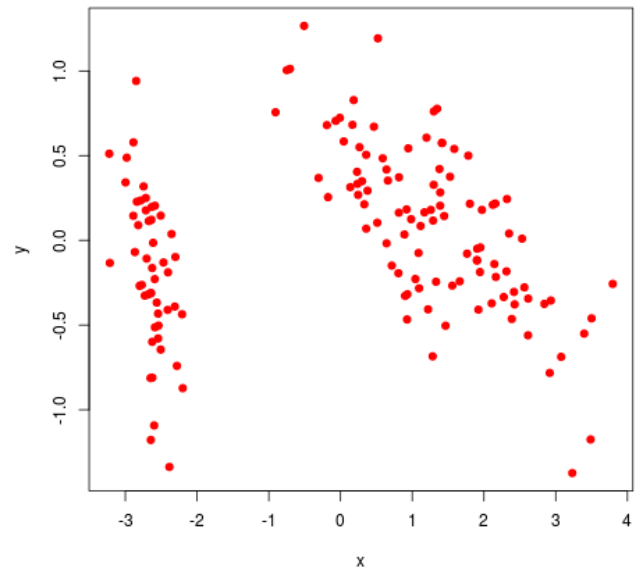
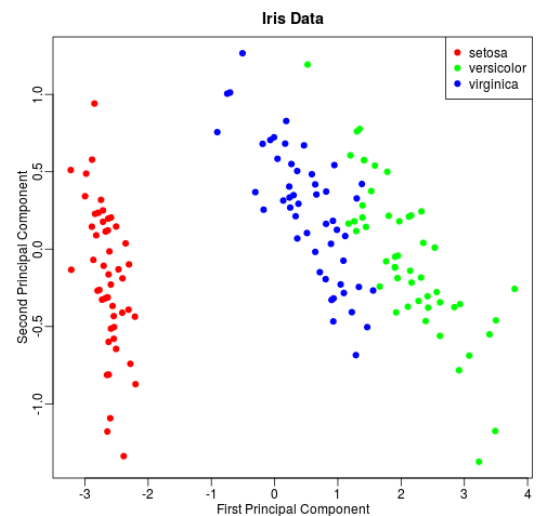
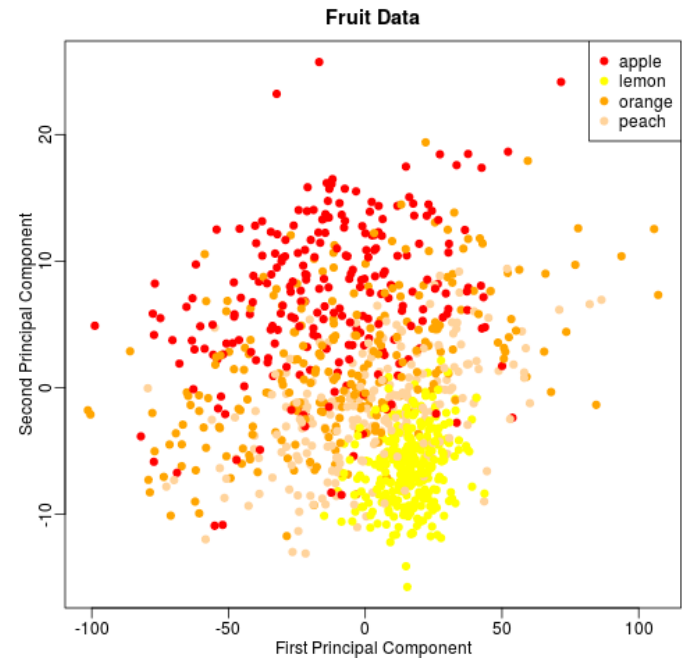
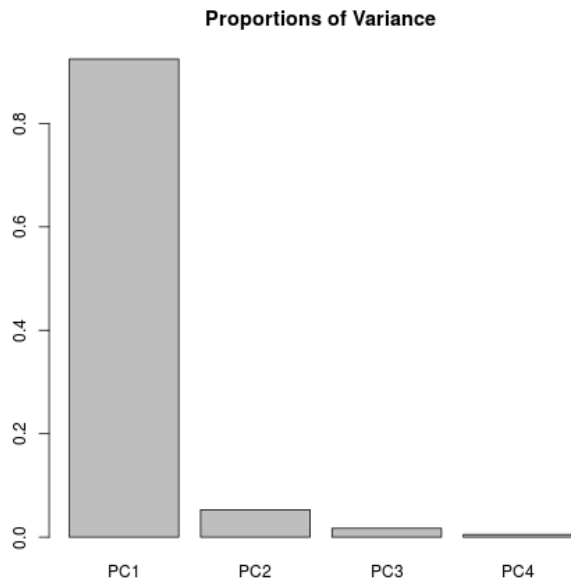


Figure 1: PCA-plot showing what appears to be two clusters, despite the fact that there are three distinct species of iris.

The plot command, a “Generic function for plotting of R objects. For more details about the graphical parameter arguments, see ‘par’.

For simple scatter plots, `plot.default` will be used. However, there are plot methods for many R objects, including function’s, `data.frame`’s, density objects, etc. Use `methods(plot)` and the documentation for these.”





## 6.1 Source code :

```
# store the iris 'classes' :
c = iris[,5]

# store the iris 'data' :
d = iris[,seq(1,4)]

# perform PCA on d :
p = prcomp(d)

# set the 1st principle component :
x = p$x[,1]

# set the 2nd principle component :
y = p$x[,2]

# plot them :
png('../doc/images/pca_plot.png')
plot(x,y)
dev.off()

# plot them in red :
png('../doc/images/pca_plot_red.png')
plot(x,y, col='red', bg='red', type='p', pch=21)
dev.off()

# store indexes of classes :
s = which(c == 'setosa')
vc = which(c == 'versicolor')
vg = which(c == 'virginica')

# color vector :
cc = as.vector(c)
cc[s] = 'red'
cc[vc] = 'blue'
cc[vg] = 'green'

# plot them colored by class :
png('../doc/images/pca_plot_class.png')
x11(width=4, height=4)
par(mar=c(2.5,2.5,2.5,.1),mgp = c(1.5, .5, 0))
plot(x,y, col=cc, bg=cc, type='p', pch=21, xlab='First Principal Component',
      ylab='Second Principal Component', main='Iris Data')
legend('topright', levels(c),
      col = c('red', 'green', 'blue'),
      pt.bg = c('red', 'green', 'blue'), pch = 21)
dev.off()

# do a barplot of the proportions of variance :
sig = p$sdev**2
pvar = sig / sum(sig)
png('../doc/images/pca_pvar_barplot.png')
barplot(pvar, names.arg=c('PC1','PC2','PC3','PC4'),
        main='Proportions of Variance')
dev.off()
```

## 7 Fruit data :

While the iris data appears to be highly grouped, the fruit data appears much less so. However, the lemons seem to be clustered distinctly from the other fruit. Therefore, I believe that these data *do* show enough structure for machine learning techniques; with apples, oranges, and peaches potentially presenting the highest challenge.

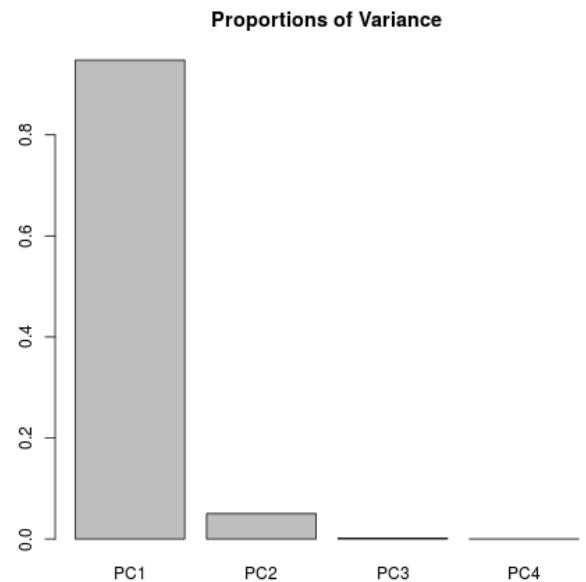
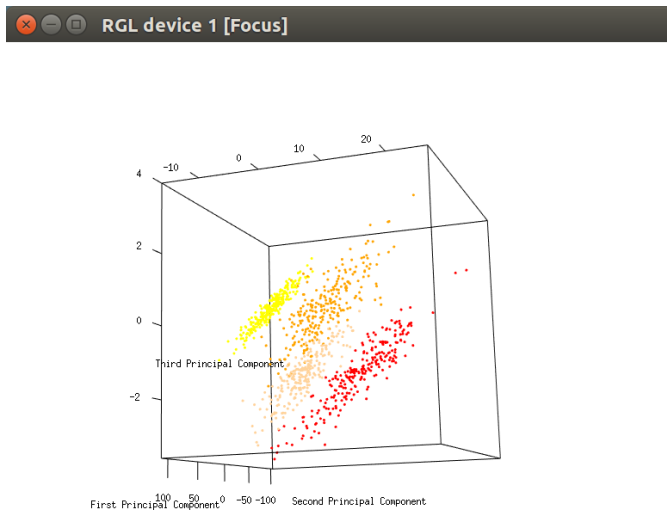


Figure 2: The proportions of the variance in the fruit data. The principle component captures  $\approx 94\%$  of the variation.



```
o = which(c == 'orange')
z = which(c == 'peach')

# color vector :
cols = c('red', 'yellow', 'orange', 'burlywood1')
cc = as.vector(c)
cc[a] = cols[1]
cc[l] = cols[2]
cc[o] = cols[3]
cc[z] = cols[4]

# plot them colored by class :
png('../doc/images/pca_plot_fruit.png')
#X11(width=4, height=4)
par(mar=c(2.5,2.5,2.5,1),mgp = c(1.5, .5, 0))
plot(x,y, col=cc, bg=cc, type='p', pch=21, xlab='First Principal Component',
      ylab='Second Principal Component', main='Fruit Data')
legend('topright', levels(c), col = cols, pt.bg = cols, pch = 21)
dev.off()

# do a barplot of the proportions of variance :
sig = p$sdv**2
pvar = sig / sum(sig)
png('../doc/images/pca_pvar_fruit_barplot.png')
barplot(pvar, names.arg=c('PC1','PC2','PC3','PC4'),
        main='Proportions of Variance')
dev.off()

# import the rgl library for 3D stuff:
library(rgl)

plot3d(x,y,z, col=cc, bg=cc, type='p', pch=21,
       xlab='First Principal Component',
       ylab='Second Principal Component',
       zlab='Third Principal Component')

# plot them colored by class :
png('../doc/images/pca_plot_fruit_23.png')
#X11(width=4, height=4)
par(mar=c(2.5,2.5,2.5,1),mgp = c(1.5, .5, 0))
plot(y,z, col=cc, bg=cc, type='p', pch=21, xlab='Second Principal Component',
      ylab='Third Principal Component', main='Fruit Data')
legend('topright', levels(c), col = cols, pt.bg = cols, pch = 21)
dev.off()
```

Figure 3: In 3D, we can see much more distinct clustering.

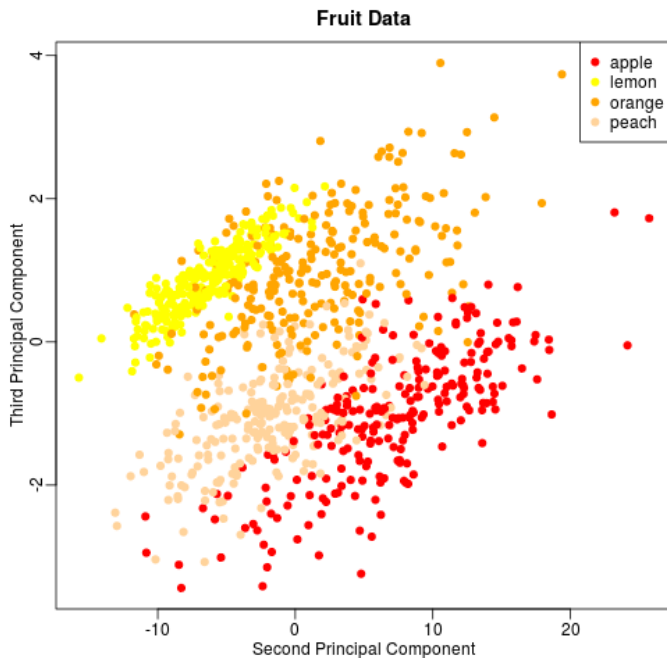


Figure 4: The second and third principle components, highlighting the clustering nature of the fruit data.

## 7.1 Source code :

```
# read the variable back in :
f = read.csv("../data/fruit.csv")

# store the fruit 'classes' :
c = f[,5]

# store the fruit 'data' :
d = f[,seq(1,4)]

# perform PCA on d :
p = prcomp(d)

# set the 1st principle component :
x = p$x[,1]

# set the 2nd principle component :
y = p$x[,2]

# set the 3rd principle component :
z = p$x[,3]

# store indexes of classes :
a = which(c == 'apple')
l = which(c == 'lemon')
```