Clustering and PCA

Yifei Sun

Contents

```
library(factoextra)
library(gridExtra)
library(corrplot)
library(RColorBrewer)
library(gplots)
library(jpeg)
```

The dataset we use contains data on 166 first generation Pokemon, including their names and basic stats: HP, Attack, Defense, Special Attack, Special Defense, and Speed. The data is from Kaggle (https://www.kaggle.com/abcsds/pokemon). We will apply unsupervised learning methods on this data. The list of Pokemon can be found at (https://pokemondb.net/pokedex/national).

```
dat <- read.csv("Pokemon.csv")
dat1 <- dat[,2:7]
dat1 <- scale(dat1)
rownames(dat1) <- dat[,1]
set.seed(1)
```

K means clustering

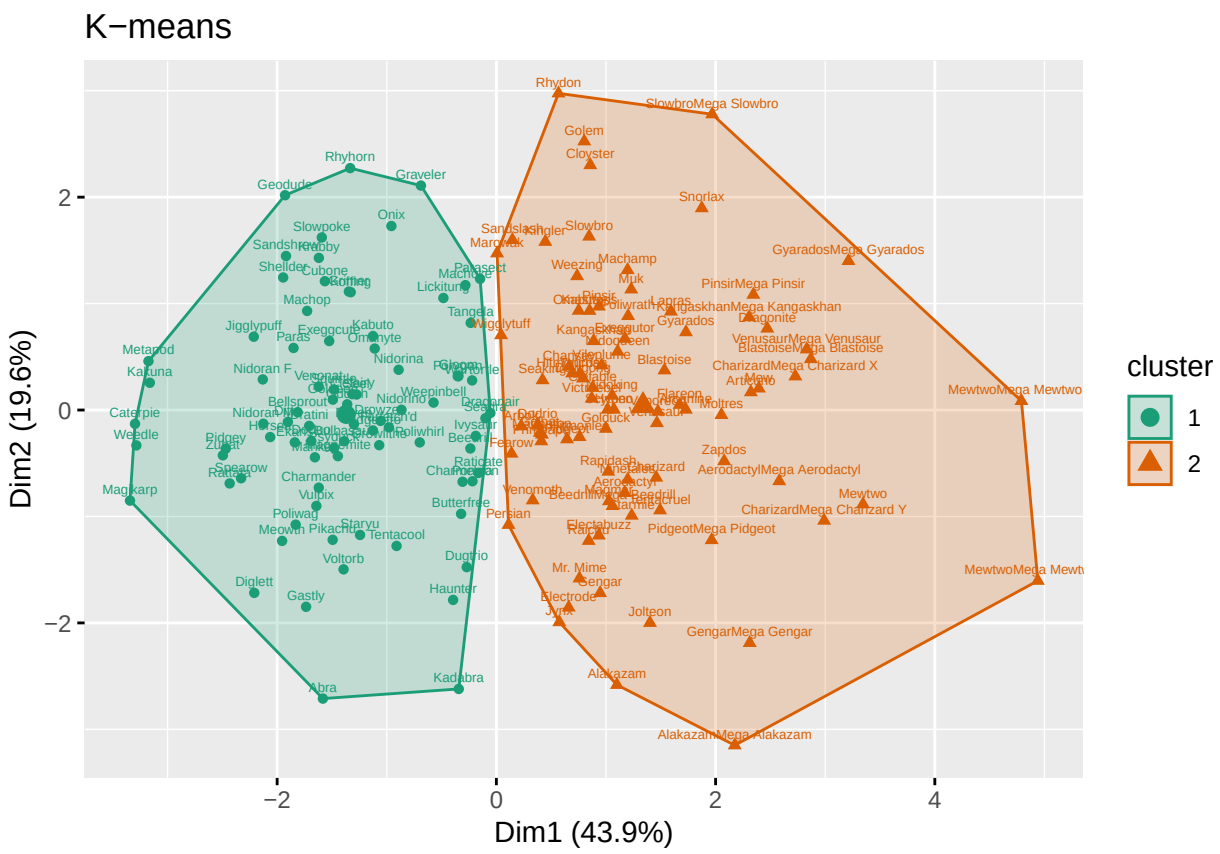
Partitioning methods such as k-means clustering require the users to specify the number of clusters to be generated. The function `fviz_nbclust()` determines and visualizes the optimal number of clusters using different methods: within cluster sums of squares, average silhouette and gap statistics. We use average silhouette, and the greater the silhouette value the better.

```
fviz_nbclust(dat1,
             FUNcluster = kmeans,
             method = "silhouette")
```


```
km <- kmeans(dat1, centers = 2, nstart = 20)
```

The function `fviz_cluster()` provides ggplot2-based visualization of partitioning methods including K means. Observations are represented by points in the plot, using principal components if $p > 2$. An ellipse is drawn around each cluster.

```
km_vis <- fviz_cluster(list(data = dat1, cluster = km$cluster),
                       ellipse.type = "convex",
                       geom = c("point","text"),
                       labelsize = 5,
                       palette = "Dark2") + labs(title = "K-means")

km_vis
```



Hierarchical clustering

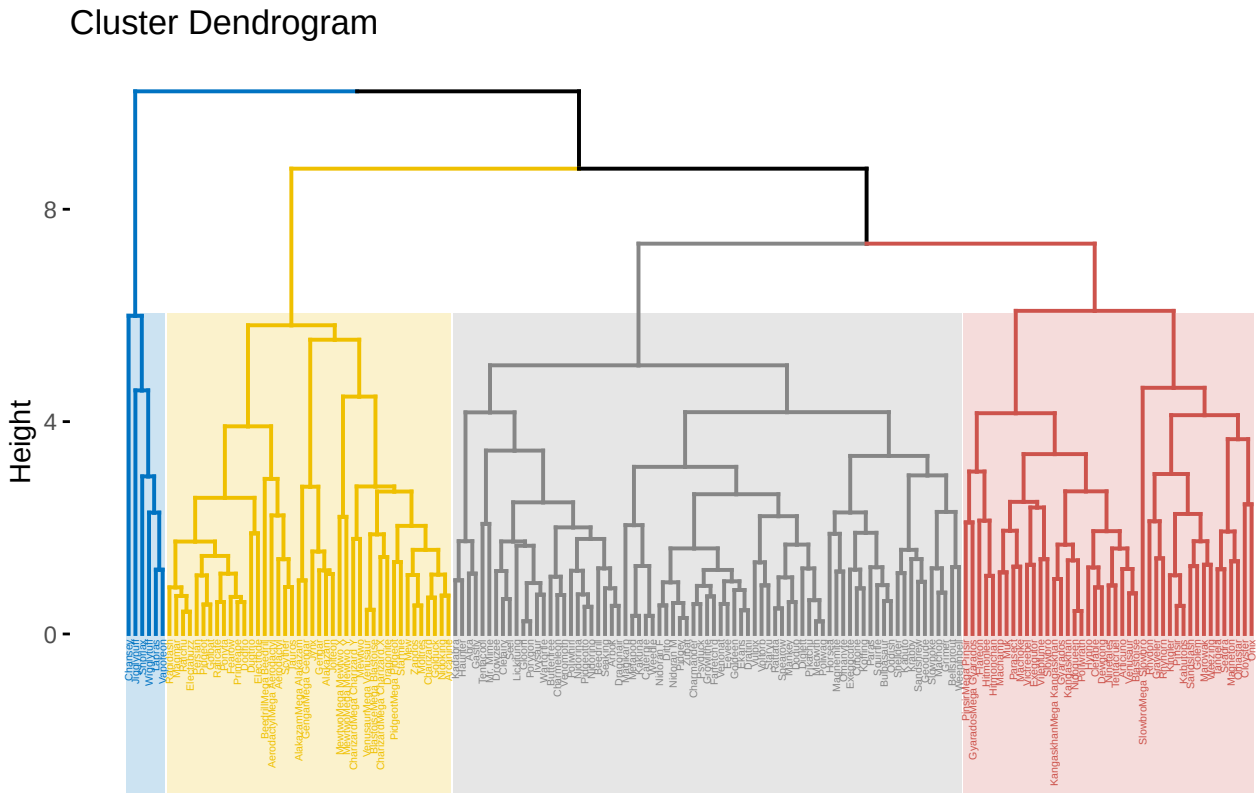
We can also apply hierarchical clustering on this data. Here we use the Euclidean distance and different types of linkage.

```
hc.complete <- hclust(dist(dat1), method = "complete")
hc.average <- hclust(dist(dat1), method = "average")
hc.single <- hclust(dist(dat1), method = "single")
hc.centroid <- hclust(dist(dat1), method = "centroid")
```

The function `fviz_dend()` can be applied to visualize the dendrogram.

```
fviz_dend(hc.complete, k = 4,
          cex = 0.3,
          palette = "jco",
          color_labels_by_k = TRUE,
          rect = TRUE, rect_fill = TRUE, rect_border = "jco",
          labels_track_height = 2.5)
```

```
## Warning: The `<scale>` argument of `guides()` cannot be `FALSE`. Use "none" instead as
## of ggplot2 3.3.4.
## i The deprecated feature was likely used in the factoextra package.
##   Please report the issue at <https://github.com/kassambara/factoextra/issues>.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

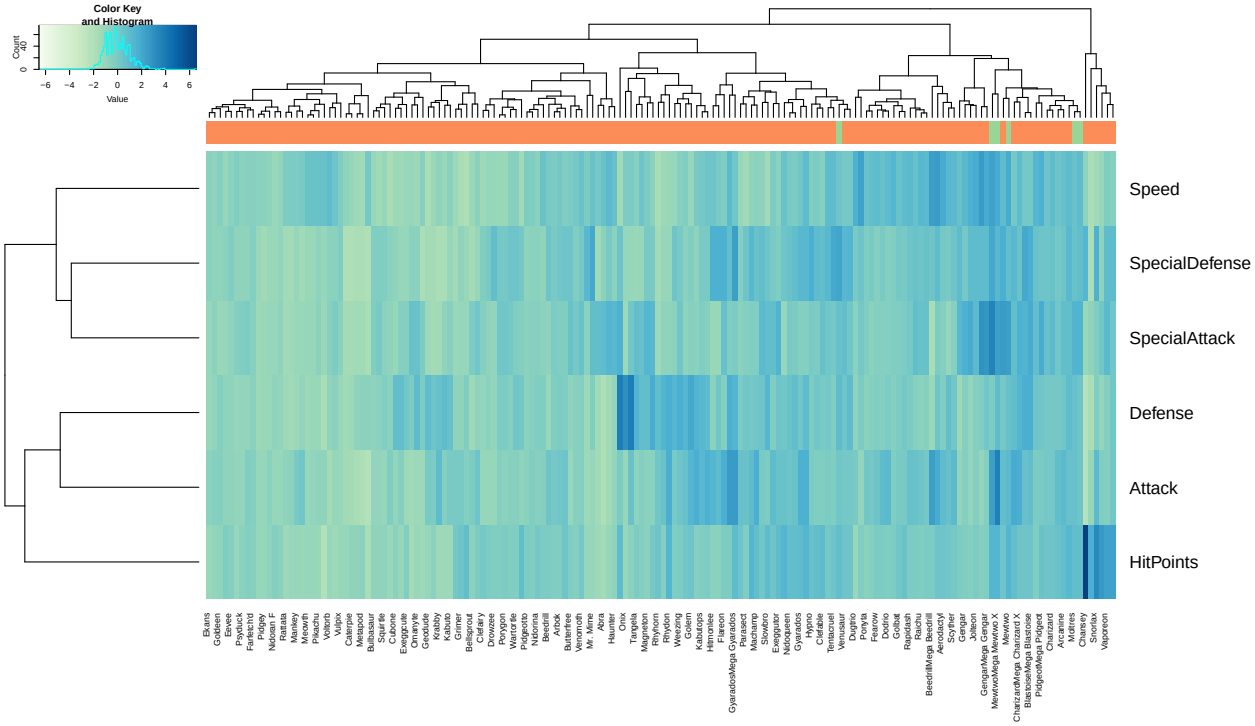



```
ind4.complete <- cutree(hc.complete, 4)

# Who are in the fourth cluster?
dat[ind4.complete == 4,]
```

```
##           Name HitPoints Attack Defense SpecialAttack SpecialDefense Speed
## 45  Jigglypuff       115     45      20            45             25    20
## 46  Wigglytuff       140     70      45            85             50    45
## 122    Chansey       250      5       5            35            105    50
## 143     Lapras       130     85      80            85             95    60
## 146   Vaporeon       130     65      60           110             95    65
## 156    Snorlax       160    110      65            65            110    30
##     Legendary
## 45      FALSE
## 46      FALSE
## 122     FALSE
## 143     FALSE
## 146     FALSE
## 156     FALSE
```

To display more details, we show the heatmap of the data.

```
#display.brewer.all(n=NULL, type="all", select=NULL, exact.n=TRUE)
col1 <- colorRampPalette(brewer.pal(9, "GnBu"))(100)
col2 <- colorRampPalette(brewer.pal(3, "Spectral"))(2)

heatmap.2(t(dat1),
          col = col1, keysize=.8, key.par = list(cex=.5),
          trace = "none", key = TRUE, cexCol = 0.75,
          labCol = as.character(dat[,1]),
          ColSideColors = col2[as.numeric(dat[,"Legendary"])+1],
          margins = c(10, 10))
```



PCA

The function `prcomp()` can be used to perform PCA.

```
pca <- prcomp(dat1)
pca$rotation
```

```
##                     PC1        PC2         PC3          PC4         PC5
## HitPoints     0.3638022  0.2862972  0.72425610 -0.078135517 -0.42663445
## Attack        0.4363956  0.3149994 -0.27779372 -0.573757403 -0.12333177
## Defense       0.3031184  0.5812622 -0.48929801  0.361032760  0.03453292
## SpecialAttack 0.4378985 -0.3119077 -0.03743076  0.654754892 -0.29724064
## SpecialDefense 0.5204254 -0.1331800  0.25037584 -0.006718302  0.80453025
## Speed         0.3503261 -0.6049135 -0.30786700 -0.324966961 -0.25682461
##                      PC6
## HitPoints     -0.27020899
## Attack         0.53736079
## Defense       -0.44643458
## SpecialAttack  0.43874986
```

```
## SpecialDefense -0.03766086
## Speed          -0.49498168
```

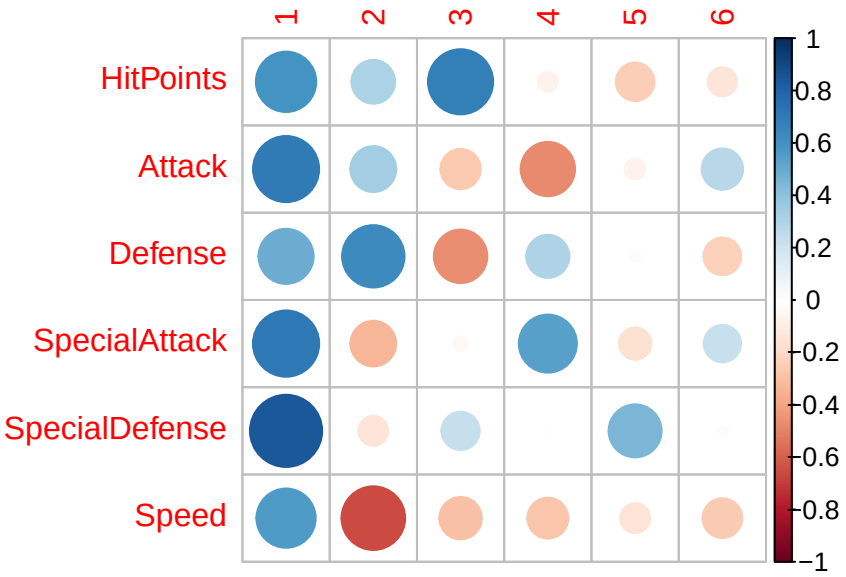
```
pca$sdev
```

```
## [1] 1.6238460 1.0848056 0.9487926 0.8345883 0.5670204 0.5177487
```

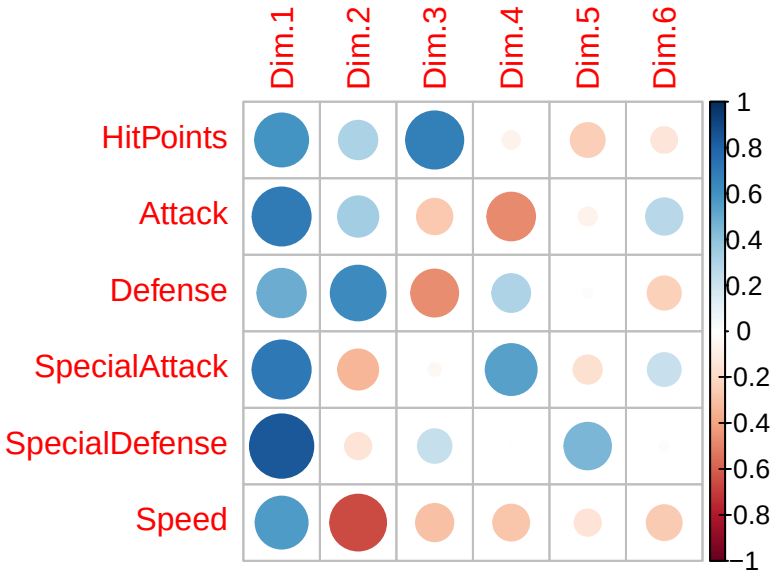
```
pca$rotation %*% diag(pca$sdev)
```

```
##                     [,1]       [,2]        [,3]         [,4]        [,5]
## HitPoints      0.5907587  0.3105768  0.68716880 -0.065210990 -0.24191044
## Attack         0.7086393  0.3417131 -0.26356862 -0.478851234 -0.06993163
## Defense        0.4922176  0.6305564 -0.46424231  0.301313729  0.01958087
## SpecialAttack  0.7110798 -0.3383592 -0.03551403  0.546450792 -0.16854151
## SpecialDefense 0.8450908 -0.1444744  0.23755473 -0.005607016  0.45618508
## Speed          0.5688756 -0.6562135 -0.29210193 -0.271213634 -0.14562479
##                       [,6]
## HitPoints      -0.13990035
## Attack          0.27821784
## Defense        -0.23114091
## SpecialAttack   0.22716216
## SpecialDefense -0.01949886
## Speed          -0.25627611
```

```
corrplot(pca$rotation %*% diag(pca$sdev))
```

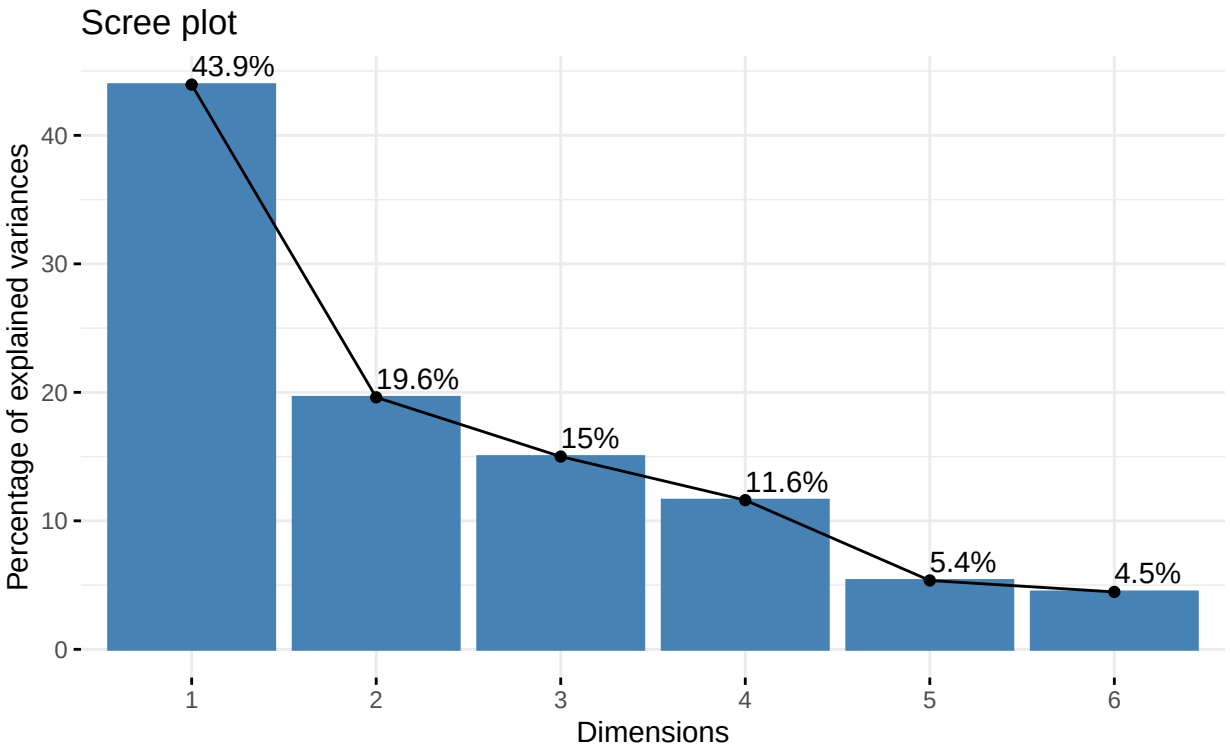



```
var <- get_pca_var(pca)
corrplot(var$cor)
```



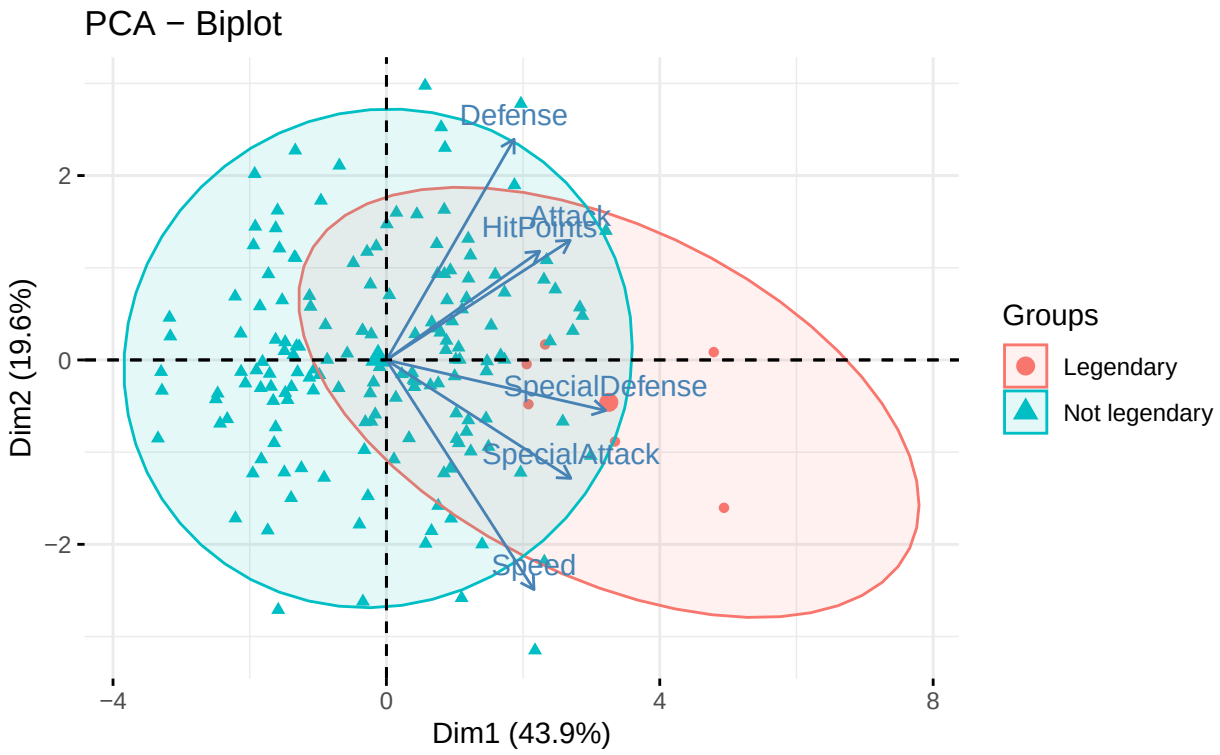
The function `fviz_eig()` plots the eigenvalues/variances against the number of dimensions.

```
fviz_eig(pca, addlabels = TRUE)
```

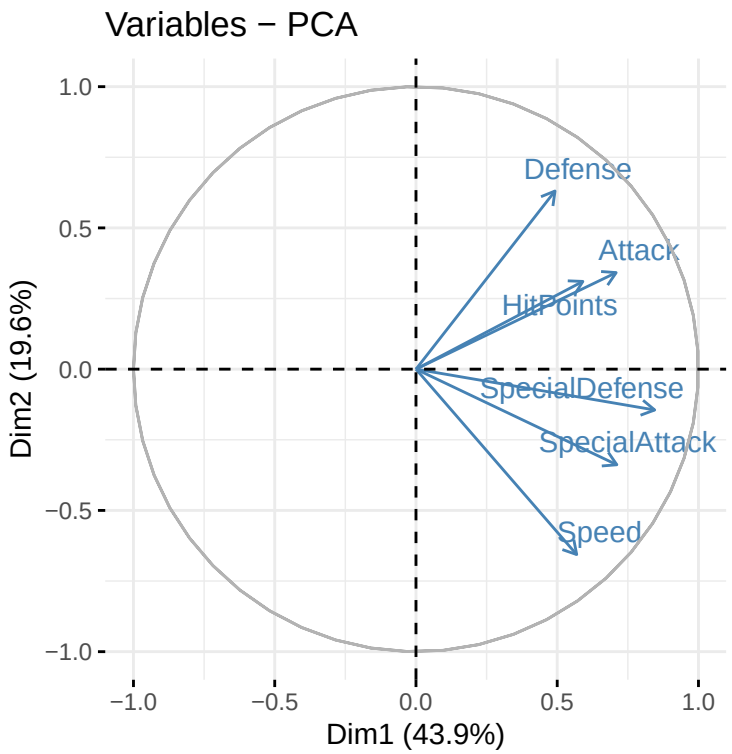


The function `fviz_pca_biplot()` can be used to obtain the biplot of individuals and variables.

```
fviz_pca_biplot(pca, axes = c(1,2),
                habillage = ifelse(dat$Legendary==TRUE, "Legendary","Not legendary"),
                label = c("var"),
                addEllipses = TRUE)
```




```
fviz_pca_var(pca, col.var = "steelblue", repel = TRUE)
```




```
fviz_pca_ind(pca,
             habillage = ifelse(dat$Legendary==TRUE,"Legendary","Not legendary"),
             label = "none",
             addEllipses = TRUE)
```

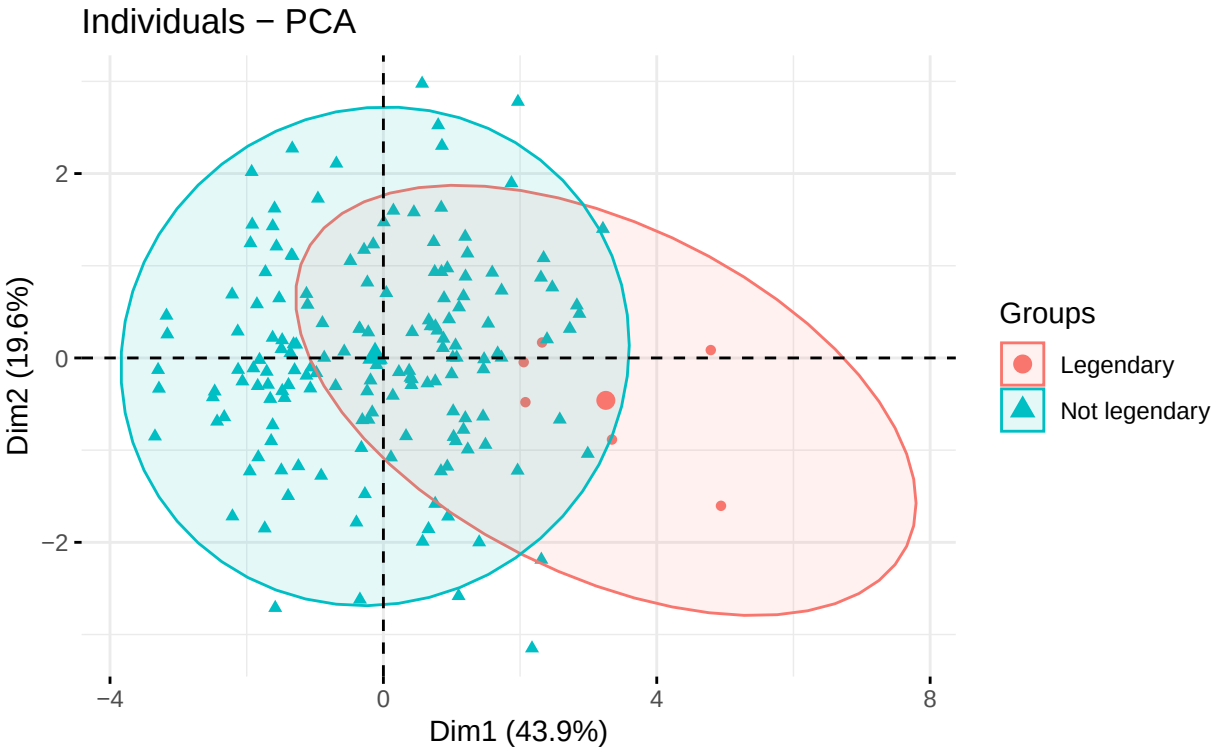
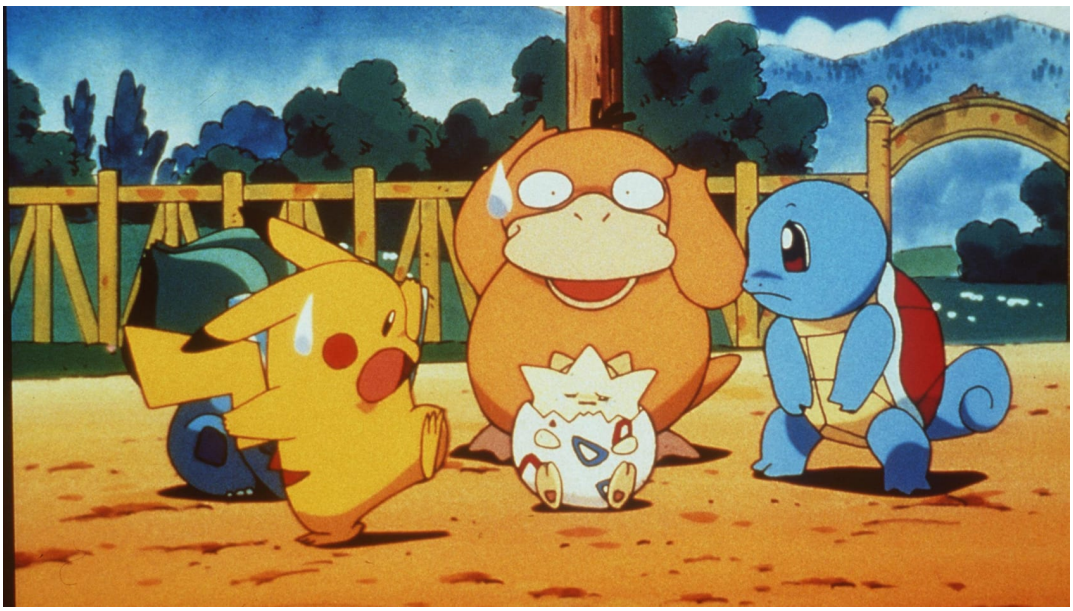


Image compression

```
img <- readJPEG("image.jpg")
dim(img)
```

```
## [1]  948 1685    3
```

```
knitr::include_graphics("image.jpg")
```



```
r <- img[,,1]
g <- img[,,2]
b <- img[,,3]

img.r.pca <- prcomp(r, center = FALSE)
img.g.pca <- prcomp(g, center = FALSE)
img.b.pca <- prcomp(b, center = FALSE)

rgb.pca <- list(img.r.pca, img.g.pca, img.b.pca)

# Approximate X with XV_kV_k^T
compress <- function(pr, k)
{
  compressed.img <- pr$x[,1:k] %*% t(pr$rotation[,1:k])
  compressed.img
}

# Using first 20 PCs
pca20 <- sapply(rgb.pca,
                compress,
                k = 20,
                simplify = "array")

writeJPEG(pca20, "pca20.jpeg")
knitr::include_graphics("pca20.jpeg")
```