```
> wine <- read.csv("C:/Users/admin/desktop/wineR3.csv")
> str(wine)
'data.frame':   178 obs. of  14 variables:
  $ Alcohol             : num  14.2 13.2 13.2 14.4 13.2 ...
$ Malic.acid          : num  1.71 1.78 2.36 1.95 2.59 1.76 1.87 2.15 1.64 1.35 ...
$ Ash                 : num  2.43 2.14 2.67 2.5 2.87 2.45 2.45 2.61 2.17 2.27 ...
$ Acl                 : num  15.6 11.2 18.6 16.8 21 15.2 14.6 17.6 14 16 ...
$ Mg                  : int  127 100 101 113 118 112 96 121 97 98 ...
$ Phenols             : num  2.8 2.65 2.8 3.85 2.8 3.27 2.5 2.6 2.8 2.98 ...
$ Flavanoids          : num  3.06 2.76 3.24 3.49 2.69 3.39 2.52 2.51 2.98 3.15 ...
$ Nonflavanoid.phenols: num  0.28 0.26 0.3 0.24 0.39 0.34 0.3 0.31 0.29 0.22 ...
$ Proanth             : num  2.29 1.28 2.81 2.18 1.82 1.97 1.98 1.25 1.98 1.85 ...
$ Color.int           : num  5.64 4.38 5.68 7.8 4.32 6.75 5.25 5.05 5.2 7.22 ...
$ Hue                 : num  1.04 1.05 1.03 0.86 1.04 1.05 1.02 1.06 1.08 1.01 ...
$ OD                  : num  3.92 3.4 3.17 3.45 2.93 2.85 3.58 3.58 2.85 3.55 ...
$ Proline             : int  1065 1050 1185 1480 735 1450 1290 1295 1045 1045 ...
$ Wine                : int  1 1 1 1 1 1 1 1 1 1 ...
>
  > wine.PCA <- princomp(wine)
> summary(wine.PCA)
Importance of components:
  Comp.1       Comp.2       Comp.3       Comp.4
Standard deviation     314.0775636 13.098369709 3.0785792121 2.252144e+00
Proportion of Variance   0.9980876  0.001735919 0.0000958949 5.132007e-05
Cumulative Proportion    0.9980876  0.999823544 0.9999194388 9.999708e-01
Comp.5       Comp.6       Comp.7       Comp.8
Standard deviation     1.130736e+00 9.291336e-01 5.342233e-01 3.929461e-01
Proportion of Variance 1.293652e-05 8.734764e-06 2.887623e-06 1.562287e-06
Cumulative Proportion  9.999837e-01 9.999924e-01 9.999953e-01 9.999969e-01
Comp.9      Comp.10      Comp.11      Comp.12
Standard deviation     3.362951e-01 2.930753e-01 2.143433e-01 1.863628e-01
Proportion of Variance 1.144289e-06 8.690673e-07 4.648520e-07 3.514092e-07
Cumulative Proportion  9.999980e-01 9.999989e-01 9.999994e-01 9.999997e-01
Comp.13      Comp.14
Standard deviation     1.436873e-01 8.970616e-02
Proportion of Variance 2.088966e-07 8.142155e-08
Cumulative Proportion  9.999999e-01 1.000000e+00
>
  > colnames(wine) <-
c("Alcohol","Malic.acid","Ash","Acl","Mg","Phenols","Flavanoids","Nonflavanoid.phenols","Proanth","Color.int","Hue","OD","Proline","Wi
>
  > library(vegan)
Ładowanie wymaganego pakietu: permute
Ładowanie wymaganego pakietu: lattice
This is vegan 2.6-8
> wine.rda <- rda(wine ~ Alcohol + Malic.acid + Ash + Acl + Mg + Phenols + Flavanoids + Nonflavanoid.phenols + Proanth + Color.int +
Hue + OD + Proline, data = wine, scale = T)
> wine.rda
Call: rda(formula = wine ~ Alcohol + Malic.acid + Ash + Acl + Mg + Phenols +
            Flavanoids + Nonflavanoid.phenols + Proanth + Color.int + Hue + OD +
            Proline, data = wine, scale = T)

-- Model Summary --

  Inertia Proportion Rank
Total         14.000000   1.000000
Constrained   13.900089   0.992863   13
Unconstrained  0.099911   0.007137    1

Inertia is correlations

-- Eigenvalues --

  Eigenvalues for constrained axes:
  RDA1  RDA2  RDA3  RDA4  RDA5  RDA6  RDA7  RDA8  RDA9 RDA10 RDA11 RDA12 RDA13
5.521 2.497 1.446 0.927 0.875 0.669 0.553 0.350 0.293 0.259 0.226 0.169 0.115

Eigenvalues for unconstrained axes:
  PC1
0.09991

> RsquareAdj(wine.rda)
$r.squared
[1] 0.9928635

$adj.r.squared
[1] 0.9922978

> screeplot(wine.rda)
>
  > signif.full <- anova.cca(wine.rda, parallel=getOption("mc.cores"))
> signif.full
Permutation test for rda under reduced model
Permutation: free
Number of permutations: 999

Model: rda(formula = wine ~ Alcohol + Malic.acid + Ash + Acl + Mg + Phenols + Flavanoids + Nonflavanoid.phenols + Proanth +
Color.int + Hue + OD + Proline, data = wine, scale = T)
Df Variance      F Pr(>F)
Model     13  13.9001 1755.1  0.001 ***
  Residual 164   0.0999
---
  Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
>
  > vif.cca(wine.rda)
Alcohol           Malic.acid                  Ash
2.460372            1.656647            2.185448
Acl                   Mg             Phenols
2.238732            1.417855            4.334519
Flavanoids Nonflavanoid.phenols             Proanth
7.029350            1.796380            1.975683
Color.int                 Hue                  OD
3.026304            2.551447            3.785473
Proline
```

```
2.823849
>
  > plot(wine.rda, scaling=3)
>
  > load.rda <- scores(wine.rda, choices=c(1:3), display="species")
> outliers <- function(x,z){
  + lims <- mean(x) + c(-1, 1) * z * sd(x)
  + x[x< lims[1] | x > lims[2]]
  + }
> hist(load.rda[,1], main="Loadings on RDA1")
>
  > hist(load.rda[,2], main="Loadings on RDA2")
>
```