# MVN package: Multivariate Normality Tests

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**Abstract**

Assessing the assumption of multivariate normality is required by many parametric multivariate statistical methods, such as discriminant analysis, principal component analysis, MANOVA, etc. Here, we present an R package to asses multivariate normality. The MVN package contains three most widely used multivariate normality tests, including Mardia's, Henze-Zirkler's and Royston's multivariate normality tests.

## Contents

# 1 Preparation of input data

`MVN` package expects a numeric matrix or a data frame that contains minimum two variables. In this vignette, we will work with the *Iris* data set. This data set is a multivariate data set introduced by Ronald A. Fisher (1936) as an application of discriminant analysis [1]. It is also called Anderson's Iris data set because Edgar Anderson collected the data to measure the morphologic variation of Iris flowers of three related species [2]. The data set consists of 50 samples from each of three species of Iris including *setosa*, *virginica* and *versicolor*. For each sample, four variables were measured including the length and the width of the *sepals* and *petals*, in centimeters. We will check the multivariate normality of the *Iris* data set by using three multivariate normality tests, including Mardia's, Royston's and Henze-Zirkler's multivariate normality tests.

First, we can call our data set using `data` function and display it using `head` function as follows:

```
data(iris)
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
```

The *Iris* data is in `data.frame` format which consists of 5 variables (*Sepal.Length*, *Sepal.Width*, *Petal.Length*, *Petal.Width*, and *Species*) and 150 samples.

```
class(iris)

## [1] "data.frame"

dim(iris)

## [1] 150   5
```

For simplicity, we will work with a subset of the *Iris* data with first 50 samples without class label.

```
Iris=iris[1:50, 1:4]
head(Iris)

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

## 2 Multivariate Normality Tests

We will introduce three multivariate normality tests below, including Mardia's, Henze-Zirkler's and Royston's Multivariate Normality Tests.

Before using our multivariate normality tests, we need to load our `MVN` package as follows:

```
library(MVN)
```

### 2.1 Mardia's Multivariate Normality Test

Mardia's test is based on multivariate extensions of *skewness* and *kurtosis* measures [3]. Now, we will check the multivariate normality of the *Iris* data using `mardiaTest` function in the `MVN` package. This function calculates the Mardia's multivariate skewness and kurtosis coefficients as well as their corresponding statistical tests. For large sample size the multivariate skewness is asymptotically distributed as a chi-square random variable; here it is corrected for small sample size. Likewise, the multivariate kurtosis is distributed as a unit-normal [4–6].

```
result <- mardiaTest(Iris, cov = TRUE, qqplot = FALSE)
result

##    Mardia's Multivariate Normality Test
## ---------------------------------------
##    data : Iris
##
##    g1p             : 3.08
##    chi.skew        : 25.66
##    p.value.skew    : 0.1772
##
##    g2p             : 26.54
##    z.kurtosis      : 1.295
##    p.value.kurt    : 0.1953
##
##    chi.small.skew  : 27.86
##    p.value.small   : 0.1128
##
##    Result          : Data is multivariate normal.
## ---------------------------------------
```

Here:
`g1p`: Mardia's estimation of multivariate skewness,
`chi.skew`: Chi-square value of the skewness statistic,
`p.value.skew`: Significance value of skewness statistic,
`g2p`: Mardia's estimation of multivariate kurtosis,
`z.kurtosis`: z value of the kurtosis statistic,
`p.value.kurt`: Significance value of kurtosis statistic,
`chi.small.skew`: Chi-square value of the small sample skewness statistic,
`p.value.small`: Significance value of small sample skewness statistic.

As seen above results, both skewness ($p = 0.1772$) and kurtosis ($p = 0.1953$) values indicate multivariate normality.

`mardiaTest` function has an S4 class called `mardia`. We can use `getSlots` function in order to get the slots in this S4 class.

```
getSlots("mardia")
```

```
##            g1p       chi.skew   p.value.skew chi.small.skew  p.value.small
##      "numeric"      "numeric"      "numeric"      "numeric"      "numeric"
##            g2p     z.kurtosis   p.value.kurt          dname      dataframe
##      "numeric"      "numeric"      "numeric"    "character"   "data.frame"
```

To access the informations which are stored in these slots, we can use `@` operator as follow:

```
result@p.value.skew
```

```
## [1] 0.1772
```

```
result@p.value.kurt
```

```
## [1] 0.1953
```

## 2.2 Henze-Zirkler's Multivariate Normality Test

The Henze-Zirkler test is based on a non-negative functional distance that measures the distance between two distribution functions. If the data is multivariate normal, the test statistic is approximately log-normally distributed. It proceeds to calculate the mean, variance and smoothness parameter. Then, mean and variance are log-normalized and the p-value is estimated. We can use `hzTest` function in the `MVN` package to calculate the Henze-Zirkler's Multivariate Normality Test [7–11].

```
result <- hzTest(Iris, cov = TRUE, qqplot = FALSE)
result
```

```
##   Henze-Zirkler's Multivariate Normality Test
## ---------------------------------------------
##   data : Iris
##
##   HZ      : 0.9488
##   p-value : 0.04995
##
##   Result  : Data is not multivariate normal.
## ---------------------------------------------
```

Here, `HZ` is the value of Henze-Zirkler statistic at significance level 0.05 and `p-value` is a p-value for the Henze-Zirkler's Multivariate Normality Test.

Since the p-value, which optain from the `hzTest`, lower than 0.05, one can conclude that this multivariate data set deviates from multivariate normality.

`hzTest` function has an S4 class called `hz`. We can use `getSlots` function in order to get the slots in this S4 class.

```
getSlots("hz")

##           HZ      p.value        dname    dataframe
##    "numeric"    "numeric"  "character" "data.frame"
```

To access the informations which are stored in these slots, we can use `@` operator as follow:

```
result@HZ

## [1] 0.9488

result@p.value

## [1] 0.04995
```

### 2.3 Royston's Multivariate Normality Test

Royston's H test uses `Shapiro-Wilk's W` statistic for multivariate normality. However, if kurtosis of the data greater than 3 then `Shapiro-Francia` test is used for leptokurtic samples else `Shapiro-Wilk` test is used for platykurtic samples [10, 12–18].

```
result <- roystonTest(Iris, qqplot = FALSE)
result

##   Royston's Multivariate Normality Test
## ---------------------------------------------
##   data : Iris
##
##   H       : 31.52
##   p-value : 2.188e-06
##
##   Result  : Data is not multivariate normal.
## ---------------------------------------------
```

Here, `H` is the value of Royston's H statistic at significance level `0.05` and `p-value` is an approximate p-value for the test with respect to equivalent degrees of freedom (`edf`).

According to the Royston's Multivariate Normality Test, the *Iris* data set does not appear to follow a multivariate normal distribution ($p < 0.001$).

`roystonTest` function has an S4 class called `royston`. We can use `getSlots` function in order to get the slots in this S4 class.

```
getSlots("hz")

##           HZ      p.value        dname    dataframe
##    "numeric"    "numeric"  "character" "data.frame"
```

To access the informations which are stored in these slots, we can use `@` operator as follow:

```
result@H
```

```
## [1] 31.52
```

```
result@p.value
```

```
## [1] 2.188e-06
```

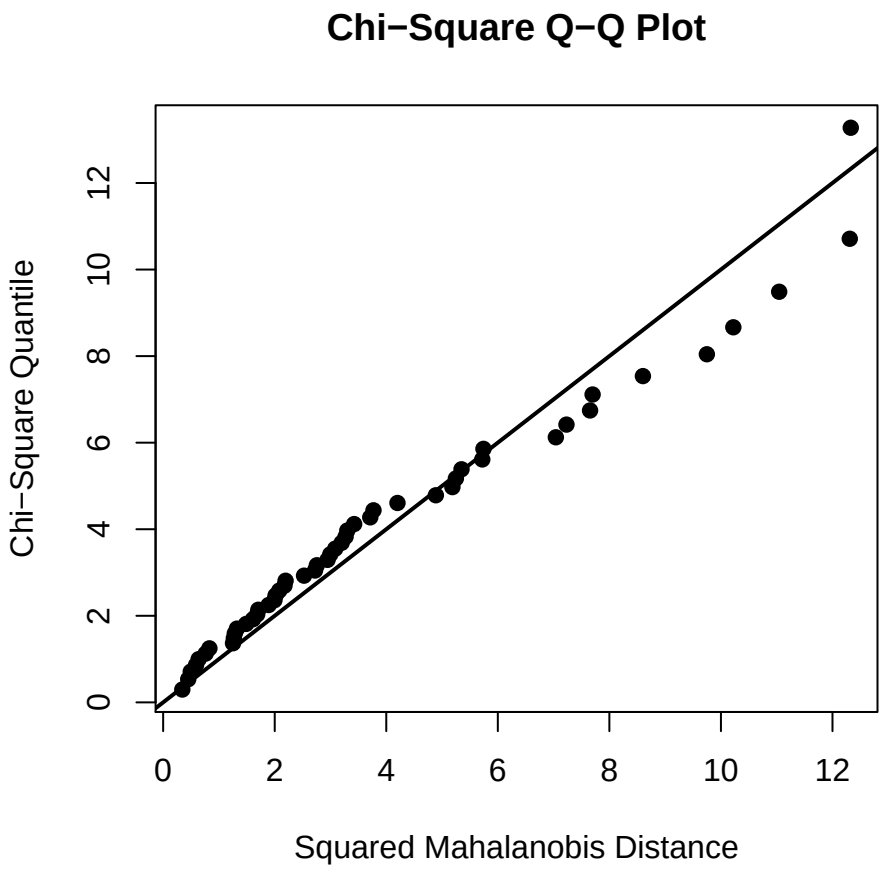
# 3 Multivariate Normality Plots

Our `MVN` package has ability to create three multivariate plots. We can use `qqplot = TRUE` option in the `mardiaTest`, `hzTest` and `roystonTest` functions to create a chi-suqare Q-Q plot. Furthermore, we can use `mvnPlot` function in our `MVN` package to create perspective and contour plots for binary data sets.

## 3.1 Q-Q Plot

We can create a chi-square Q-Q plot for our *Iris* data set to see whether there is any deviation from multivariate normality.

```
result <- roystonTest(Iris, qqplot = TRUE)
```



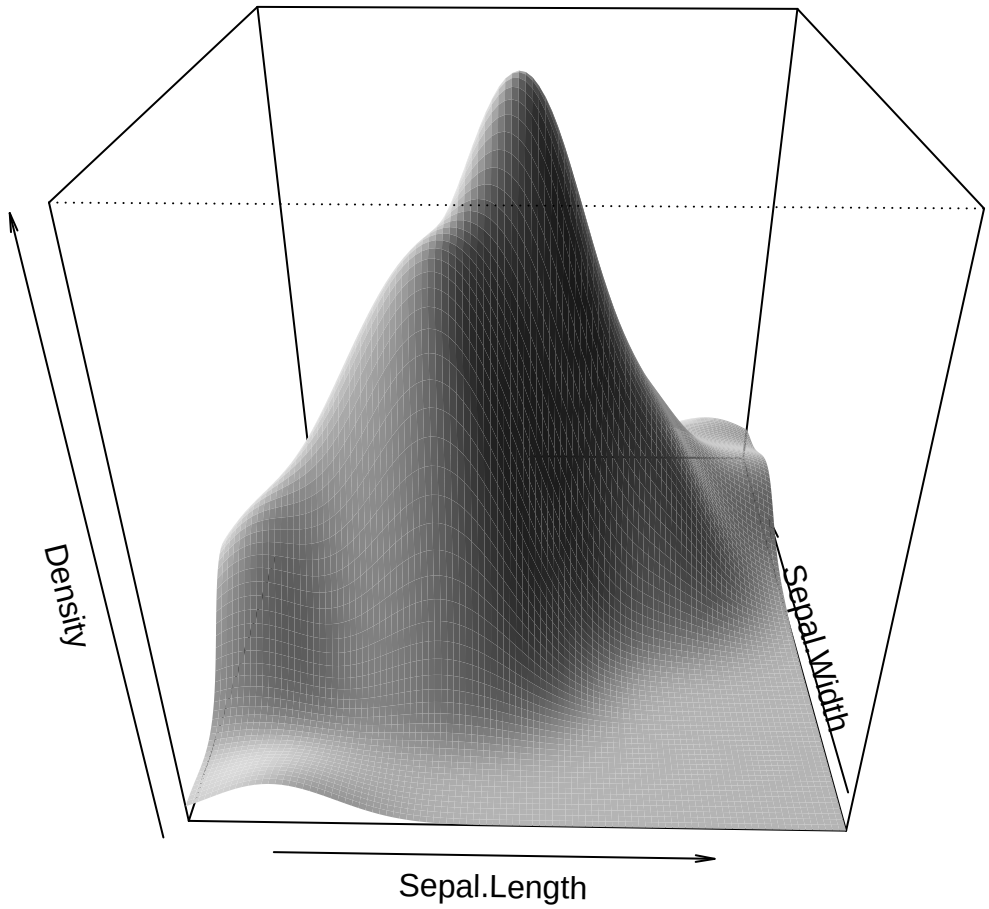
```
result

##   Royston's Multivariate Normality Test
## --------------------------------------------
##   data : Iris
##
##   H       : 31.52
##   p-value : 2.188e-06
##
##   Result  : Data is not multivariate normal.
## --------------------------------------------
```

If the data set follows approximately a multivariate normal distribution, the resulting plot should be roughly straight line. As you can see from the chi-square Q-Q plot above, there are some deviations from the straight line and this indicates possible departures from a multivariate normal distribution.

### 3.2 Perspective and Contour Plots

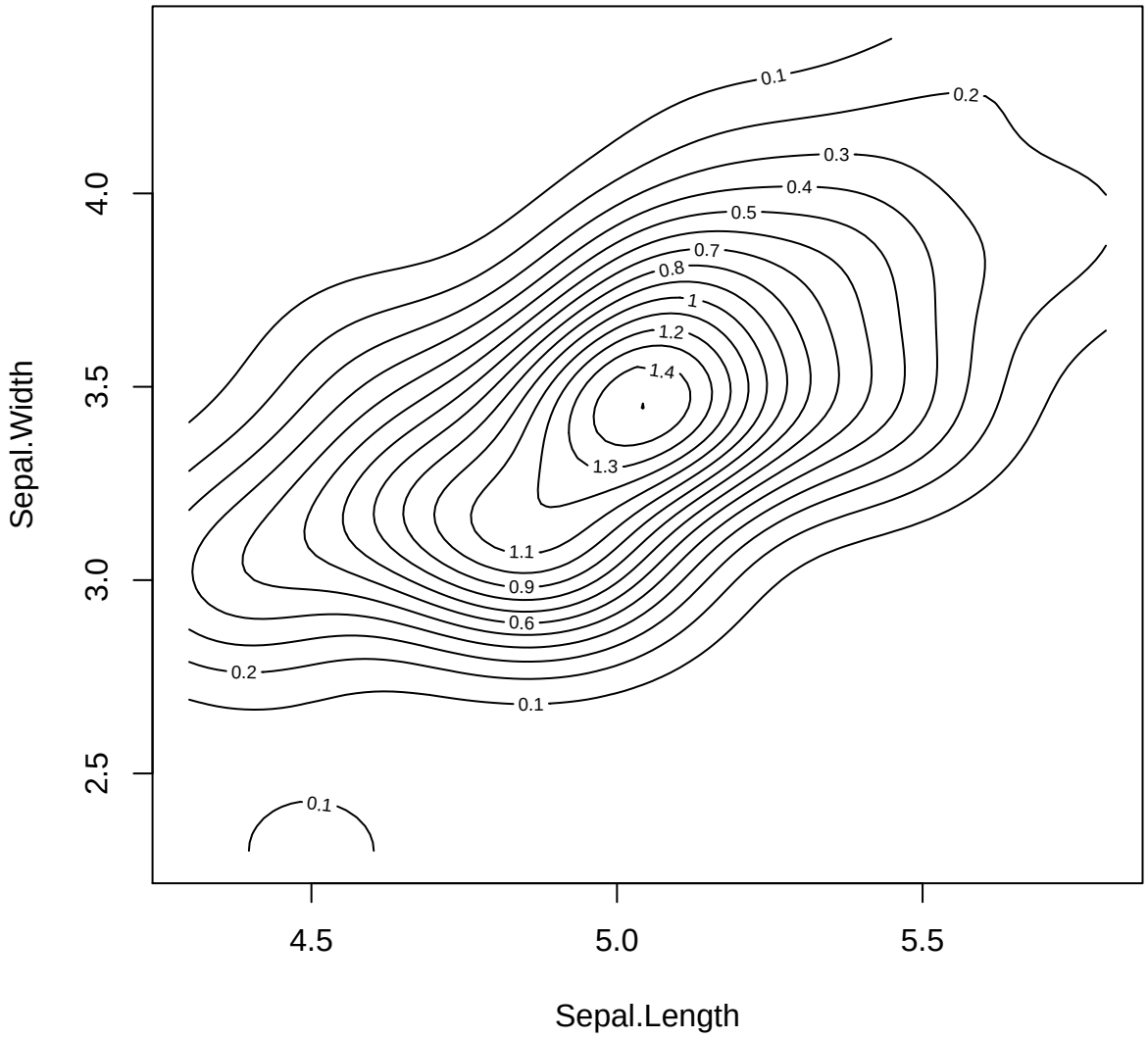
We can use the `mvnPlot` function in the `MVN` package to create a perspective plot for a binary data set. In order to get a perspective plot, we should continue with two variables, i.e., bivariate normal distribution. As an example, we subset first 50 rows and *sepal* measures of *Iris* data. Sepal measures of first 50 samples are bivariate normal. We can see that from the perspective plot. Perspective plot produces 3-dimensional bell-shaped graph when data is bivariate normal.

```
Iris = iris[1:50, 1:2]
result = hzTest(Iris)
mvnPlot(result, type = "persp", default = TRUE)
```




Another alternative is to use 2-dimensional contour graphs. We can use the `mvnPlot` function in the `MVN` package to create a contour plot for a binary data set. Contour graphs are very useful since it gives information about normality and correlation at the same time.

```
mvnPlot(result, type = "contour", default = TRUE)
```




From contour graph above, we can say that there is a positive correlation among *sepal* measures of flowers since contour lines lie around main diagonal.

# 4 Multivariate Outlier Detection

There are two multivariate outlier detection methods which are based on Mahalanobis distance in the `MVN` package.

## 4.1 Mahalanobis Distance

This methodology has following steps:

1 Compute robust Mahalanobis distances (MD(xi))

2 Compute the 97.5 percent-Quantile Q of the Chi-Square distribution

3 Declare MD(xi) > Q as possible outlier

For this task `mvnPlot` function can be used as follows:

```
Iris = iris[1:50, 1:3]
result <- mvOutlier(Iris, qqplot = FALSE, method="quan")
head(result$outlier)

##        MD Outlier
## 23 14.961    TRUE
## 25 12.660    TRUE
## 15 11.890    TRUE
## 45 11.586    TRUE
## 14  9.081   FALSE
## 42  7.733   FALSE

head(result$newData)

##    Sepal.Length Sepal.Width Petal.Length
## 1           5.1         3.5          1.4
## 10          4.9         3.1          1.5
## 11          5.4         3.7          1.5
## 12          4.8         3.4          1.6
## 13          4.8         3.0          1.4
## 14          4.3         3.0          1.1
```

Here, user can get outlier set based on Mahalanobis distance and data set without outliers.

## 4.2 Adjusted Mahalanobis Distance

This methodology has following steps:

1 Compute robust Mahalanobis distances (MD(xi))

2 Compute the 97.5 percent Adjsuted Quantile (AQ) of the Chi-Square distribution

3 Declare MD(xi) > AQ as possible outlier

Likewise, `mvnPlot` function can be used as follows:

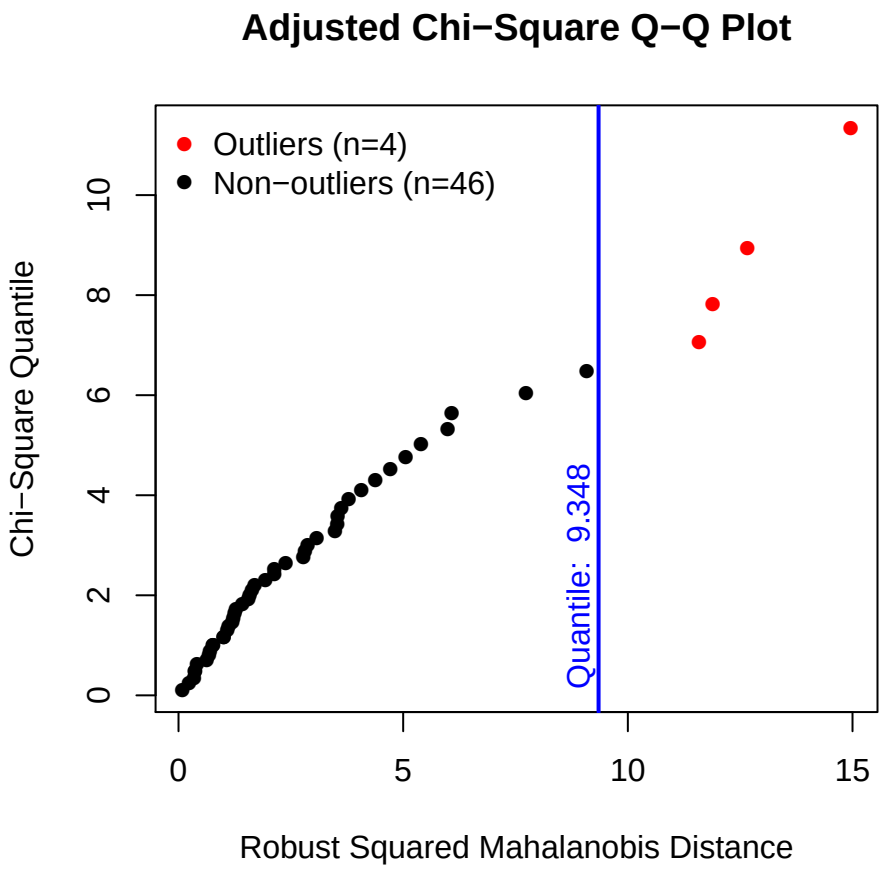
```
result <- mvOutlier(Iris, qqplot = FALSE, method="adj.quan")
head(result$outlier)

##        MD Outlier
## 23 14.961    TRUE
## 25 12.660    TRUE
## 15 11.890    TRUE
## 45 11.586    TRUE
## 14  9.081   FALSE
## 42  7.733   FALSE
```

```
head(result$newData)

##    Sepal.Length Sepal.Width Petal.Length
## 1           5.1         3.5          1.4
## 10          4.9         3.1          1.5
## 11          5.4         3.7          1.5
## 12          4.8         3.4          1.6
## 13          4.8         3.0          1.4
## 14          4.3         3.0          1.1
```

Here, user can get outlier set based on adjusted Mahalanobis distance and data set without outliers.

A Q-Q plot can be created with using `qqplot = TRUE` option in the `mvOutlier` function for visual inspection.

```
result <- mvOutlier(Iris, qqplot = TRUE, method="adj.quan")
```



# 5 Session info

```
sessionInfo()

## R version 3.1.1 (2014-07-10)
## Platform: x86_64-apple-darwin13.1.0 (64-bit)
##
## locale:
## [1] C/tr_TR.UTF-8/tr_TR.UTF-8/C/tr_TR.UTF-8/tr_TR.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] MVN_3.5           mvoutlier_2.0.5   sgeostat_1.0-25   robustbase_0.91-1
## [5] MASS_7.3-34       moments_0.13      nortest_1.0-2     knitr_1.6
##
## loaded via a namespace (and not attached):
##  [1] DEoptimR_1.0-1        GGally_0.4.8          Rcpp_0.11.2
##  [4] codetools_0.2-9       colorspace_1.2-4      digest_0.6.4
##  [7] evaluate_0.5.5        formatR_1.0           ggplot2_1.0.0
## [10] grid_3.1.1            gtable_0.1.2          highr_0.3
## [13] munsell_0.4.2         mvtnorm_1.0-0         pcaPP_1.9-50
## [16] pls_2.4-3             plyr_1.8.1            proto_0.3-10
## [19] reshape_0.8.5         reshape2_1.4          robCompositions_1.9.0
## [22] rrcov_1.3-4           scales_0.2.4          stats4_3.1.1
## [25] stringr_0.6.2         tools_3.1.1
```

# References


[1] R. A. Fisher (1936). "The use of multiple measurements in taxonomic problems". Annals of Eugenics 7 (2): 179-188. doi:10.1111/j.1469-1809.1936.tb02137.x

[2] Edgar Anderson (1936). "The species problem in Iris". Annals of the Missouri Botanical Garden 23 (3): 457-509. JSTOR 2394164.

[3] Mardia, K. V. (1970). "Measures of multivariate skewness and kurtosis with applications". Biometrika 57 (3): 519-530. doi:10.1093/biomet/57.3.519.

[4] Mardia, K. V. (1974), Applications of some measures of multivariate skewness and kurtosis for testing normality and robustness studies. Sankhy A, 36:115-128.

[5] Trujillo-Ortiz, A. and R. Hernandez-Walls. (2003). Mskekur: Mardia's multivariate skewness and kurtosis coefficients and its hypotheses testing. A MATLAB file. URL http://www.mathworks.com/matlabcentral/fileexchange/loadFile.do?objectId=3519

[6] Stevens, J. (1992), Applied Multivariate Statistics for Social Sciences. 2nd. ed. New-Jersey:Lawrance Erlbaum Associates Publishers. pp. 247-248.

[7] Trujillo-Ortiz, A., R. Hernandez-Walls, K. Barba-Rojo and L. Cupul-Magana. (2007). HZmvntest:Henze-Zirkler's Multivariate Normality Test. A MATLAB file. URL http://www.mathworks.com/matlabcentral/fileexchange/loadFile.do?objectId=17931

[8] Henze, N. and Zirkler, B. (1990), A Class of Invariant Consistent Tests for Multivariate Normality. Commun. Statist.-Theor. Meth., 19(10): 35953618.

[9] Henze, N. and Wagner, Th. (1997), A New Approach to the BHEP tests for multivariate normality. Journal of Multivariate Analysis, 62:1-23.

[10] Johnson, R.A. and Wichern, D. W. (1992). Applied Multivariate Statistical Analysis. 3rd. ed. New-Jersey:Prentice Hall.

[11] Mecklin, C. J. and Mundfrom, D. J. (2003), On Using Asymptotic Critical Values in Testing for Multivariate Normality.

[12] Mecklin, C.J. and Mundfrom, D.J. (2005). A Monte Carlo comparison of the Type I and Type II error rates of tests of multivariate normality. Journal of Statistical Computation and Simulation, 75:93-107.

[13] Royston, J.P. (1982). An Extension of Shapiro and Wilks W Test for Normality to Large Samples. Applied Statistics, 31(2):115124.

[14] Royston, J.P. (1983). Some Techniques for Assessing Multivariate Normality Based on the Shapiro-Wilk W. Applied Statistics, 32(2).

[15] Royston, J.P. (1992). Approximating the Shapiro-Wilk W-Test for non-normality. Statistics and Computing, 2:117-119.121133.

[16] Royston, J.P. (1995). Remark AS R94: A remark on Algorithm AS 181: The W test for normality. Applied Statistics, 44:547-551.

[17] Shapiro, S. and Wilk, M. (1965). An analysis of variance test for normality. Biometrika, 52:591611.

[18] Trujillo-Ortiz, A., R. Hernandez-Walls, K. Barba-Rojo and L. Cupul-Magana. (2007). Roystest:Royston's Multivariate Normality Test. A MATLAB file. URL http://www.mathworks.com/matlabcentral/fileexchange/17811