Topic 6: Basic Statistical Analysis

2023-08-16

In this topic, you will learn about :

- Test of association (Pearson Chi-Square and Fisher's Exact test)
- Correlation test

Pearson Chi-Square Test

Pearson's Chi-Square Test for Independence in R

Pearson's Chi-Square test for independence is a statistical test used to determine if there is a significant association between two categorical variables. It assesses whether the observed frequency distribution differs significantly from the expected frequency distribution under the assumption of independence.

Performing Pearson's Chi-Square Test:

1. Using **chisq.test()**: The **chisq.test()** function in R is used to perform Pearson's Chi-Square test.

Example: Pearson's Chi-Square Test

Suppose we have survey data on the relationship between gender and favorite color and want to test if there is a significant association between the two variables.

```r
# Sample data for gender and favorite color
gender <- c("Male", "Female", "Male", "Female", "Male", "Female", "Male", "Female")
favorite_color <- c("Blue", "Red", "Blue", "Blue", "Red", "Red", "Blue", "Red")

# Create a contingency table
cont_table <- table(gender, favorite_color)

# Perform Pearson's Chi-Square test
chi_square_result <- chisq.test(cont_table)
```

```
## Warning in chisq.test(cont_table): Chi-squared approximation may be incorrect
```

```r
# Print the test result
print(chi_square_result)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  cont_table
## X-squared = 0.5, df = 1, p-value = 0.4795
```

Interpreting the Output:

The output of the **chisq.test()** function includes the Chi-Square statistic, degrees of freedom, and the p-value. The p-value indicates the probability of obtaining the observed contingency table or more extreme tables under the assumption of independence.

If the p-value is below a pre-defined significance level (commonly 0.05), we reject the null hypothesis and conclude that there is a significant association between gender and favorite color.

2. Using **Residuals:**

The residuals can be helpful in interpreting the direction and magnitude of the deviation from independence.

```
# Extract residuals from the chi-square result
residuals <- chi_square_result$residuals

# Print the residuals
print(residuals)
```

```
##         favorite_color
## gender         Blue        Red
##   Female -0.7071068  0.7071068
##   Male    0.7071068 -0.7071068
```

Summary:

1. Pearson's Chi-Square test for independence is used to determine if there is a significant association between two categorical variables.
2. The **chisq.test()** function in R is used to perform Pearson's Chi-Square test.
3. The p-value obtained from the test helps to make a decision about rejecting or failing to reject the null hypothesis of independence between the two categorical variables.
4. Residuals can be used to interpret the direction and magnitude of the deviation from independence.

Fisher's Exact test

Fisher's Exact Test in R Programming

Fisher's Exact test is a statistical test used to determine if there is a significant association between two categorical variables in a 2x2 contingency table. It is particularly useful when the sample size is small or when the assumptions of the Chi-Square test are not met.

Performing Fisher's Exact Test:

1. Using **fisher.test():** The **fisher.test()** function in R is used to perform Fisher's Exact test.

Example: Fisher's Exact Test

Suppose we have survey data on the relationship between gender and voting preference and want to test if there is a significant association between the two variables.

```
# Sample data for gender and voting preference
gender <- c("Male", "Female", "Male", "Female")
voting_preference <- c("Republican", "Democrat", "Democrat", "Republican")

# Create a contingency table
cont_table <- table(gender, voting_preference)

# Perform Fisher's Exact test
fisher_result <- fisher.test(cont_table)

# Print the test result
print(fisher_result)
```

```
##
##  Fisher's Exact Test for Count Data
##
```

```
## data:  cont_table
## p-value = 1
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  6.412991e-03 1.559335e+02
## sample estimates:
## odds ratio
##          1
```

Interpreting the Output:

The output of the **fisher.test()** function includes the p-value. The p-value indicates the probability of obtaining the observed contingency table or more extreme tables under the assumption of independence.

If the p-value is below a pre-defined significance level (commonly 0.05), we reject the null hypothesis and conclude that there is a significant association between gender and voting preference.

2. Using **Odds Ratio**:

The odds ratio is a measure of association between two categorical variables in a 2x2 contingency table. It quantifies the strength and direction of the relationship.

```r
# Extract odds ratio from the Fisher's Exact test result
odds_ratio <- fisher_result$estimate

# Print the odds ratio
print(odds_ratio)
```

```
## odds ratio
##          1
```

Summary:

1. Fisher's Exact test is used to determine if there is a significant association between two categorical variables in a 2x2 contingency table, especially when sample sizes are small or Chi-Square test assumptions are not met.
2. The **fisher.test()** function in R is used to perform Fisher's Exact test.
3. The p-value obtained from the test helps to make a decision about rejecting or failing to reject the null hypothesis of independence between the two categorical variables.
4. The odds ratio can be used to measure the strength and direction of the association between the variables.

Correlation test

Correlation Test in R Programming

Correlation is a statistical measure that indicates the extent to which two continuous variables are linearly related to each other. Correlation tests in R help to determine if there is a significant association between two continuous variables and to quantify the strength and direction of the relationship.

Performing Correlation Test:

1. **Pearson Correlation** (**cor.test()**): The **cor.test()** function in R is used to perform Pearson's correlation test. It tests for a linear relationship between two continuous variables.

Example: Pearson Correlation Test

```r
# Sample data for two continuous variables
x <- c(1, 2, 3, 4, 5)
y <- c(3, 5, 7, 9, 11)
```

```r
# Perform Pearson correlation test
cor_test_result <- cor.test(x, y)

# Print the test result
print(cor_test_result)
```

```
##
##  Pearson's product-moment correlation
##
## data:  x and y
## t = 82191237, df = 3, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  1 1
## sample estimates:
## cor
##   1
```

Interpreting the Output:

The output of the **cor.test()** function includes the correlation coefficient (r), the p-value, and the confidence interval for the correlation coefficient. The correlation coefficient (r) measures the strength and direction of the linear relationship between the two variables.

If the p-value is below a pre-defined significance level (commonly 0.05), we reject the null hypothesis and conclude that there is a significant correlation between the two variables.

2. **Spearman Correlation** (**cor.test()**): You can also use the **cor.test()** function to perform Spearman's correlation test, which tests for a monotonic relationship between two variables. Spearman's correlation is more appropriate for data that are not normally distributed or have outliers.

Example: Spearman Correlation Test

```r
# Sample data for two continuous variables
x <- c(1, 2, 3, 4, 5)
y <- c(3, 5, 7, 9, 11)

# Perform Spearman correlation test
cor_test_result <- cor.test(x, y, method = "spearman")

# Print the test result
print(cor_test_result)
```

```
##
##  Spearman's rank correlation rho
##
## data:  x and y
## S = 4.4409e-15, p-value = 0.01667
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
##   1
```

3. **Kendall Correlation** (**cor.test()**): The **cor.test()** function can also perform Kendall's correlation test, which tests for a monotonic relationship between two variables similar to Spearman's correlation. Kendall's correlation is appropriate when dealing with small sample sizes.

Example: Kendall Correlation Test

```r
# Sample data for two continuous variables
x <- c(1, 2, 3, 4, 5)
y <- c(3, 5, 7, 9, 11)

# Perform Kendall correlation test
cor_test_result <- cor.test(x, y, method = "kendall")

# Print the test result
print(cor_test_result)
```

```
##
##  Kendall's rank correlation tau
##
## data:  x and y
## T = 10, p-value = 0.01667
## alternative hypothesis: true tau is not equal to 0
## sample estimates:
## tau
##   1
```

Summary:

1. Correlation tests in R help to determine if there is a significant association between two continuous variables.
2. Pearson correlation is used for normally distributed data with a linear relationship.
3. Spearman and Kendall correlations are used for non-normally distributed data or data with outliers, and they test for monotonic relationships.
4. The p-value obtained from the correlation test helps to make a decision about rejecting or failing to reject the null hypothesis of no correlation between the two variables.

Additional notes

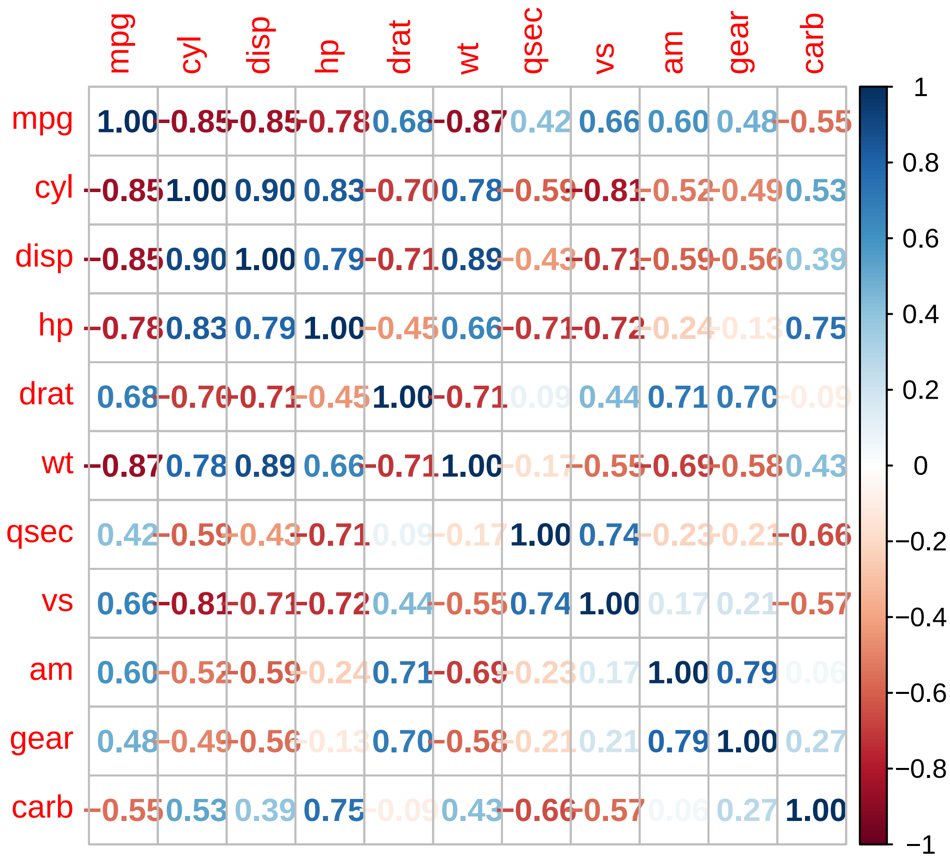
An Introduction to corrplot Package

R package corrplot provides a visual exploratory tool on correlation matrix that supports automatic variable reordering to help detect hidden patterns among variables.

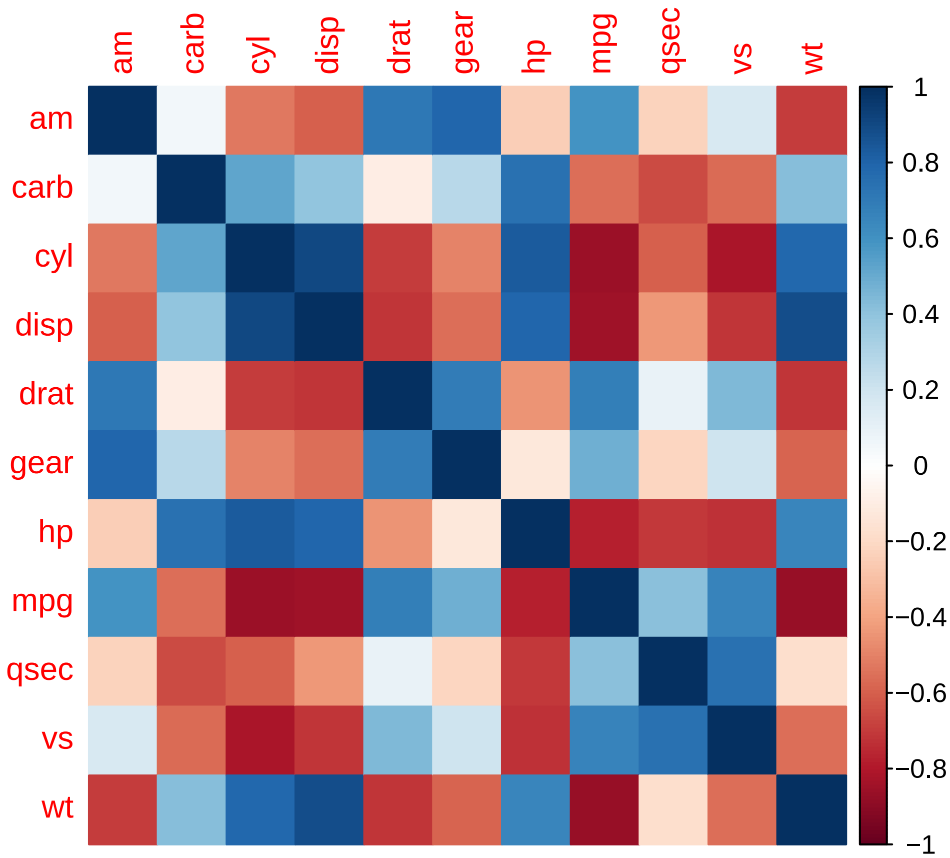
```r
library(corrplot)
```

```
## corrplot 0.92 loaded
```

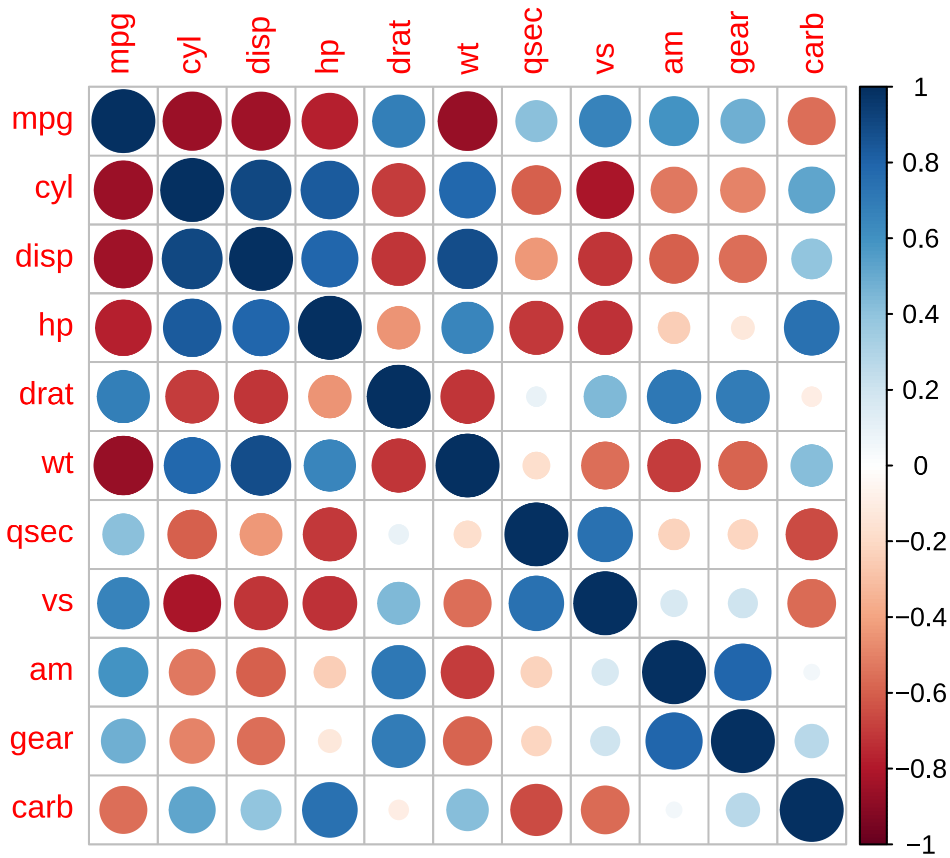
```r
M = cor(mtcars)
corrplot(M, method = 'number') # colorful number
```



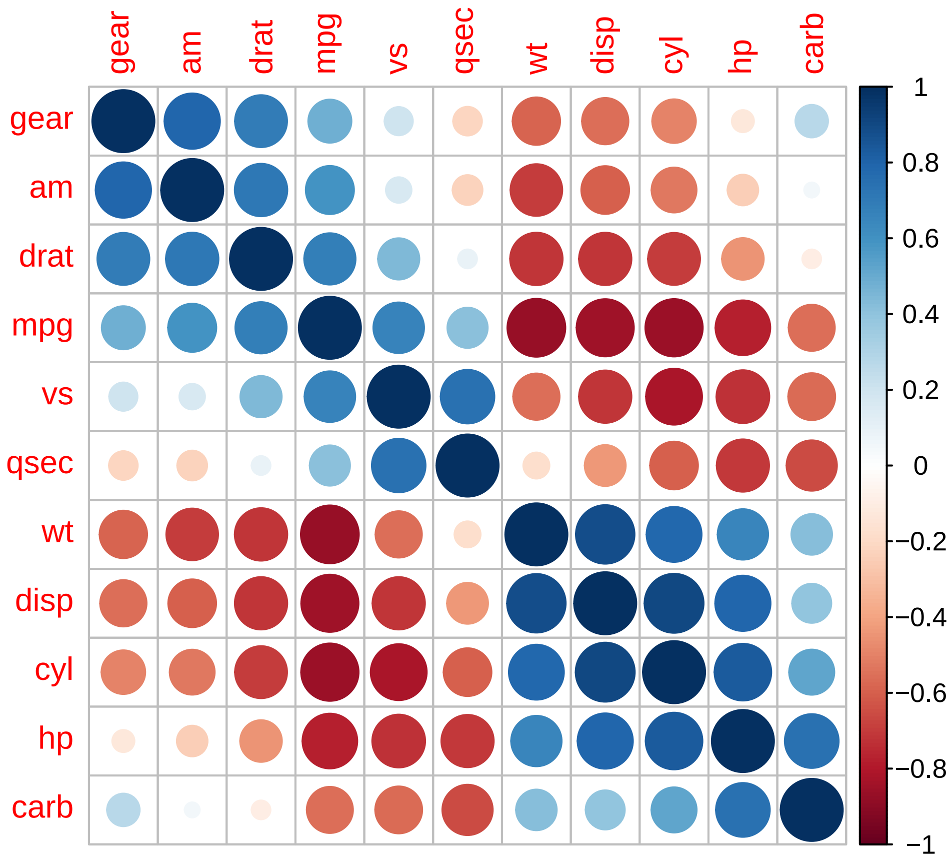

```
corrplot(M, method = 'color', order = 'alphabet')
```



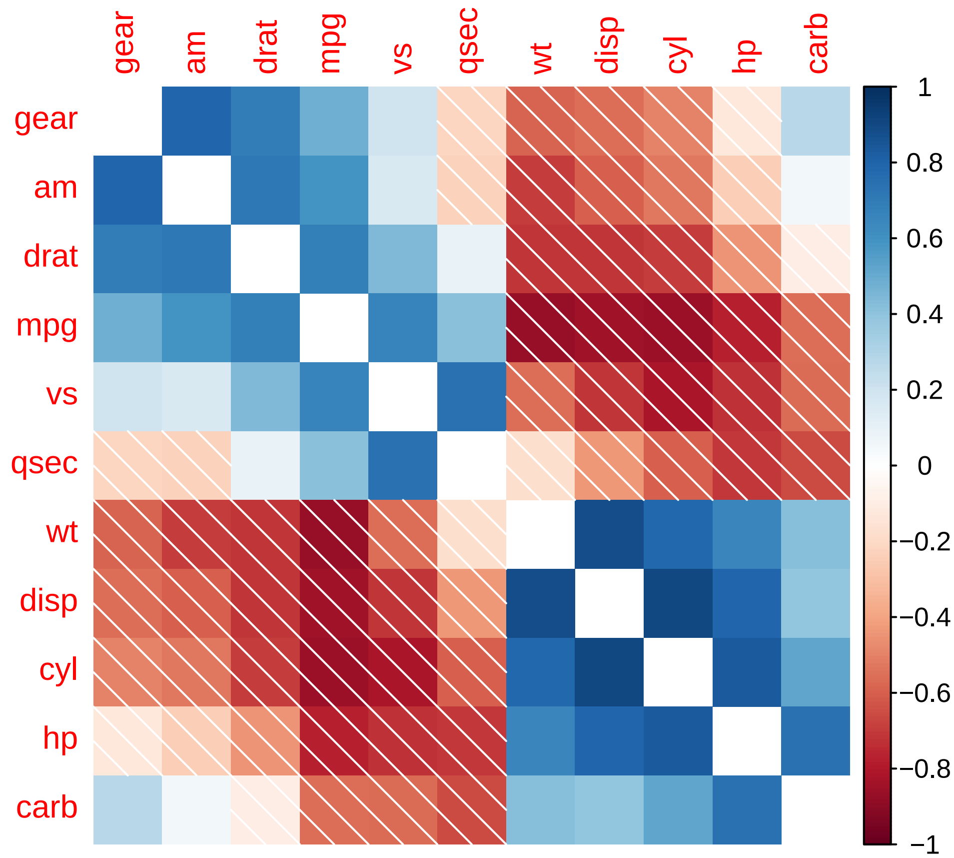

```
corrplot(M) # by default, method = 'circle'
```



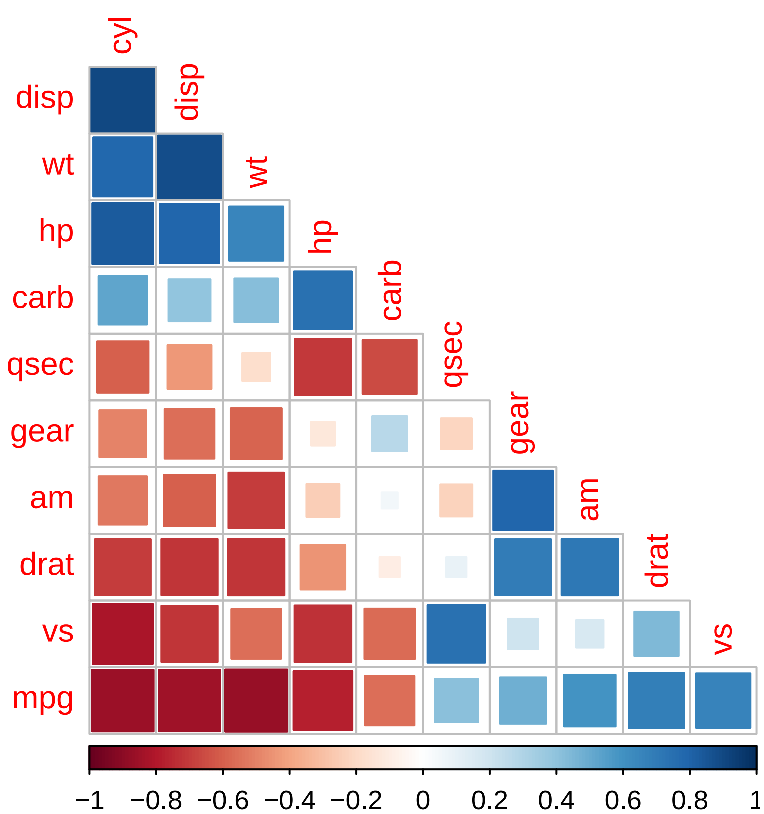

```
corrplot(M, order = 'AOE') # after 'AOE' reorder
```



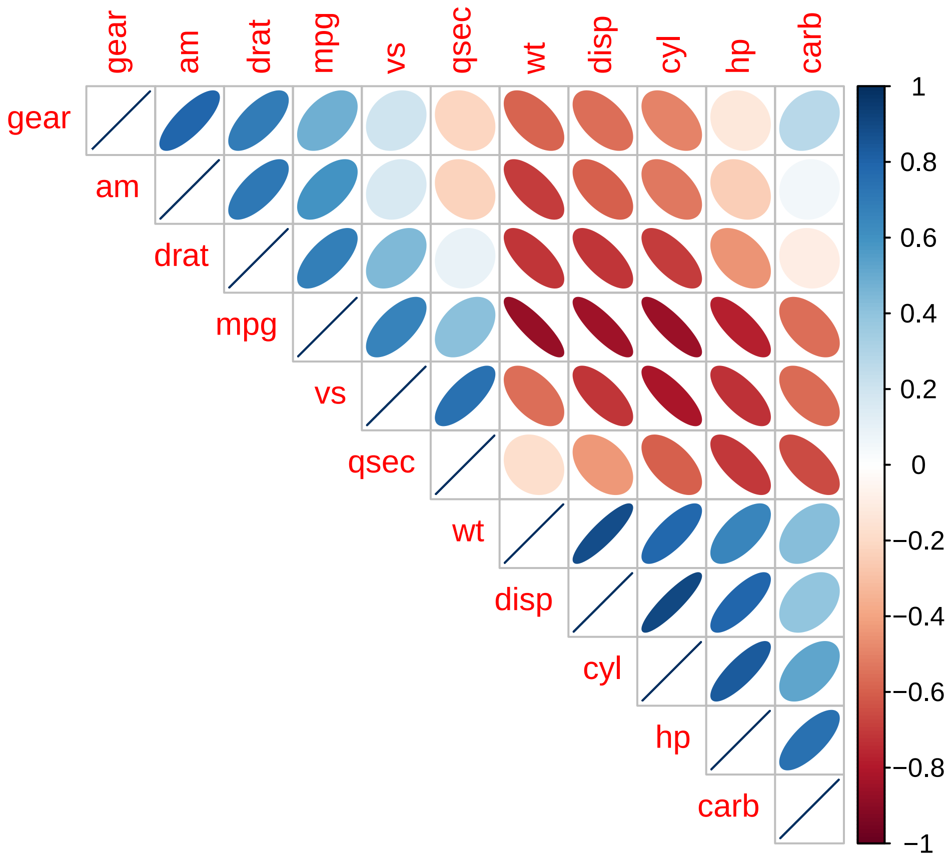

```
corrplot(M, method = 'shade', order = 'AOE', diag = FALSE)
```



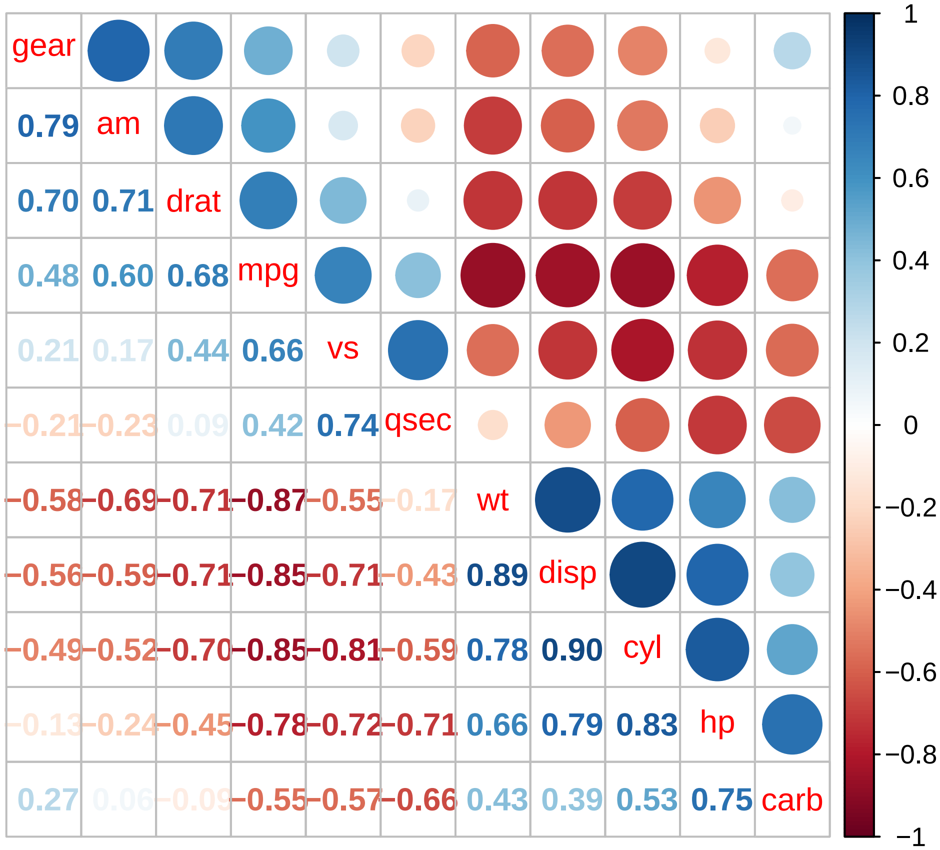

```r
corrplot(M, method = 'square', order = 'FPC', type = 'lower', diag = FALSE)
```



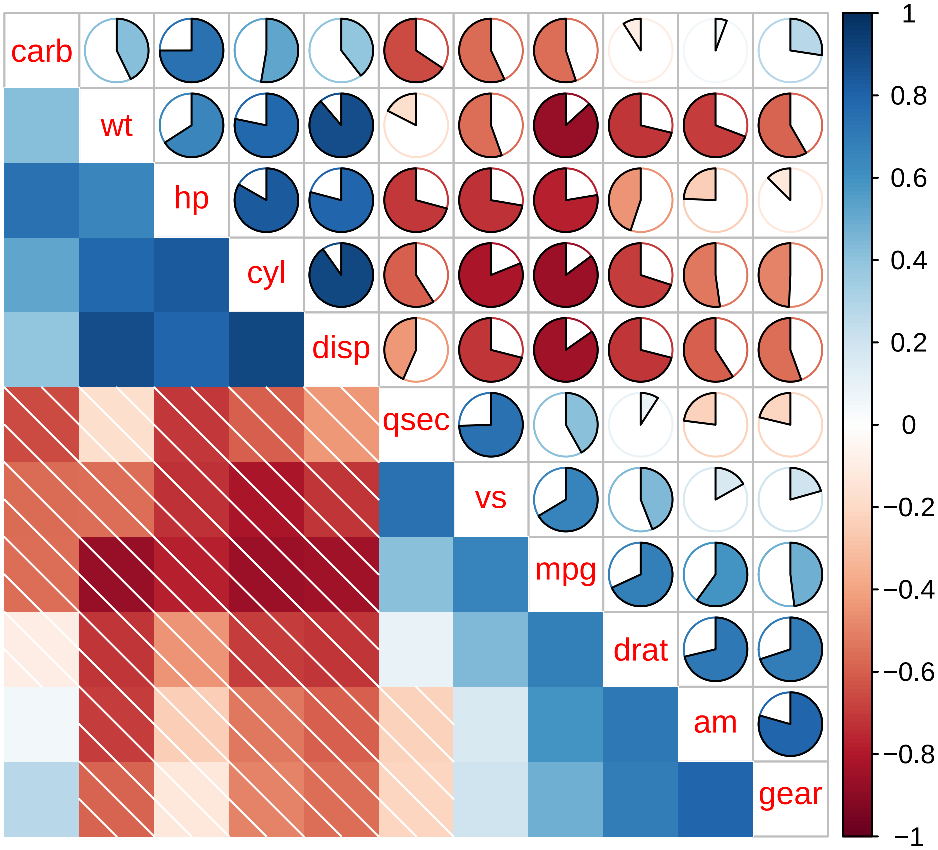
```r
corrplot(M, method = 'ellipse', order = 'AOE', type = 'upper')
```



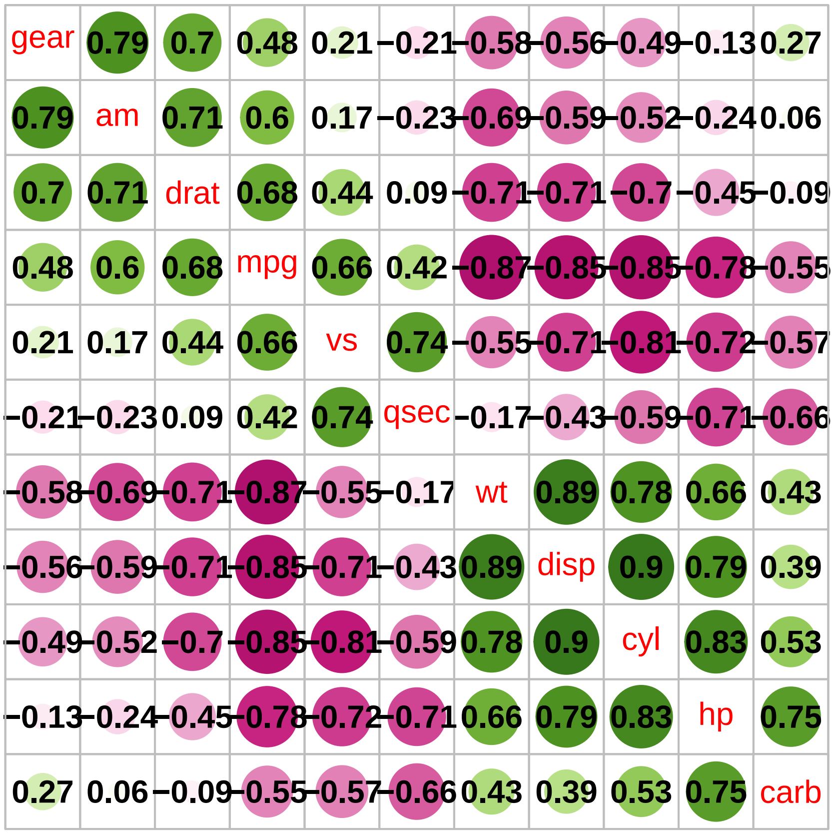

```r
corrplot.mixed(M, order = 'AOE')
```



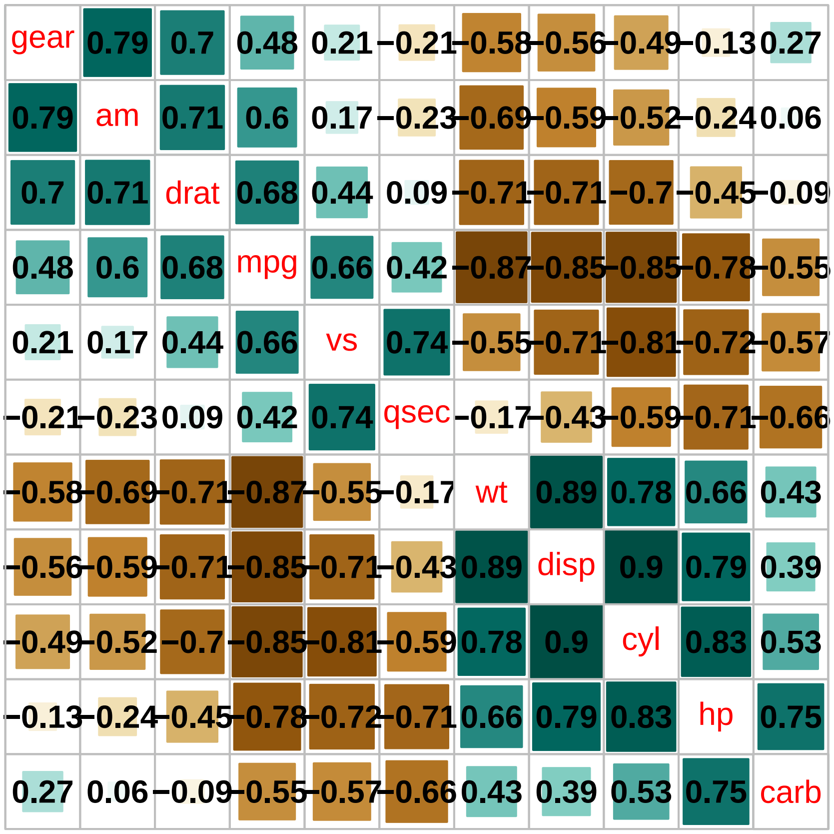

```
corrplot.mixed(M, lower = 'shade', upper = 'pie', order = 'hclust')
```



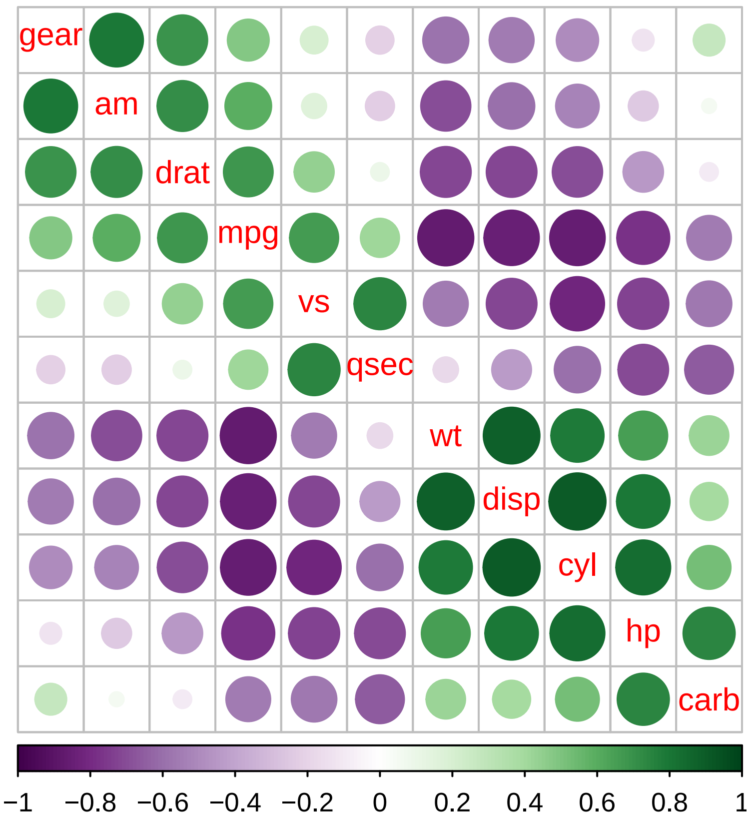

```r
corrplot(M, order = 'AOE', addCoef.col = 'black', tl.pos = 'd',
         cl.pos = 'n', col = COL2('PiYG'))
```



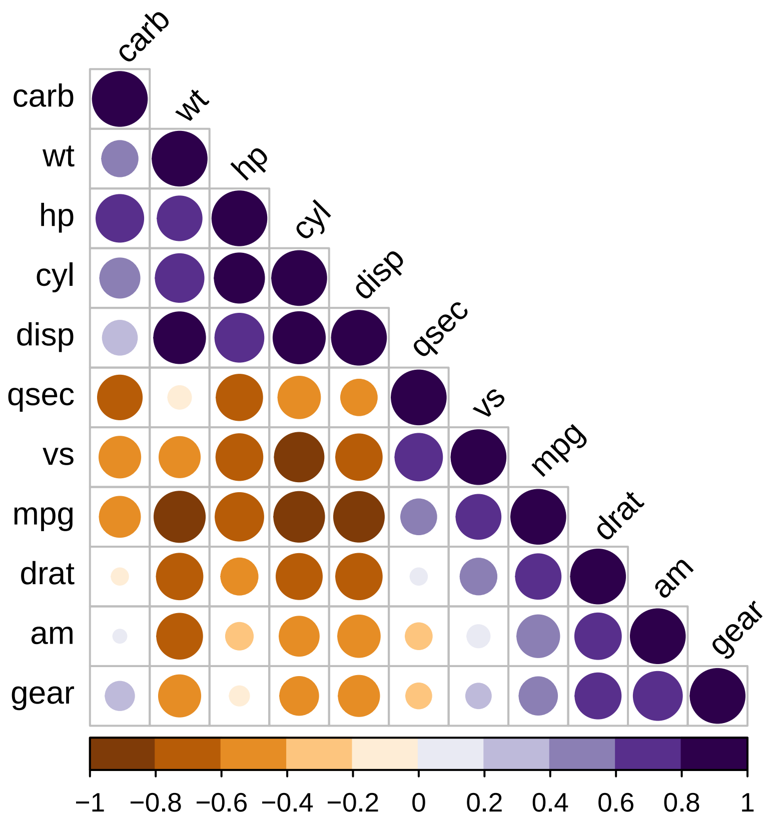

```r
corrplot(M, method = 'square', order = 'AOE', addCoef.col = 'black', tl.pos = 'd',
         cl.pos = 'n', col = COL2('BrBG'))
```




```r
## bottom color legend, diagonal text legend, rotate text label
corrplot(M, order = 'AOE', cl.pos = 'b', tl.pos = 'd',
         col = COL2('PRGn'), diag = FALSE)
```

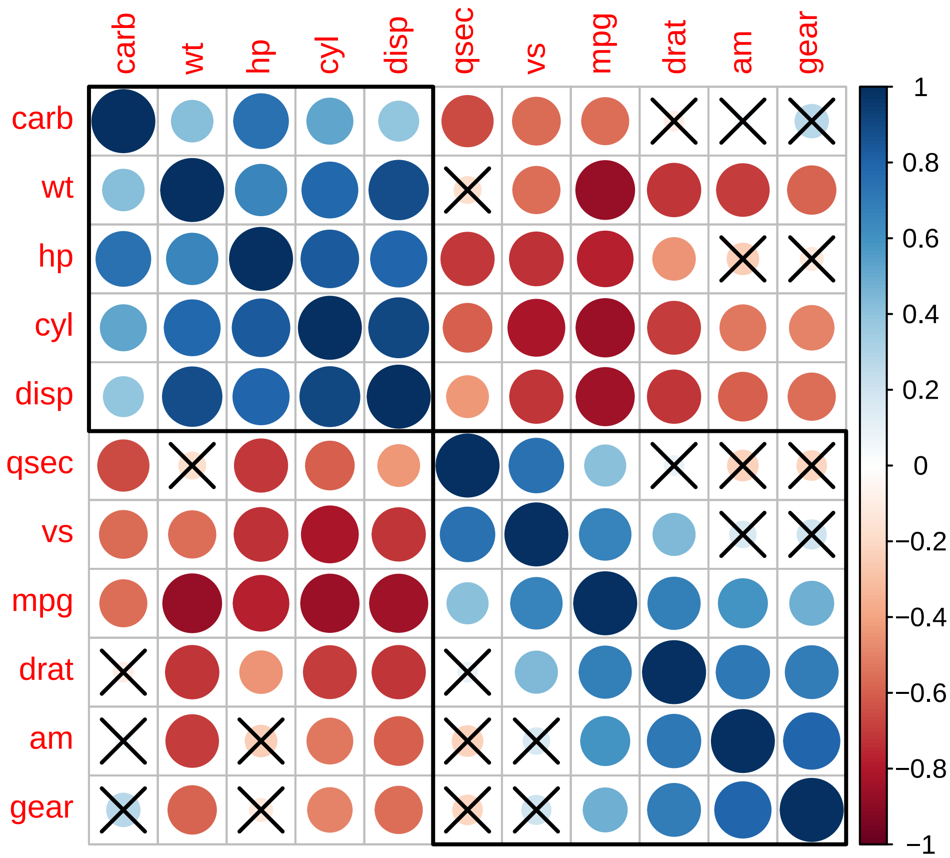



```
## text labels rotated 45 degrees and  wider color legend with numbers right aligned
corrplot(M, type = 'lower', order = 'hclust', tl.col = 'black',
         cl.ratio = 0.2, tl.srt = 45, col = COL2('PuOr', 10))
```

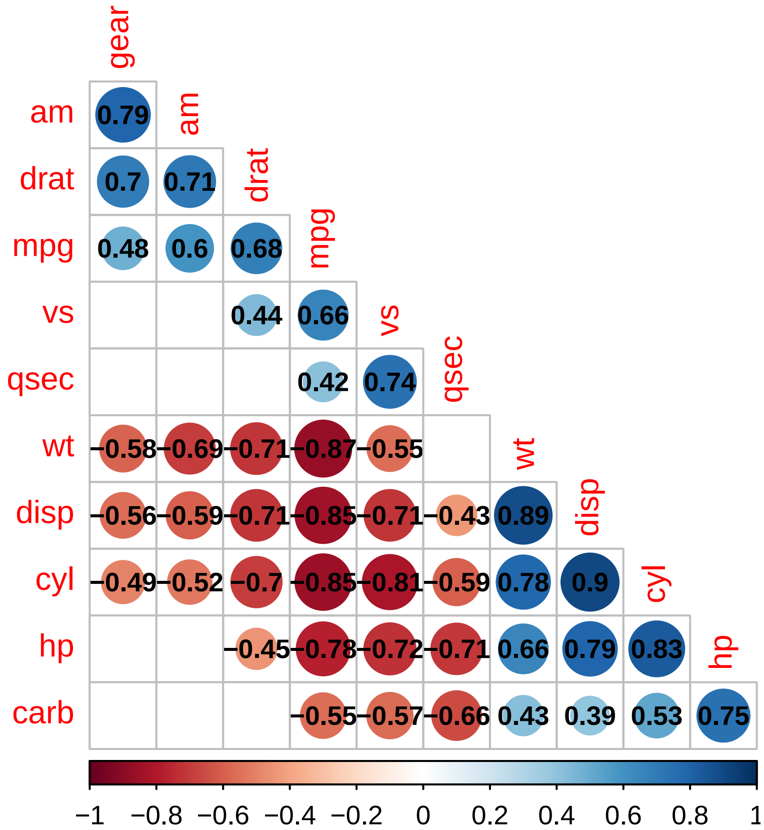


Visualize p-value and confidence interval

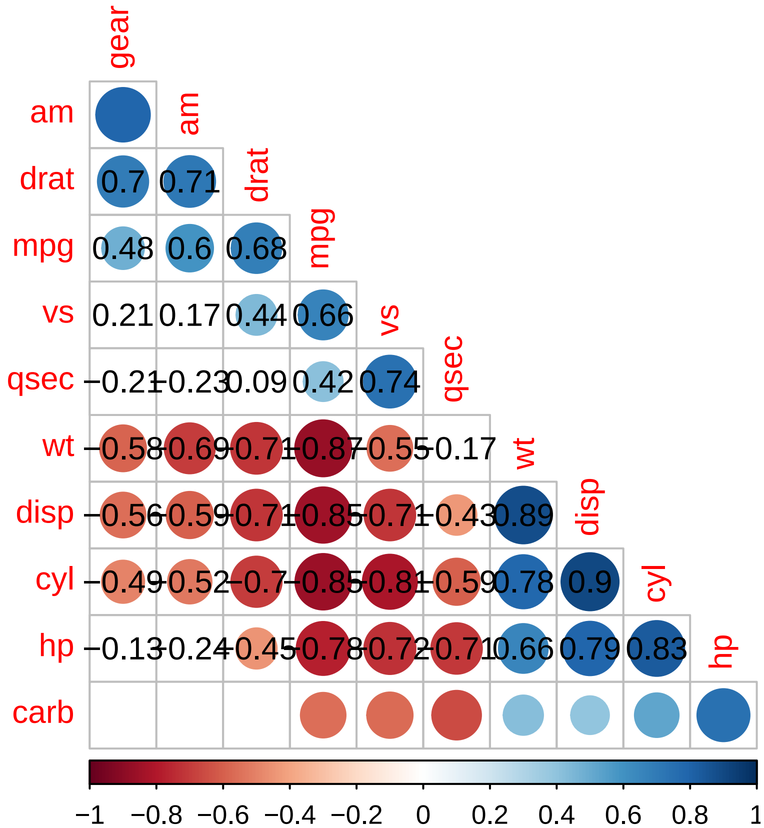
```
testRes = cor.mtest(mtcars, conf.level = 0.95)

## specialized the insignificant value according to the significant level
corrplot(M, p.mat = testRes$p, sig.level = 0.10, order = 'hclust', addrect = 2)
```



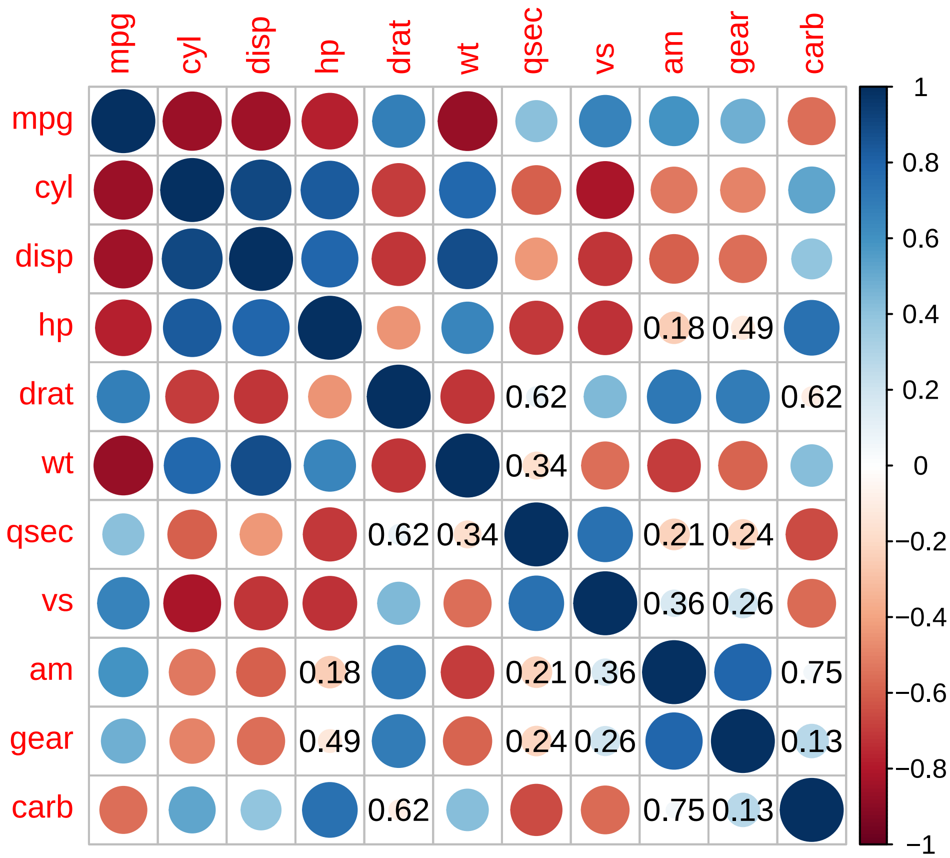

```r
## leave blank on non-significant coefficient
## add significant correlation coefficients
corrplot(M, p.mat = testRes$p, method = 'circle', type = 'lower', insig='blank',
         addCoef.col ='black', number.cex = 0.8, order = 'AOE', diag=FALSE)
```



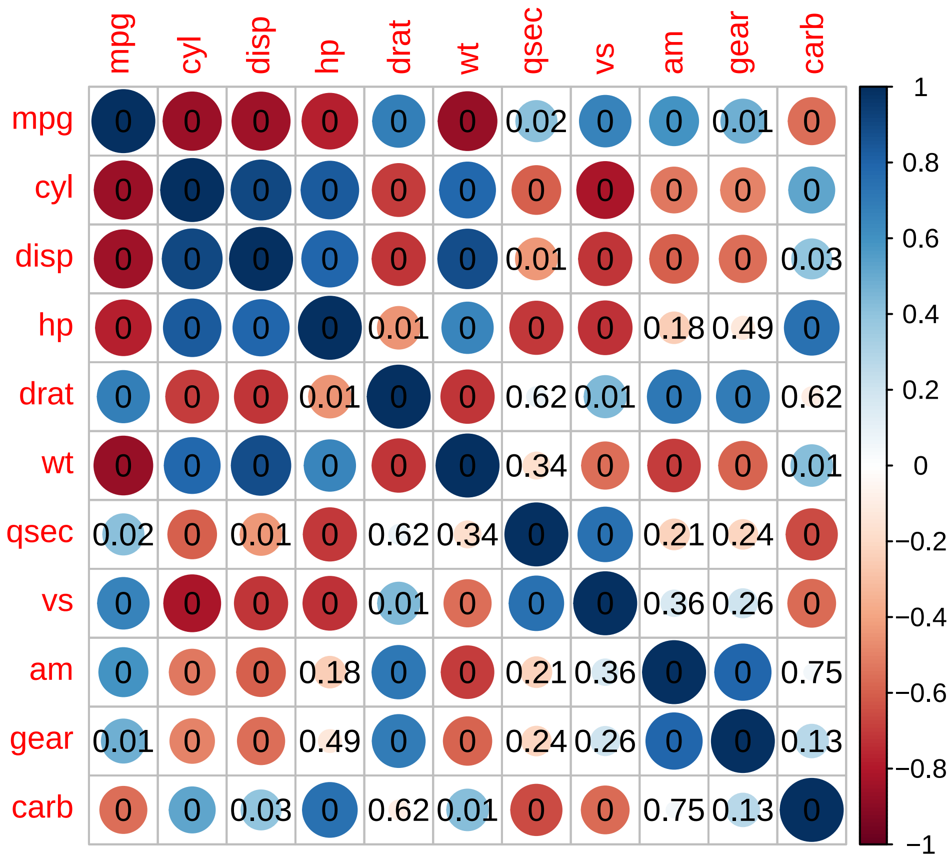
```r
## leave blank on non-significant coefficient
## add all correlation coefficients
corrplot(M, p.mat = testRes$p, method = 'circle', type = 'lower', insig='blank',
         order = 'AOE', diag = FALSE)$corrPos -> p1
text(p1$x, p1$y, round(p1$corr, 2))
```



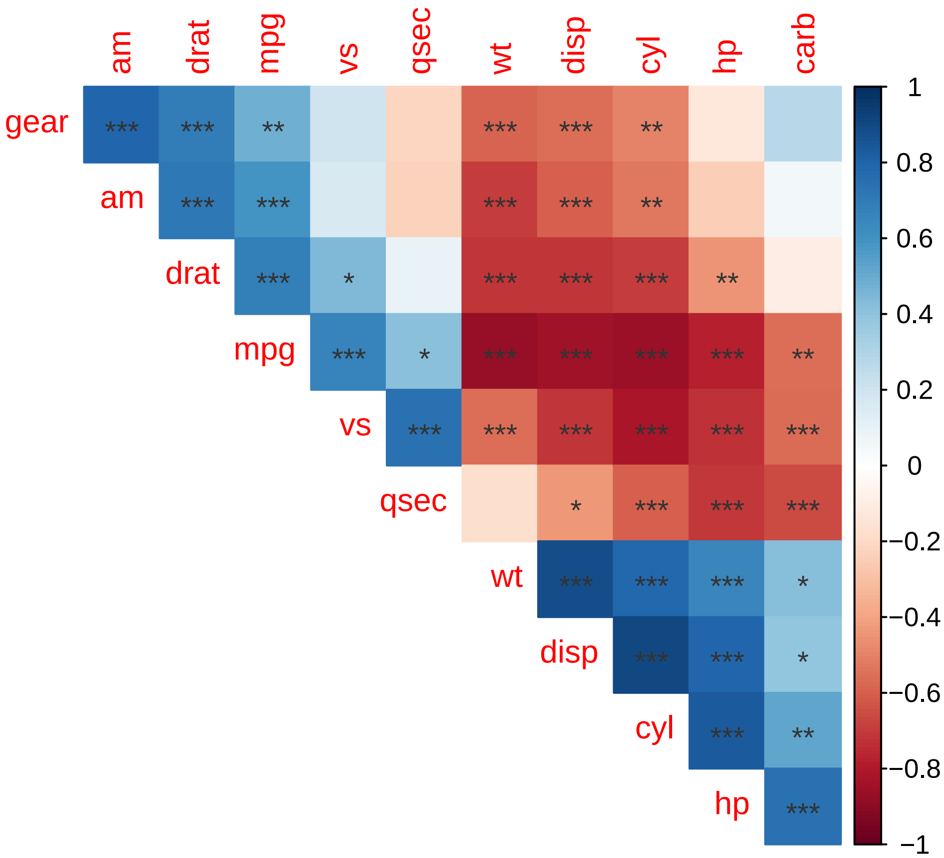

```r
## add p-values on no significant coefficients
corrplot(M, p.mat = testRes$p, insig = 'p-value')
```




```r
## add all p-values
corrplot(M, p.mat = testRes$p, insig = 'p-value', sig.level = -1)
```




```r
## add significant level stars
corrplot(M, p.mat = testRes$p, method = 'color', diag = FALSE, type = 'upper',
         sig.level = c(0.001, 0.01, 0.05), pch.cex = 0.9,
         insig = 'label_sig', pch.col = 'grey20', order = 'AOE')
```



References

- Michael Friendly (2002). Corrgrams: Exploratory displays for correlation matrices. The American Statistician, 56, 316–324.
- D.J. Murdoch, E.D. Chow (1996). A graphical display of large correlation matrices. The American Statistician, 50, 178–180.
- Michael Hahsler, Christian Buchta and Kurt Hornik (2020). seriation: Infrastructure for Ordering Objects Using Seriation. R package version 1.2-9. https://CRAN.R-project.org/package=seriation
- Hahsler M, Hornik K, Buchta C (2008). "Getting things in order: An introduction to the R package seriation." Journal of Statistical Software, 25(3), 1-34. ISSN 1548-7660, doi: 10.18637/jss.v025.i03 (URL: https://doi.org/10.18637/jss.v025.i03), <URL: https://www.jstatsoft.org/v25/i03/>.
- https://cran.r-project.org/web/packages/corrplot/vignettes/corrplot-intro.html