Basic statistics

Note updated August 19, 2019. Not for sale :-)

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- Purpose: To compare MEANS of TWO independent samples/groups.
- Assumptions:
    1. Numerical outcome.

2. Normal data distribution for each group.
3. Equal variance between groups.

- *t*-statistics.

1.1.1.2 Analysis

1. Load `cholest.sav` dataset,

```
library(foreign)
cholest = read.spss("cholest.sav", to.data.frame = TRUE)
str(cholest)
```

```
## 'data.frame':    80 obs. of  5 variables:
##  $ chol    : num  6.5 6.6 6.8 6.8 6.9 7 7 7.2 7.2 7.2 ...
##  $ age     : num  38 35 39 36 31 38 33 36 40 34 ...
##  $ exercise: num  6 5 6 5 4 4 5 5 4 6 ...
##  $ sex     : Factor w/ 2 levels "female","male": 2 2 2 2 2 2 2 2 2 2 ...
##  $ categ   : Factor w/ 3 levels "Grp A","Grp B",..: 1 1 1 1 1 1 1 1 1 1 ...
##  - attr(*, "variable.labels")= Named chr  "cholesterol in mmol/L" "age in year" "duration of exercis
##   ..- attr(*, "names")= chr  "chol" "age" "exercise" "sex" ...
##  - attr(*, "codepage")= int 65001
```

```
head(cholest)
```

```
##   chol age exercise  sex categ
## 1  6.5  38        6 male Grp A
## 2  6.6  35        5 male Grp A
## 3  6.8  39        6 male Grp A
## 4  6.8  36        5 male Grp A
## 5  6.9  31        4 male Grp A
## 6  7.0  38        4 male Grp A
```

Explore the data. Obtain the basic descriptive statistics.

Mean and SD,

```
by(cholest$chol, cholest$sex, mean)
```

```
## cholest$sex: female
## [1] 8.9275
## ------------------------------------------------------------------------
## cholest$sex: male
## [1] 7.5325
```

```
by(cholest$chol, cholest$sex, sd)
```

```
## cholest$sex: female
## [1] 0.4551627
## ------------------------------------------------------------------------
## cholest$sex: male
## [1] 0.4687066
```

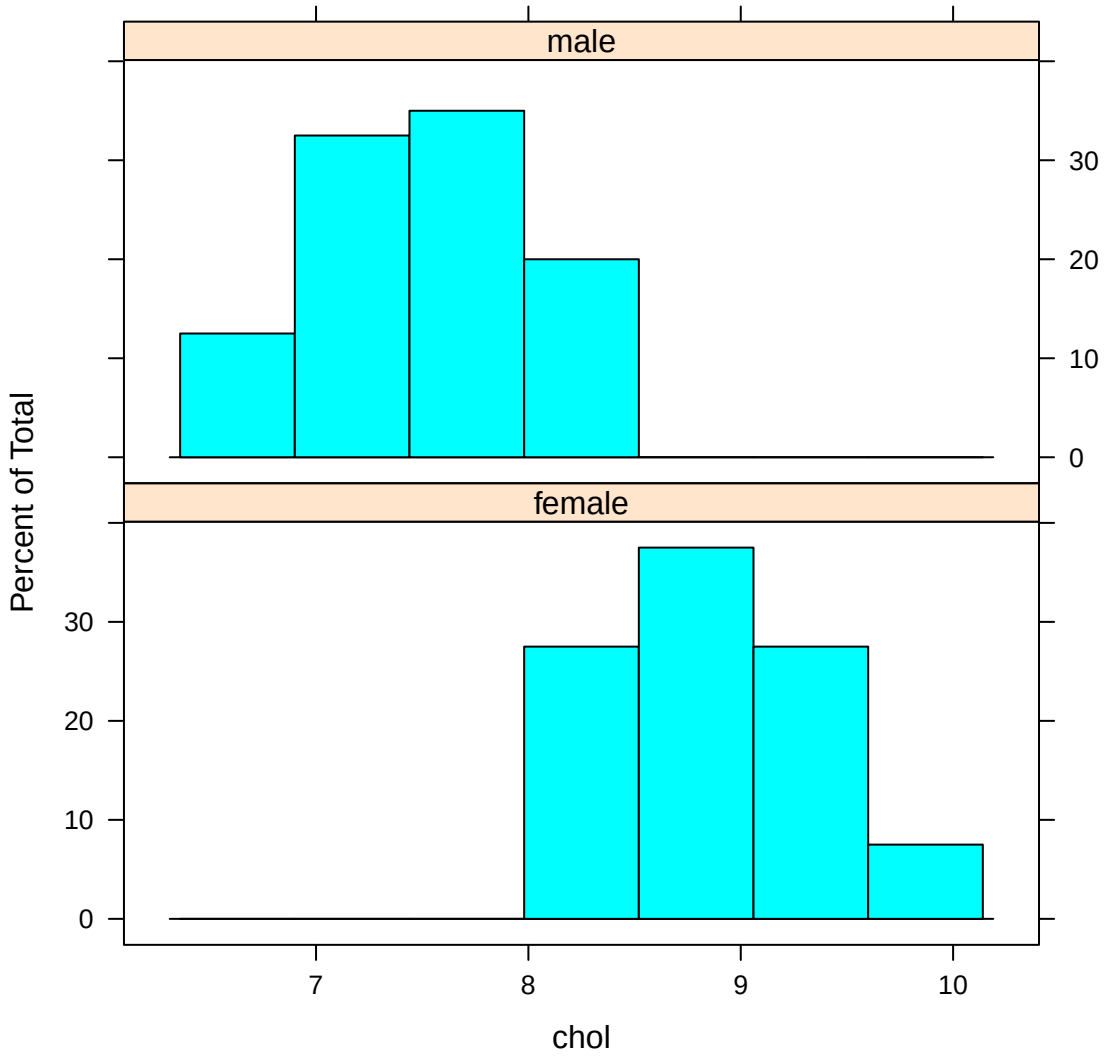
and the number of subjects per group,

```
table(cholest$sex)
```

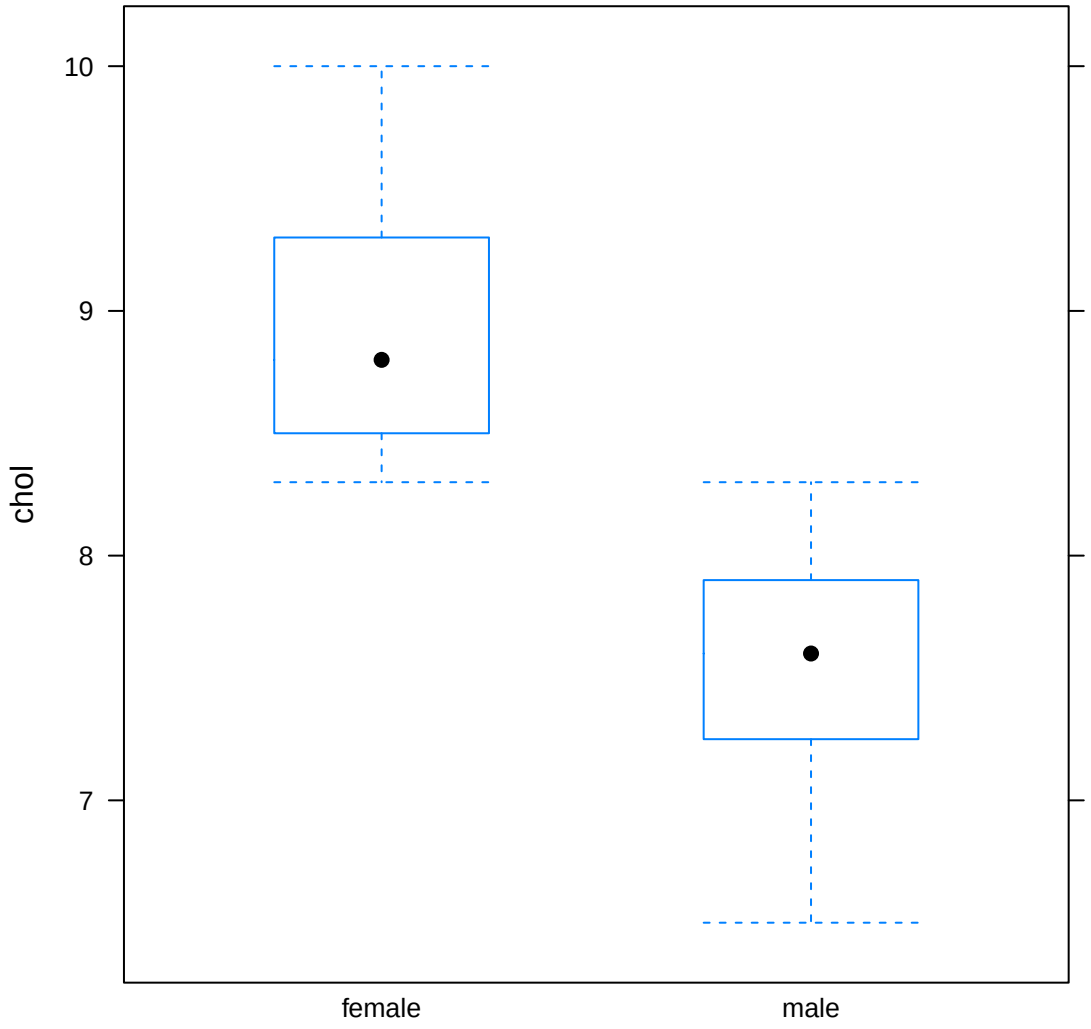
```
##
## female   male
##     40     40
```

2. Check the **normality assumption** of the data by group,

```
library(lattice)
histogram(~ chol | sex, data = cholest, layout = c(1, 2))
```




```
bwplot(chol ~ sex, data = cholest)
```



3. Check the **equality of variance assumption**,

```
var.test(chol ~ sex, data = cholest)  # equal*
```

```
##
##  F test to compare two variances
##
## data:  chol by sex
## F = 0.94304, num df = 39, denom df = 39, p-value = 0.8556
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  0.4987744 1.7830278
## sample estimates:
## ratio of variances
##          0.9430422
```

*Choose:

- Equal variance = Standard Two Sample t-test.

- Unequal variance = Welch Two Sample t-test.

4. Perform independent t-test,

```
t.test(chol ~ sex, data = cholest)  # significant difference
```

```
##
##  Welch Two Sample t-test
##
## data:  chol by sex
## t = 13.504, df = 77.933, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  1.189337 1.600663
## sample estimates:
## mean in group female   mean in group male
##               8.9275               7.5325
```

The function default is **Welch Two Sample *t*-test** (takes car the unequal variance).

You can also obtain the standard t-test (equal variance assumed),

```
t.test(chol ~ sex, data = cholest, var.equal = TRUE)
```

```
##
##  Two Sample t-test
##
## data:  chol by sex
## t = 13.504, df = 78, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  1.18934 1.60066
## sample estimates:
## mean in group female   mean in group male
##               8.9275               7.5325
```

1.1.2 Mann-Whitney U test (Wilcoxon rank-sum test)

1.1.2.1 About the test

- Non-parametric test.
- Purpose: To compare RANKS of TWO independent samples/groups.
- Assumption: Numerical/ordinal outcome.
- Data per group are not normally distributed.
- Involves ranking all observations (regardless of groups) and obtaining the sums per group.
- W-statistics.

1.1.2.2 Analysis

1. Obtain descriptive statistics for non-normal data, median and IQR,

```
by(cholest$chol, cholest$sex, median)
```

```
## cholest$sex: female
## [1] 8.8
## ------------------------------------------------------------
## cholest$sex: male
```

```
## [1] 7.6
```

```
by(cholest$chol, cholest$sex, IQR)
```

```
## cholest$sex: female
## [1] 0.8
## ------------------------------------------------------------
## cholest$sex: male
## [1] 0.625
```

2. Perform Mann-Whitney U test,

```
wilcox.test(chol ~ sex, data = cholest, exact = FALSE)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  chol by sex
## W = 1598, p-value = 1.568e-14
## alternative hypothesis: true location shift is not equal to 0
```

1.2 Two dependent samples

1.2.1 Paired *t*-test

1.2.1.1 About the test

- Parametric test.
- Purpose: To compare MEAN DIFFERENCE between TWO related samples, i.e. equal to ZERO if there is no difference.
- Assumptions:
  1. Numerical outcome.
  2. Normal distribution of the DIFFERENCES between TWO paired observations (e.g. $SBP\ after\ treatment - SBP\ before\ treatment$).
- *t*-statistics.

1.2.1.2 Analysis

1. Load `sbp.csv` dataset,

```
sbp = read.csv("sbp.csv")
str(sbp)
```

```
## 'data.frame':    11 obs. of  2 variables:
##  $ S1: int  110 120 120 130 100 120 135 100 140 130 ...
##  $ S2: int  100 120 130 130 100 130 140 100 140 130 ...
```

```
sbp
```

```
##     S1  S2
## 1  110 100
## 2  120 120
## 3  120 130
## 4  130 130
## 5  100 100
```

```
## 6  120 130
## 7  135 140
## 8  100 100
## 9  140 140
## 10 130 130
## 11 130 130
```

Explore the data. Obtain the basic descriptive statistics.

Mean and SD,

```
mean(sbp$S1); sd(sbp$S1)
```

```
## [1] 121.3636
```

```
## [1] 13.43334
```

```
mean(sbp$S2); sd(sbp$S2)
```

```
## [1] 122.7273
```

```
## [1] 15.5505
```

```
mean(sbp$S2 - sbp$S1); sd(sbp$S2 - sbp$S1)
```

```
## [1] 1.363636
```

```
## [1] 5.518564
```

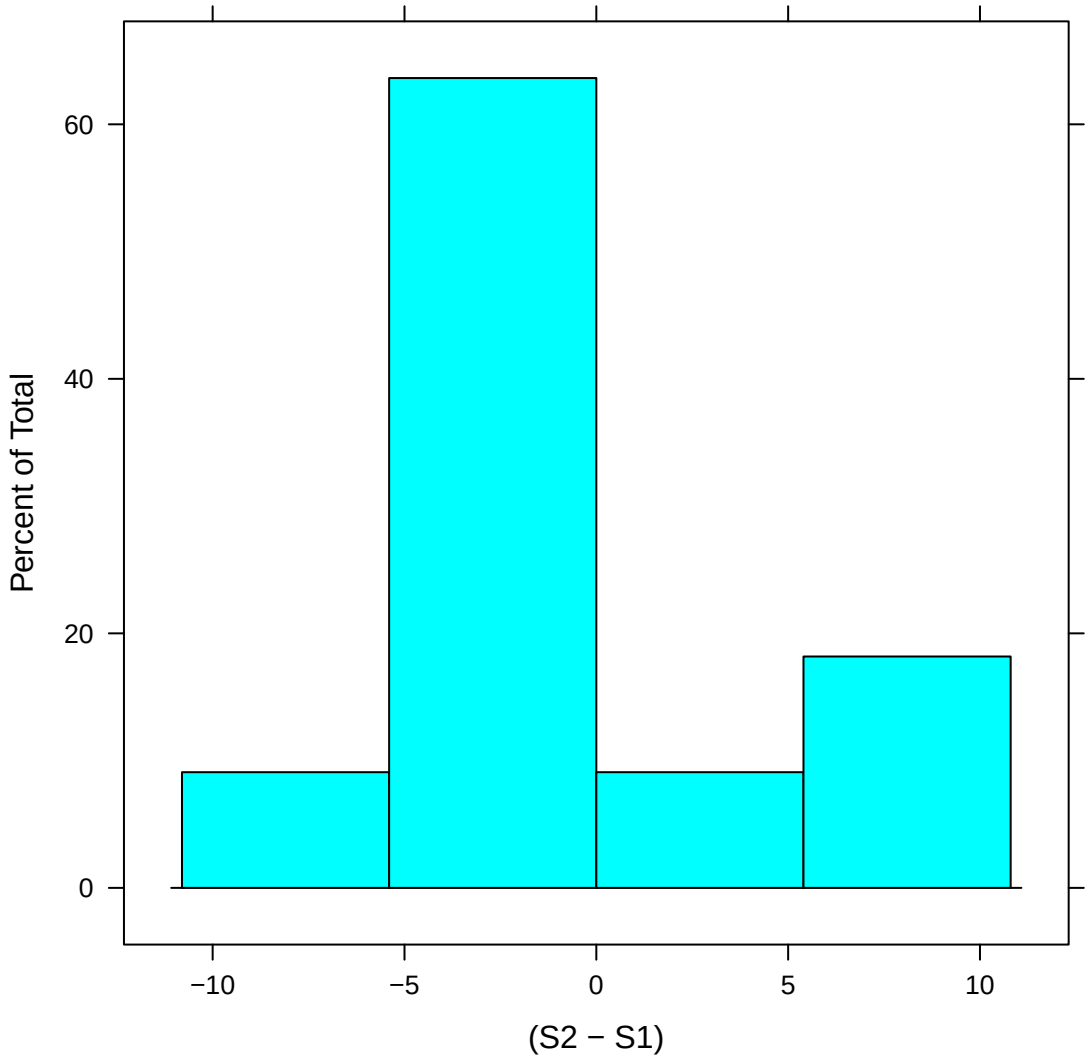
and the number of subjects,

```
lengths(sbp)
```

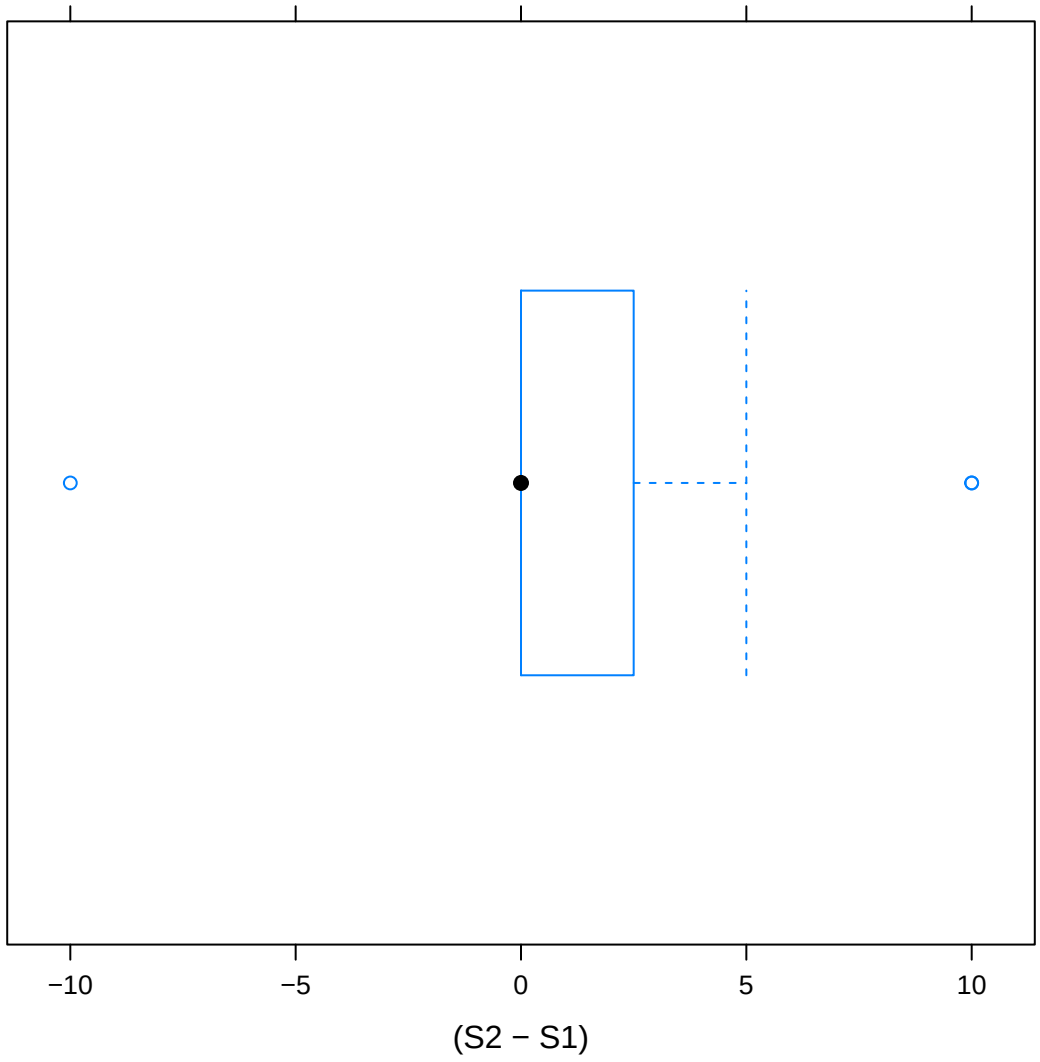
```
## S1 S2
## 11 11
```

2. Check the **normality assumption** of the differences ($S2 - S1$),

```
histogram(~ (S2 - S1), data = sbp)  # not perfectly normal
```




```
bwplot(~ (S2 - S1), data = sbp)
```



3. Perform paired t-test,

```
t.test(sbp$S1, sbp$S2, paired = TRUE)  # no significant difference
```

```
##
##  Paired t-test
##
## data:  sbp$S1 and sbp$S2
## t = -0.81954, df = 10, p-value = 0.4316
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -5.071058  2.343785
## sample estimates:
## mean of the differences
##               -1.363636
```

1.2.2 Wilcoxon signed-rank test

1.2.2.1 About the test

- Non-parametric test.
- Purpose: To compare SIGNED RANKS of the DIFFERENCES between TWO related samples, i.e. equal to ZERO if there is no difference.
- Assumption: Numerical/ordinal outcome.
- The differences are not normally distributed.
- Involves signing (+/-) and ranking the differences (hence *signed-rank* test).
- V-statistics.

1.2.2.2 Analysis

1. Obtain descriptive statistics for non-normal data: median and IQR,

```
median(sbp$S1); IQR(sbp$S1)
```

```
## [1] 120
```

```
## [1] 15
```

```
median(sbp$S2); IQR(sbp$S2)
```

```
## [1] 130
```

```
## [1] 20
```

2. Perform Wilcoxon signed-rank test,

```
wilcox.test(sbp$S2, sbp$S1, paired = TRUE, exact = FALSE)
```

```
##
##  Wilcoxon signed rank test with continuity correction
##
## data:  sbp$S2 and sbp$S1
## V = 7, p-value = 0.5708
## alternative hypothesis: true location shift is not equal to 0
```

1.3 More than two independent samples

1.3.1 One-way ANOVA

1.3.1.1 About the test

- Parametric test.
- **AN**alysis **O**f **VA**riance.
- Purpose: Compare MEANS of THREE/MORE independent samples/groups.
- Assumptions:
    1. Numerical outcome.
    2. Normal data distribution for each group.
    3. Equal variance between groups.
- F-statistics.

1.3.1.2 Analysis

1. Explore the data. Obtain basic descriptive statistics,

```
by(cholest$chol, cholest$categ, mean)
```

```
## cholest$categ: Grp A
## [1] 7.248
## ------------------------------------------------------------
## cholest$categ: Grp B
## [1] 8.293939
## ------------------------------------------------------------
## cholest$categ: Grp C
## [1] 9.25
```

```
by(cholest$chol, cholest$categ, sd)
```

```
## cholest$categ: Grp A
## [1] 0.3355592
## ------------------------------------------------------------
## cholest$categ: Grp B
## [1] 0.3091717
## ------------------------------------------------------------
## cholest$categ: Grp C
## [1] 0.3569047
```

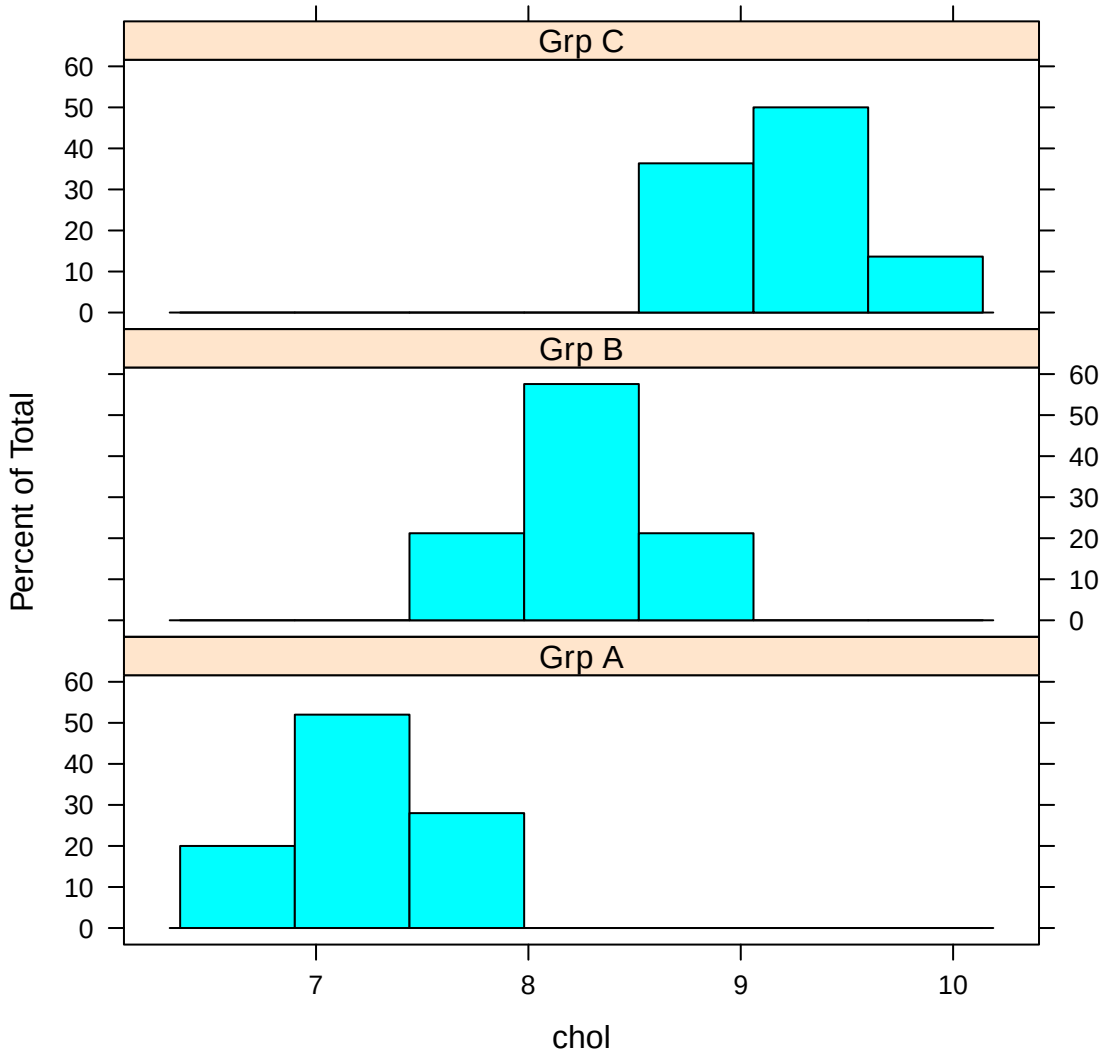
and the number of subjects per group,

```
table(cholest$categ)
```

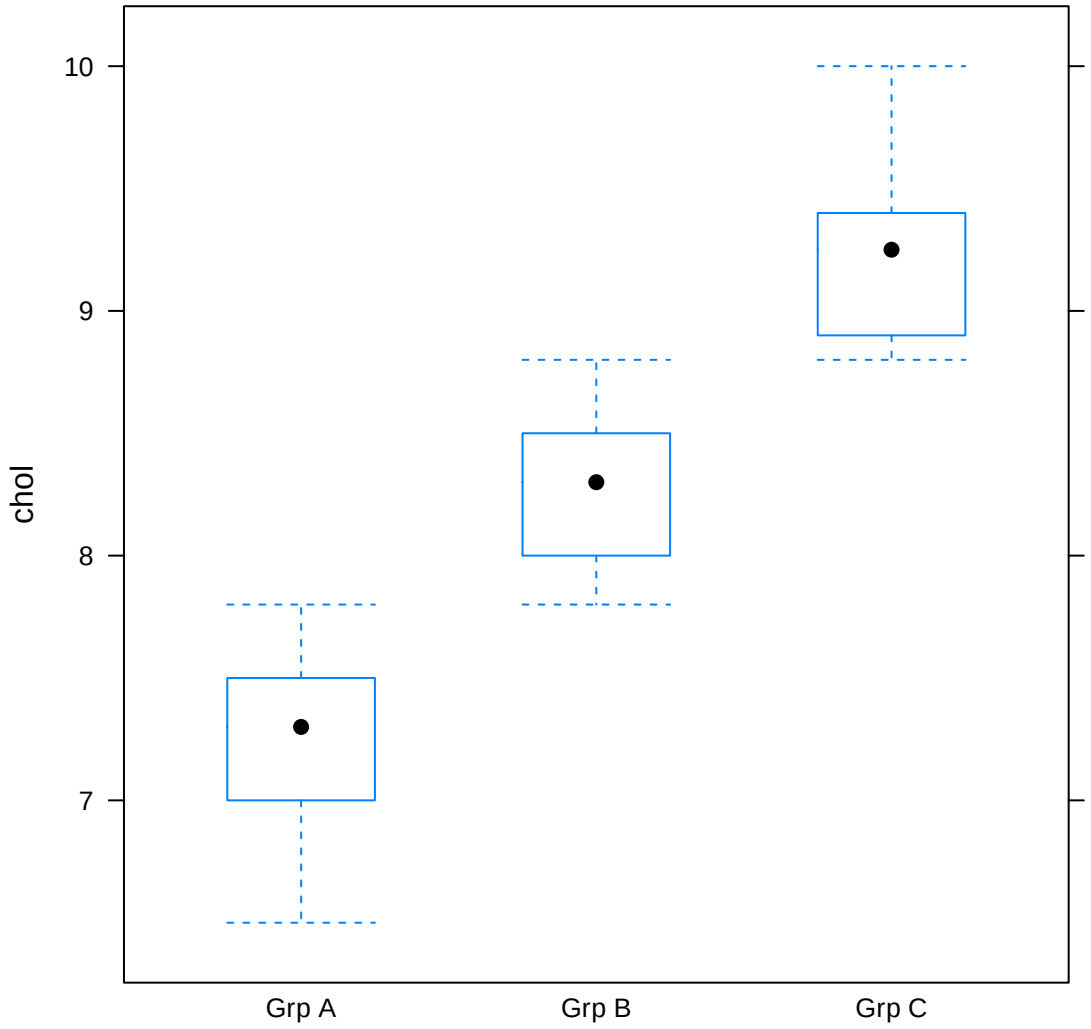
```
##
## Grp A Grp B Grp C
##    25    33    22
```

2. Check the **normality assumption** of the data per group,

```
histogram(~ chol | categ, data = cholest, layout = c(1, 3))
```




```
bwplot(chol ~ categ, data = cholest)
```



However, we will mainly rely on **residuals** for the normality assessment.

3. Check the **equality of variance assumption**,

```
bartlett.test(chol ~ categ, data = cholest)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  chol by categ
## Bartlett's K-squared = 0.53515, df = 2, p-value = 0.7652
```

4. Perform one-way ANOVA test,

```
aov_chol = aov(chol ~ categ, data = cholest)
summary(aov_chol)  # significant difference between three groups
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## categ        2  47.13   23.57   215.1 <2e-16 ***
## Residuals   77   8.44    0.11
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Notice here we save the output of `aov()` into `aov_chol` first. This allows further extraction of full output from `aov_chol` ANOVA object.

Alternatively, for unequal variance, we can use Welch's version of ANOVA

```
oneway.test(chol ~ categ, data = cholest)
```

```
##
##  One-way analysis of means (not assuming equal variances)
##
## data:  chol and categ
## F = 194.55, num df = 2.000, denom df = 46.546, p-value < 2.2e-16
```

5. Post-hoc test, to look for significant group pairs,

```
pairwise.t.test(cholest$chol, cholest$categ, p.adj = "bonferroni")
```

```
##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  cholest$chol and cholest$categ
##
##       Grp A  Grp B
## Grp B <2e-16 -
## Grp C <2e-16 5e-16
##
## P value adjustment method: bonferroni
```

```
# all pairs significant difference
```

Here, it works as if we do multiple independent t-tests. We adjust for multiple comparison by Bonferroni correction.

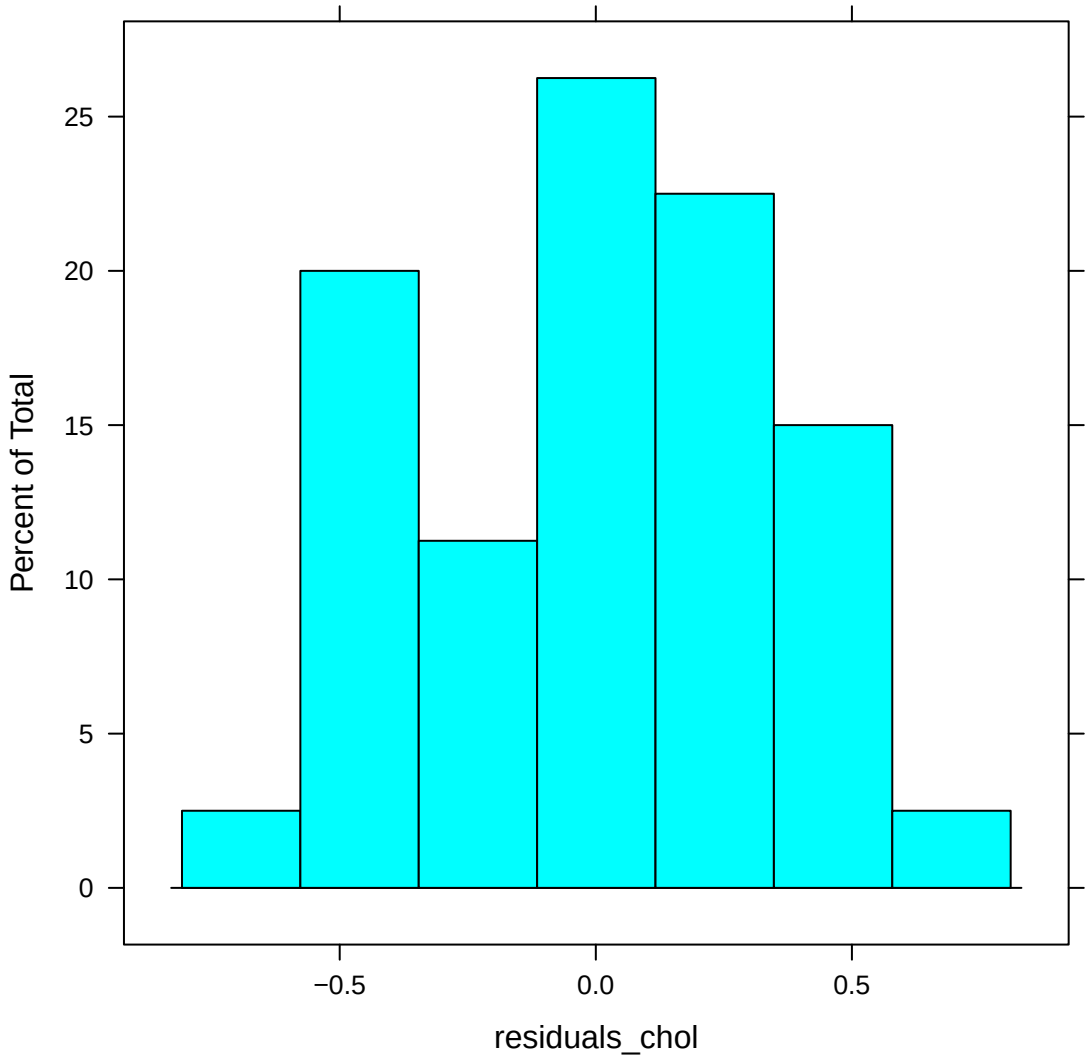
6. Check the **normality of the residuals**,

Save the residuals as `residual_chol`. We also need to use `as.numeric()` to extract proper numerical data from `aov_chol` ANOVA object, and save it again to `residuals_chol`

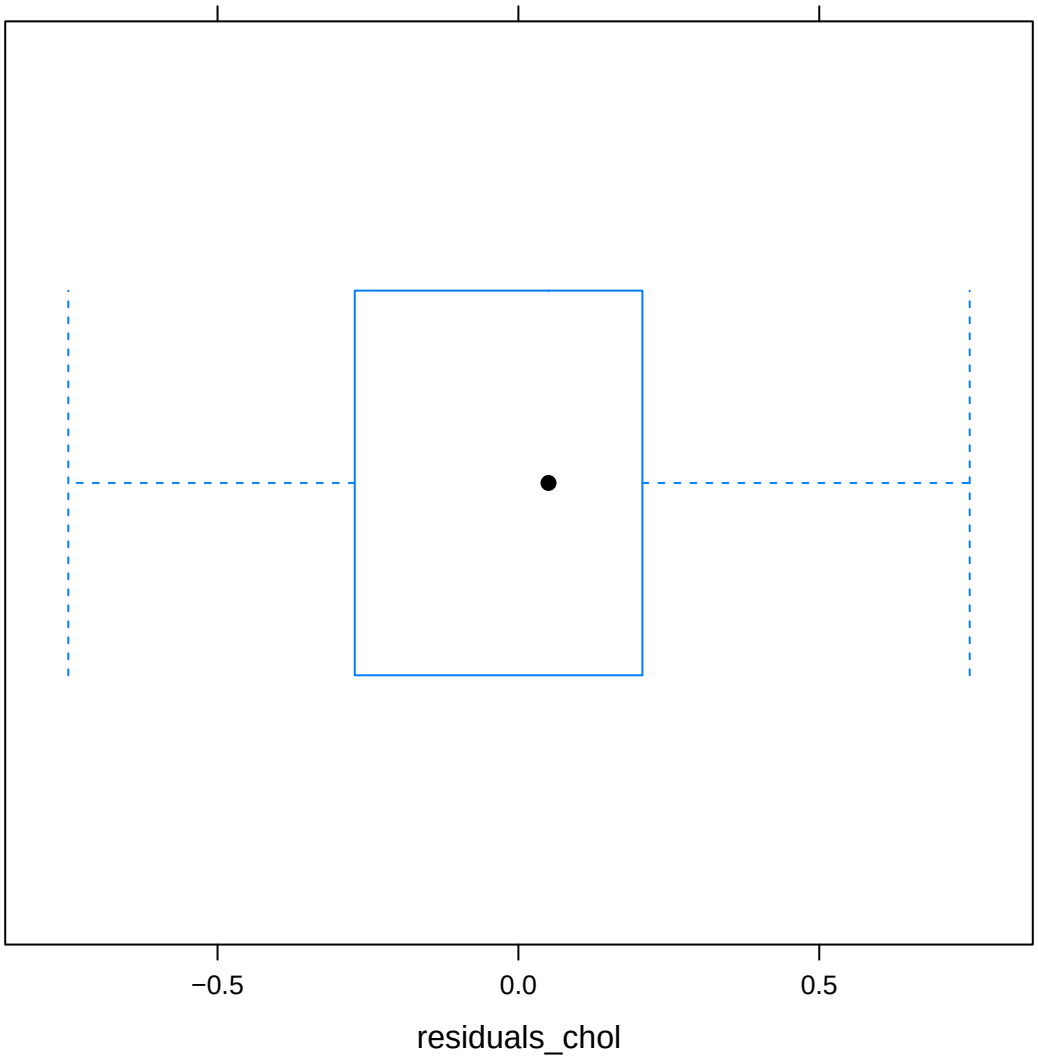
```
residuals_chol = residuals(aov_chol)
residuals_chol = as.numeric(residuals_chol)
```

Then, check the normality,

```
histogram(~ residuals_chol)  # normal
```




```
bwplot(~ residuals_chol)
```



1.3.2 Kruskal-Wallis test

1.3.2.1 About the test

- Non-parametric alternative of ANOVA, ANOVA on ranks.
- Purpose: To compare RANKS of THREE/MORE independent samples/groups.
- Assumption: Numerical/ordinal outcome.
- Involves ranking all observations (regardless of groups) and obtaining the average of ranks per group.
- H-statistics.

1.3.2.2 Analysis

1. Obtain descriptive statistics for non-normal data, median and IQR,

```
by(cholest$chol, cholest$categ, median)
```

```
## cholest$categ: Grp A
```

```
## [1] 7.3
## ------------------------------------------------------------------------
## cholest$categ: Grp B
## [1] 8.3
## ------------------------------------------------------------------------
## cholest$categ: Grp C
## [1] 9.25
```

```
by(cholest$chol, cholest$categ, IQR)
```

```
## cholest$categ: Grp A
## [1] 0.5
## ------------------------------------------------------------------------
## cholest$categ: Grp B
## [1] 0.5
## ------------------------------------------------------------------------
## cholest$categ: Grp C
## [1] 0.475
```

2. Perform Kruskal-Wallis test,

```
kruskal.test(chol ~ categ, data = cholest)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  chol by categ
## Kruskal-Wallis chi-squared = 69.188, df = 2, p-value = 9.464e-16
```

3. Post-hoc test, to look for significant group pairs,

```
pairwise.wilcox.test(cholest$chol, cholest$categ, p.adj = "bonferroni")
```

```
## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute exact p-value
## with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute exact p-value
## with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute exact p-value
## with ties
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test
##
## data:  cholest$chol and cholest$categ
##
##       Grp A   Grp B
## Grp B 3.3e-10 -
## Grp C 1.4e-08 1.5e-09
##
## P value adjustment method: bonferroni
```

Here, it works as if we do multiple Mann-Whitney U tests (remember the test is also known as Wilcoxon rank-sum test). We adjust for multiple comparison by Bonferroni correction.

2 Comparison of Categorical Data

2.1 Two independent samples

2.1.1 Chi-squared test for association

2.1.1.1 About the test

- Non-parametric test.
- Purpose: To determine the association between TWO categorical variables.
- Cross-tabulation between the variables, usually 2 x 2, but can be any levels.
- The association between the variables are made by comparing the **observed** cell counts with the **expected** cell counts if the variables are not associated to each other.
- Assumption: $< \frac{25}{20}\%$ **expected** cell counts < 5.
- χ^2 statistics.

2.1.1.2 Analysis

1. The data.

```
           cancer
smoking      lung cancer no lung cancer
  smoking             20             12
  no smoking          55            113
```

Now, load `lung.csv`,

```
lung = read.csv("lung.csv")
str(lung)
```

```
## 'data.frame':    200 obs. of  2 variables:
##  $ Smoking: Factor w/ 2 levels "no smoking","smoking": 2 2 2 2 2 2 2 2 2 2 ...
##  $ Cancer : Factor w/ 2 levels "cancer","no cancer": 1 1 1 1 1 1 1 1 1 1 ...
```

```
head(lung)
```

```
##   Smoking Cancer
## 1 smoking cancer
## 2 smoking cancer
## 3 smoking cancer
## 4 smoking cancer
## 5 smoking cancer
## 6 smoking cancer
```

Now, we create cross-tabulation of the categorical variables,

```
tab_lung = table(Smoking = lung$Smoking, Cancer = lung$Cancer)
str(tab_lung)
```

```
##  'table' int [1:2, 1:2] 55 20 113 12
##  - attr(*, "dimnames")=List of 2
##   ..$ Smoking: chr [1:2] "no smoking" "smoking"
##   ..$ Cancer : chr [1:2] "cancer" "no cancer"
```

and view the table,

```
tab_lung
```

```
##             Cancer
## Smoking      cancer no cancer
##   no smoking     55       113
##   smoking        20        12
```

```
addmargins(tab_lung)
```

```
##             Cancer
## Smoking      cancer no cancer Sum
##   no smoking     55       113 168
##   smoking        20        12  32
##   Sum            75       125 200
```

2. Perform chi-squared test for association. Two ways to do,

by using the table,

```
chisq.test(tab_lung)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  tab_lung
## X-squared = 8.9286, df = 1, p-value = 0.002807
```

or by using the variables directly,

```
chisq.test(lung$Smoking, lung$Cancer)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  lung$Smoking and lung$Cancer
## X-squared = 8.9286, df = 1, p-value = 0.002807
```

But remember, for chi-squared test, you must review the table to get an idea about the association.

3. Check assumption – $< 25\%$ **expected** cell counts < 5.

The expected cell counts,

```
chisq.test(tab_lung)$expected
```

```
##             Cancer
## Smoking      cancer no cancer
##   no smoking     63       105
##   smoking        12        20
```

No count < 5, thus we can rely on chi-squared test.

2.1.2 Fisher's exact test

2.1.2.1 About the test

- Alternative of chi-squared test.
- Usually small cell counts, i.e. chi-squared test requirement is not fulfilled.
- Gives exact P-value, no statistical distribution involved.

2.1.2.2 Analysis

1. Perform Fisher's exact test,

```
fisher.test(tab_lung)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  tab_lung
## p-value = 0.002414
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.1215695 0.6836086
## sample estimates:
## odds ratio
##  0.2940024
```

2.2 Two dependent samples

2.2.1 McNemar's test

2.2.1.1 About the test

- Non-parametric test.
- Purpose: To determine the association between TWO repeated categorical outcomes.
- Cross-tabulation is limited to 2 x 2 only.
- The concern is whether the subjects still have the same outcomes (concordant) or different outcomes (discordant) upon repetition (pre-post).
- The association is determined by looking at the discordant cells.
- χ^2 statistics.

2.2.1.2 Analysis

1. The data.

```
            second
first        approve disapprove
  approve        794        150
  disapprove      86        570
```

*Data from Agresti (2003), Table 10.1 Rating of Performance of Prime Minister

Now, we are going to enter the data in form of counts directly. This is done as follows,

```
tab_pm = read.table(header = FALSE, text = "
794 150
86  570
")
tab_pm
```

```
##    V1  V2
## 1 794 150
## 2  86 570
```

```
str(tab_pm)
```

```
## 'data.frame':    2 obs. of  2 variables:
##  $ V1: int  794 86
##  $ V2: int  150 570
```

which is a data frame.

To properly format the data into a table, do as follows in two steps,

```
tab_pm = as.matrix(tab_pm)  # first convert to a matrix
tab_pm = as.table(tab_pm)  # then convert to a table
str(tab_pm)
```

```
##  'table' int [1:2, 1:2] 794 86 150 570
##  - attr(*, "dimnames")=List of 2
##   ..$ : chr [1:2] "A" "B"
##   ..$ : chr [1:2] "V1" "V2"
```

Now it is a proper table from `str()`.

The table needs proper headers. Now we give them proper names,

```
dimnames(tab_pm) = list(first = c("approve", "disapprove"), second = c("approve", "disapprove"))
str(tab_pm)
```

```
##  'table' int [1:2, 1:2] 794 86 150 570
##  - attr(*, "dimnames")=List of 2
##   ..$ first : chr [1:2] "approve" "disapprove"
##   ..$ second: chr [1:2] "approve" "disapprove"
```

Now we view the table,

```
tab_pm
```

```
##             second
## first        approve disapprove
##   approve        794        150
##   disapprove      86        570
```

```
addmargins(tab_pm)
```

```
##             second
## first        approve disapprove  Sum
##   approve        794        150  944
##   disapprove      86        570  656
##   Sum            880        720 1600
```

2. Perform McNemar's test,

```
mcnemar.test(tab_pm)
```

```
##
##  McNemar's Chi-squared test with continuity correction
##
## data:  tab_pm
## McNemar's chi-squared = 16.818, df = 1, p-value = 4.115e-05
```

References

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