Basic Statistics: guide to R

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Contents

Part 1

General pointers

- Relationship analysis $\neq$ group comparison
- Always inspect the `str` of your data and coerce correct types
  - ☐ Coerce nominal:

    ```
    dataset$var <- factor(dataset$var,
                    levels = c(), labels = c())
    ```

    or

    ```
    dataset$var <- as.factor(dataset$var)
    ```

  - ☐ Coerce ordinal:

    ```
    dataset$var <- ordered(dataset$var,
                    levels = c(), labels = c())
    ```

    or

    ```
    dataset$var <- as.ordered(dataset$var)
    ```

- Check order of factor levels, can be changed for interpretability:
  `dataset$var <- factor(dataset$var, c(level1, level2, ...))`
- Always summarize data, plot data, and check assumptions
- Interaction effects and extra predictors require extra (*explicitly stated*) hypotheses
- Include in report:
  - ☐ Captions for figures and tables
    - Figures: use `fig.cap=""`
    - Tables: use inline text
  - ☐ Direction of effect and group summaries ($M = \ldots$, $SD = \ldots$)
  - ☐ Test statistic and p-value(s)
  - ☐ Effect size estimation
  - ☐ Power analysis (if available in `pwr` package)
- Discussing meaningfulness: sample size, reliability, validity

Part 2

Group comparison

2.1 T-TEST ← (1 DV, 1 IV)

2.1.1 Independent samples

2.1.1.1 Descriptives

```
# Mean, SD, Min, Max
library(pastecs)
stat.desc(dataset, basic = FALSE, norm = TRUE)
```

2.1.1.2 Assumptions

2.1.1.2.1 Normality

```
# Shapiro-Wilk & -1 < Skewness.2SE / Kurtosis.2SE < 1
stat.desc(dataset, norm = TRUE)

# Plots: repeat for sub-groups (avoid for small sample sizes)
hist(dataset$DV[dataset$factor == "level"],
        probability = TRUE,
        ylim = c(0,max))

curve(dnorm(x,
        mean = mean(dataset$DV[dataset$factor == "level"]),
        sd = sd(dataset$DV[dataset$factor == "level"]))),
        add = TRUE)
```

2.1.1.2.2 Homogeneity of variance

```
library(car)
leveneTest(DV ~ Factor, data = dataset)
```

2.1.1.3 Analysis

```
# homogeneity of variance violated
t.test(DV ~ IV, data = dataset)

# homogeneity of variance not violated
t.test(DV ~ IV, data = dataset, var.equal = TRUE)
```

2.1.1.4 Effect size

```
# Cohen's D: .2 < .5 < .8
library(effsize)
cohen.d(DV ~ IV, data = dataset)
```

2.1.1.5 Power analysis

```
library(pwr)

# checking current power
pwr.t.test(n = sample size, d = cohen's d, sig.level = p-value)

# checking desired sample size
pwr.t.test(d = cohen's d, sig.level = alpha level, power = desired power)
```

2.1.2 Dependent samples

2.1.2.1 Descriptives

```
# Mean, SD, Min, Max
library(pastecs)
stat.desc(dataset, norm = TRUE)
```

2.1.2.2 Assumptions

2.1.2.2.1 Normality

```
# the difference between the two groups should be normally distributed
# Shapiro-Wilk & -1 < Skewness.2SE / Kurtosis.2SE < 1
stat.desc(dataset$DV[dataset$factor == level1] - dataset$DV[dataset$factor ==
    level2]], norm = TRUE)

# Plots: repeat for sub-groups (avoid for small sample sizes)
hist(dataset$DV[dataset$factor == "level"],
    probability = TRUE,
    ylim = c(0,max))

curve(dnorm(x,
        mean = mean(dataset$DV[dataset$factor == "level"]),
        sd = sd(dataset$DV[dataset$factor == "level"]))),
        add = TRUE)
```

2.1.2.3 Analysis

```
t.test(DV ~ IV, data = dataset, paired = TRUE)
```

2.1.2.4 Effect size

```
# Cohen's D: .2 < .5 < .8
library(effsize)
cohen.d(DV ~ IV, data = dataset, paired = TRUE)
```

2.1.2.5 Power analysis

```
library(pwr)

# checking current power
pwr.t.test(n = sample size, d = cohen's d, sig.level = p-value, type = "paired")

# checking desired sample size
pwr.t.test(d = cohen's d, sig.level = alpha level, power = desired power, type = "
    paired")
```

2.2 ONE-WAY ANOVA ← (1 DV, 1 IV: >2 LEVELS)

2.2.1 Descriptives

```
# Mean, SD, Min, Max
library(pastecs)
by(dataset$DV, dataset$factor, stat.desc,
    norm = TRUE)
```

2.2.2 Assumptions

2.2.2.1 Normality

```
# Shapiro-Wilk & -1 < Skewness.2SE / Kurtosis.2SE < 1
by(dataset$DV, dataset$factor, stat.desc,
    norm = TRUE)

# Plots: repeat for sub-groups
hist(dataset$DV[dataset$factor == "level"],
    probability = TRUE,
    ylim = c(0,max))

curve(dnorm(x,
        mean = mean(dataset$DV[dataset$factor == "level"]),
        sd = sd(dataset$DV[dataset$factor == "level"]))),
        add = TRUE)
```

2.2.2.2 Homogeneity of variance

```
library(car)
leveneTest(DV ~ Factor, data = dataset)
```

2.2.3 Analysis

2.2.3.1 Computing the test

```
model <- aov(DV ~ IV, data=dataset)
summary(model)
```

2.2.3.2 Post-hoc analysis

```
TukeyHSD(model)
```

2.2.4 Effect size

```
# Omega^2: 0.01 < 0.06 < 0.14
library(sjstats)
omega_sq(model)

# Cohen's F (for power analysis): 0.14 < 0.39 < 0.59
cohens_f(model)
```

2.2.5 Power analysis

```
library(pwr)

# check current power
pwr.anova.test(k = number of groups, n = sample size in each group, f = Cohen's F,
     sig.level = p-value)

# check desired sample size
pwr.anova.test(k = number of groups, f = Cohen's F, sig.level = alpha level, power
     = desired power)
```

2.3 Chi-square ← (Nominal variables)

2.3.1 Entering data manually

	Yes	No
Level 1	a	x
Level 2	b	y
Level 3	c	z

! Important: Enter the data from top to bottom, not from left to right. See below. !

```
tableName <- cbind(c(a, b, c), c(x, y, z))
rownames(tableName) <- c("Level 1","Level 2","Level 3")
colnames(tableName) <- c("Yes","No")
```

2.3.2 Assumptions

2.3.2.1 Expected count > 5 for each cell

```
# check the expected values of each cell
library(gmodels)
CrossTable(tableName, chisq = TRUE, expected = TRUE)
```

2.3.3 Analysis

```
library(gmodels)
CrossTable(tableName, chisq = TRUE, expected = TRUE)
```

2.3.4 Effect size

```
# Cramer's V: 0.1 < 0.3 < 0.5
library(vcd)
assocstats(tableName)
```

```
# a grouped barplot
barplot(tableName,
    beside = TRUE,
    xlab = "",
    ylab = "",
    ylim = c(0,max),
    col = c("","",""), # preferably dark-variants, e.g. "darkred"
    legend.text = c("Level 1", "Level 2", "Level 3"))
```

2.4 Factorial ANOVA ← (1 DV, >1 IV)

2.4.1 Without interaction

2.4.1.1 Descriptives

```
# Mean, SD, Min, Max
library(pastecs)

# Repeat for each factor
by(dataset$DV, dataset$factor), stat.desc,
    norm = TRUE)
```

2.4.1.2 Assumptions

2.4.1.2.1 Normality

```
# Shapiro-Wilk & -1 < Skewness.2SE / Kurtosis.2SE < 1

# Repeat for each factor
by(dataset$DV, dataset$factor), stat.desc,
    norm = TRUE)

# Plots: repeat for sub-groups
hist(dataset$DV[dataset$factor == "level"],
                probability = TRUE,
                ylim = c(0,max))
curve(dnorm(x,
        mean = mean(dataset$DV[dataset$factor == "level"]),
        sd = sd(dataset$DV[dataset$factor == "level"])),
        add = TRUE)
```

2.4.1.2.2 Homogeneity of variance

```
library(car)
leveneTest(dataset$DV, dataset$factor)
```

2.4.1.3 Analysis

2.4.1.3.1 Computing the test

```
# if necessary: make contrasts orthogonal
contrasts(dataset$factor1) <- c(-1, 1)
contrasts(dataset$factor2) <- c(-1, 1)

# Type III ANOVA
library(car)
model <- aov(dataset$DV ~ dataset$factor1 + dataset$factor2)
Anova(model, type="III")
```

2.4.1.3.2 Post-hoc analysis

```
TukeyHSD(model)
```

2.4.1.4 Effect size

```
# Omega^2: 0.01 < 0.06 < 0.14
library(sjstats)
omega_sq(model, partial = TRUE)
```

2.4.2 With interaction

2.4.2.1 Descriptives

```
# Mean, SD, Min, Max
library(pastecs)
by(dataset$DV, list(dataset$factor1, dataset$factor2), stat.desc,
    norm = TRUE)
```

2.4.2.2 Assumptions

2.4.2.2.1 Normality

```
# Shapiro-Wilk & -1 < Skewness.2SE / Kurtosis.2SE < 1
by(dataset$DV, list(dataset$factor1, dataset$factor2), stat.desc,
    norm = TRUE)

# Plots: repeat for sub-groups ; only do this if you hate yourself
hist(dataset$DV[dataset$factor1 == "level" &
                dataset$factor2 == "level"],
                probability = TRUE,
                ylim = c(0,max))
curve(dnorm(x,
        mean = mean(dataset$DV[dataset$factor1 == "level" &
                                   dataset$factor2 == "level"]),
        sd = sd(dataset$DV[dataset$factor1 == "level" &
                                   dataset$factor2 == "level"])),
        add = TRUE)
```

2.4.2.2.2 Homogeneity of variance

```
library(car)
leveneTest(dataset$DV,
    interaction(dataset$factor1, dataset$factor2))
```

2.4.2.3 Analysis

2.4.2.3.1 Computing the test

```
# if necessary: make contrasts orthogonal
contrasts(dataset$factor1) <- c(-1, 1)
contrasts(dataset$factor2) <- c(-1, 1)

# Type III ANOVA
library(car)
model <- aov(dataset$DV ~ dataset$factor1 + dataset$factor2)
Anova(model, type="III")
```

2.4.2.3.2 Post-hoc analysis

```
TukeyHSD(model)
```

2.4.2.4 Effect size

```
# Omega^2: 0.01 < 0.06 < 0.14
library(sjstats)
omega_sq(model, partial = TRUE)
```

Part 3

Assessing relationships

3.1 Correlation ← (1 DV, 1 IV)

3.1.1 Descriptives

```
# Scatterplot
plot(var1~var2, data = dataset)
```

3.1.2 Assumptions

3.1.2.1 Linearity and homoscedasticity

```
# Check for linear relationship / equal distances from the line
plot(var1~var2, data = dataset)
```

3.1.3 Analysis

3.1.3.1 Pearson r

```
cor.test(dataset$var1, dataset$var2, method = "pearson")
```

3.1.3.2 Spearman ρ

```
cor.test(dataset$var1, dataset$var2, method = "spearman")
```

3.1.4 Effect size

```
# The correlation is itself a measure of effect size
```

3.1.5 Power analysis

```
# best suited for Pearson r

# check current power
pwr.r.test(n = sample size, r = correlation, sig.level = p-value)

# check desired sample size
pwr.r.test(r = correlation, sig.level = p-value, power = desired power)
```

3.2 Simple linear regression ← (1 DV, 1 IV)

3.2.1 Descriptives

```
# Scatterplot
plot(DV ~ IV, data = dataset)
```

3.2.2 Assumptions

```
# Check for linearity
plot(DV ~ IV, data = dataset)

# Check for homoscedasticity and normality by a residual plot
model <- lm(DV ~ IV, data = dataset)
plot(fitted(model), residuals(model))

# Check normality by Shapiro-Wilk test and/or QQ-plot
shapiro.test(residuals(model))
qqnorm(residuals(model))
```

3.2.3 Analysis

```
model <- lm(DV ~ IV, data = dataset)
summary(model)
```

3.2.4 Effect size

```
# Unadjusted R^2 is the effect size for a simple linear regression
summary(model)
```

3.2.5 Power analysis

```
library(pwr)
# f^2 = (R^2 / (1 - R^2))

# check current power
pwr.f2.test(u = df1, v = df2, f2 = (R^2/(1 - R^2)), sig.level = p-value)

# check desired sample size
pwr.f2.test(u = df1, v = df2, f2 = (R^2/(1 - R^2)), sig.level = alpha level, power
     = desired power)

# Df2 is n minus TOTAL number of vars, so v + number of vars = n
```

3.3 Multiple linear regression ← (1 DV, >1 IV)

3.3.1 Without interaction

3.3.1.1 Descriptives

```
# for non-continous variables
plot(DV ~ IV, data = dataset)

# for continuous variables
plot(DV ~ IV, data = dataset)
```

3.3.1.2 Assumptions

```
# linearity and homoscedasticity
model <- lm(DV ~ IV1 + IV2, data = dataset)
plot(fitted(model), residuals(model))

# normality of residuals
shapiro.test(residuals(model))
qqnorm(residuals(model))

# multicollinearity
library(car)
vif(model)
```

3.3.1.3 Analysis

```
model <- lm(DV ~ IV1 + IV2, data = dataset)
summary(model)
```

3.3.1.4 Effect size

```
# Adjusted R^2 is the effect size for a multiple linear regression
summary(model)
```

3.3.1.5 Power analysis

```
library(pwr)
# f^2 = (R^2 / (1 - R^2))

# check current power
pwr.f2.test(u = df1, v = df2, f2 = (R^2/(1 - R^2)), sig.level = p-value)

# check desired sample size
pwr.f2.test(u = df1, v = df2, f2 = (R^2/(1 - R^2)), sig.level = alpha level, power
     = desired power)

# Df2 is n minus TOTAL number of vars, so v + number of vars = n
```

3.3.2 With interaction

3.3.2.1 Descriptives

```
# for a single factor
library(pastecs)
plot(DV ~ IV, data = dataset)

# for a single interval predictor
plot(DV ~ IV, data = dataset)
```

```
# plotting subgroups (multiple factors): use descriptives
by(dataset$DV, list(dataset$factor1, dataset$factor2),
    stat.desc, norm = TRUE)

# plotting subgroups (mixed factor types, e.g. continuous + factor): use grouped
    scatterplot
library(ggplot2)
qplot(dataset$DV, dataset$contIV, col = dataset$factorIV) +
        labs(x = "contIV", y = "DV", colour = "factorIV")

# plotting subgroups (continuous variables): scatterplot matrix
pairs(dataset$DV ~ dataset$contIV1 + dataset$contIV2)
```

3.3.2.2 Assumptions

```
# linearity and homoscedasticity
model <- lm(DV ~ IV1 * IV2, data = dataset)
plot(fitted(model), residuals(model))

# normality of residuals
shapiro.test(residuals(model))
qqnorm(residuals(model))

# multicollinearity (although essentially useless)
library(car)
vif(model)
```

3.3.2.3 Analysis

```
model <- lm(DV ~ IV1 * IV2, data = dataset)
summary(model)

# to visualize the difference for factors
library(visreg)
visreg(model, xvar="contIV", by="factorIV")
```

3.3.2.4 Effect size

```
# Adjusted R^2 is the effect size for a multiple linear regression
summary(model)
```

3.3.2.5 Power analysis

```
library(pwr)
# f^2 = (R^2 / (1 - R^2))

# check current power
pwr.f2.test(u = df1, v = df2, f2 = (R^2/(1 - R^2)), sig.level = p-value)

# check desired sample size
pwr.f2.test(u = df1, v = df2, f2 = (R^2/(1 - R^2)), sig.level = alpha level, power
     = desired power)

# Df2 is n minus TOTAL number of vars, so v + number of vars = n
```

Part 4

Script frameworks

4.1 Standard options

```
---
title: ""
author: ""
date: ""
header-includes:
   - \usepackage{caption}
   - \renewcommand\caption{\newline}
   - \usepackage{tipa}
output:
  html_document:
    code_folding: show
    fig_caption: yes
    fig_height: 5
    highlight: tango
    theme: united
    toc: yes
    toc_depth: 4
    toc_float: yes
  pdf_document:
    fig_caption: yes
    highlight: tango
    latex_engine: xelatex
---
```{r setup, dpi=300}
knitr::opts_chunk$set(echo = TRUE, message=FALSE, warning=FALSE, cache = TRUE)
```
```

4.2 Group analysis

4.2.1 (In)dependent t-test

```
## Inserting the data
```{r}
```

Variable types
The dependent variable is [DV], measured on a [...]. The independent variable is [IV],
     measured on a [...].

Choosing a statistical test and defining hypotheses
An independent Student's/Welch t-test is suitable for a group comparison of this type.
```

```
H~0~: There is no significant difference in [DV] between [the levels of IV]. H~a~:
    There is a significant difference in [DV] between [the levels of IV].

## Descriptives

```{r}
library(pastecs)
by(dataset$DV, dataset$IV, stat.desc, norm = TRUE)
```

Table X: Descriptives for [DV] scores by [IV]

	Mean	SD	Min	Max
Group 1				
Group 2				

Boxplot visualization
```{r, fig.cap="**Figure X**: "}
boxplot(dataset$DV, dataset$IV,
    xlab = "",
    ylab = "")
```

Report
Report on the distribution and boxplots.

Computing the t-test

Assumptions
```{r, fig.cap="**Figure X**: "}
# REMEMBER: independent t-test requires normality of sub-groups, but dependent t-test
    requires normality of the differences between levels (e.g. pre- and post-test)

# normality: Shapiro-wilk and skewness.2SE and kurtosis.2SE
by(dataset$DV, dataset$IV, stat.desc, norm = TRUE)

# homogeneity of variance: NOT necessary for dependent samples
library(car)
leveneTest(dataset$DV, dataset$IV)
```

```{r, fig.cap="**Figure X**: "}
# OPTIONAL: histograms
hist(dataset$DV[dataset$IV == level 1], probability = TRUE, ylim = c(0,max),
    xlab = "", ylab = "")
curve(dnorm(x,
    mean = mean(dataset$DV[dataset$IV == level 1]),
    sd = sd(dataset$DV[dataset$IV == level 1])), add = TRUE)
```

```{r, fig.cap="**Figure X**: "}
hist(dataset$DV[dataset$IV == level 2], probability = TRUE, ylim = c(0,max),
    xlab = "", ylab = "")
curve(dnorm(x,
    mean = mean(dataset$DV[dataset$IV == level 2]),
    sd = sd(dataset$DV[dataset$IV == level 2])), add = TRUE)
```

Independent samples T-test
```{r}
t.test(dataset$DV ~ dataset$IV, var.equal = TRUE) # for non-violated homogeneity
```
```

````
t.test(dataset$DV ~ dataset$IV, var.equal = FALSE) # non-violated homogeneity
```

### Dependent samples T-test
```{r}
t.test(dataset$DV ~ dataset$IV, paired = TRUE)
```

### Report
Report on distributions. Report on assumptions. Report on significance and direction of effect.

## Computing effect size
```{r}
library(effsize)
cohen.d(dataset$DV, dataset$IV)
```

### Report
The value of Cohen's D is about [...]. This corresponds to a [...] effect size.

## Reporting and meaningfulness
""An [independent/dependent] samples t-test revealed that, on average, the [IV level 1] showed a [higher/lower ...] (M = , SD = ) than [IV level 2] (M = , SD = ). This difference was [significant / not significant]  (*t*(df) = , p = ). This effect was of a [...] size, *d* = .""

###  Meaningfulness
Sample size? Reliability? Validity? Operationalization?

### Power analysis
It is interesting to check the power of this study, which we can do using the ```pwr ``` in the following manner:

```{r}
library(pwr)

# for independent samples
pwr.t.test(n= sub-group sample size, d= Cohens D, sig.level= p-value, type= "two.sample")
pwr.t.test(d= Cohens D, sig.level= alpha-level, power = 0.8, type= "two.sample")

# for dependent samples
pwr.t.test(n= number of paired observations, d= Cohens D, sig.level= p-value, type= "paired")
pwr.t.test(d= Cohens D, sig.level= alpha-level, power = 0.8, type= "paired")
```

Given the above analysis, it becomes clear that the study had a power of [less/more] than 0.80.
````

4.2.2 One-way ANOVA

````
## Inserting the data
```{r}
```

## Variable types
The dependent variable is [DV], measured on a [...]. The independent variable is [IV], measured on a [...]. [IV] has the following levels: [...].

## Choosing a statistical test and defining hypotheses
A One-way ANOVA can be used for this kind of analysis.
````
````

```
H~0~: There is no significant group difference for [DV] between [the levels of IV]. H~
    a~: There is a significant group difference for [DV] between [the levels of IV], i
    .e. at least one group differs significantly from any other.

## Descriptives
```{r, fig.cap="**Figure X**: "}
library(pastecs)
by(dataset$DV, dataset$IV, stat.desc, norm = TRUE) # -> table

boxplot(dataset$DV~dataset$IV,
        xlab = "IV",
        ylab = "DV")
```

Table X:

	Mean	SD	Min	Max
Group 1				
Group 2				
Group 3				

Report
Report on the distribution and boxplots. Report on the group differences.

Computing a One-way ANOVA

Assumptions
```{r,fig.cap="**Figure X**: ")}
# normality: Shapiro-Wilk and skewness.2SE + kurtosis.2SE
by(dataset$DV, dataset$IV, shapiro.test)

# homogeneity of variance
library(car)
leveneTest(dataset$DV~dataset$IV)
```

One-way ANOVA + post-hoc tests
```{r}
model <- aov(dataset$DV ~ dataset$IV)
summary(model)
TukeyHSD(model)
```

Report
Report on distributions. Report on assumptions. Report on significance and direction
    of effect. Report on post-hoc test differences between groups.

Effect size
```{r}
library(sjstats)

# Omega^2: 0.01 < 0.06 < 0.14
omega_sq(model)

# Cohen's F (for power analysis): 0.14 < 0.39 < 0.59
cohens_f(model)
```

Report
The effect size is [...].
```

````
## Reporting and meaningfulness
"There was [a significant/no significant] effect of [IV] on [DV] (*F* (df1, df2) = ; *p* = ). This effect was of a [...] size ($\omega^2$ = ). A Tukey post-hoc analysis revealed that the [IV level 1] (*M* = , *SD* = ) scored [significantly/not significantly]  [higher/lower] than the [IV level 2] group (*M* = , *SD* = , *p* = ), and also [higher/lower] than the [IV level 3] (*M* = , *SD* = , *p* =). "

###  Meaningfulness
Sample size? Reliability? Validity? Operationalization?

### Power analysis
It is interesting to check the power of this study, which we can do using the ```pwr``` in the following manner:

```{r}
library(pwr)

pwr.anova.test(k = number of groups, n = sample size for each group, f = Cohens F, sig.level = p-value)
pwr.anova.test(k = number of groups, f = Cohens F, sig.level = 0.05, power = 0.8)
```

Given the above analysis, it becomes clear that the study had a power of [less/more] than 0.80.
````

4.2.3 Chi-square

````
## Inserting the data
```{r}
tableName <- cbind(c(a, b, c), c(x, y, z))
rownames(tableName) <- c("Level 1","Level 2","Level 3")
colnames(tableName) <- c("Level 1","Level 2")
```

## Variable types
The variables are **var1**  and **var2**, both of which are measured on a nominal scale. The levels are *level 1/Level 2* for **var1** and *Level 1/Level 2/Level 3* for **var2**.

## Defining hypotheses
H~0~: There is no association between **var1** and **var2**. H~a~: There is an association between **var1** and **var2**.

##   <sup>2</sup> computation
```{r}
library(gmodels)
CrossTable(tableName, chisq = TRUE, expected = TRUE)
```

### Report
An important assumption of chi-square testing is that the expected value for each cell must be greater than 5. This is [...] the case for the data, so this assumption is [...] violated, and therefore no correction is needed. The p-value is [...] than 0.05, so we [...] the H~0~.

## Effect size
```{r}
library(vcd)
assocstats(tableName)
```

### Report
Cramer's V is equal to [...], so the effect size is [...].
````

```
## Interpretation and barplot
Given that we [...] the null-hypothesis, we [...] that **var1** and **var2** are [...]
     associated. Specifically, participants with [...] levels of **var1** [...] levels
     of **var2**.

```{r, fig.cap="**Figure X**: Barplot showing **var1** by **var2**"}
barplot(tableName,
        beside = TRUE,
        xlab = "var1",
        ylab = "Number of participants",
        ylim = c(0,max),
        col = c("darkred","darkgreen","darkblue"),
        legend.text = c("Level 1 var2", "Level 2 var2", "Level 3 var2"))
```


Reporting and meaningfulness
"A chi-squared test of independence showed that **var1** and **var2** were [...]
    significantly associated (* ²* (df, N=) = [...], *p* = [...]). The
    effect size was [...] (*V* = [...])."

Report
Meaningfulness: Sample size? Operationalization? Reliability? Validity?

Power analysis
It is interesting to see whether or not the study had enough statistical power to even
     detect the effect that we are looking for, so in order to check this, we can use
    the ```pwr``` package, as follows:

```{r}
library(pwr)
pwr.chisq.test(w = Cramers V, N= sample size, df = 2, sig.level = p-value)
pwr.chisq.test(w = Cramers V, df = df, sig.level = 0.05, power = 0.8)
```

Given the above analysis, it becomes clear that the study [...] statistical power, and
     that in order to find a significant effect [...].
```

4.2.4 Factorial ANOVA

```
## Inserting the data
```{r}
```

Variable types
The dependent variable is [DV], measured on a [...]. One independent variables is [IV1
    ], measured on a [...]. [IV1] has the following levels: [...]. The other
    independent variable is [IV2], measured on a [...]. [IV2] has the following levels
    : [...].

Choosing a statistical test and defining hypotheses
A Factorial ANOVA can be used for this kind of analysis.

H~0~ (main effect of IV1): There is no significant group difference for [DV] between [
    the levels of IV1]. H~a~: There is a significant group difference for [DV] between
     [the levels of IV1], i.e. at least one group differs significantly from any other
    .

H~0~ (main effect of IV2): There is no significant group difference for [DV] between [
    the levels of IV2]. H~a~: There is a significant group difference for [DV] between
     [the levels of IV2], i.e. at least one group differs significantly from any other
```

```
    .

H~0~ (interaction effect): There is no significant interaction between [IV1] and [IV2
    ]. H~a~: There is a significant interaction between [IV1] and [IV2].

## Descriptives and assumptions
```{r}
# descriptives for the main effects -> table
by(dataset$DV, dataset$IV1, stat.desc, norm = TRUE)
by(dataset$DV, dataset$IV2, stat.desc, norm = TRUE)

# descriptives for the interaction effect -> table
by(dataset$DV, list(dataset$IV1, dataset$IV2), stat.desc, norm = TRUE)

# homogeneity of variance
library(car)
leveneTest(dataset$DV ~ dataset$IV1)
leveneTest(dataset$DV ~ dataset$IV2)
leveneTest(dataset$DV ~ interaction(dataset$IV1, dataset$IV2))
```

Table X:

| | | Mean | SD | Min | Max | Shapiro-
    Wilk test | Levene's test |
|------------- |--------------------------- |------ |---- |----- |-----
    |------------------- |--------------- |
| IV1 | Level 1 | | | | |
              | |
| | Level 2 | | | | |
              | |
| IV2 | Level 1 | | | | |
              | |
| | Level 2 | | | | |
              | |
| Interaction | IV1 Level 1 * IV2 Level 1 | | | | |
              | |
| | IV1 Level 1 * IV2 Level 2 | | | | |
              | |
| | IV1 Level 2 * IV2 Level 1 | | | | |
              | |
| | IV1 Level 2 * IV2 Level 2 | | | | |
              | |

Boxplots (optional)
```{r, fig.cap='**Figure X**: '}
boxplot(dataset$DV ~ dataset$IV1,
        xlab = "",
        ylab = "")
```

```{r, fig.cap='**Figure X**: '}
boxplot(dataset$DV ~ dataset$IV2,
        xlab = "",
        ylab = "")
```

```{r, fig.cap='**Figure X**: '}
library(ggplot2)
ggplot(dataset, aes(x = dataset$IV1, y = dataset$DV, fill=dataset$IV2)) +
  geom_boxplot(width = 0.75) +
  theme_classic() +
  labs(x = "IV1", y = "DV") +
  guides(fill=guide_legend(title="IV2"))
```
```

```
```

Report
Report on the distribution and boxplots. Report on the assumptions. Report on the
    direction of effects.

Computing factorial ANOVA
```{r}
# changing the orthogonal contrasts
contrasts(dataset$IV1) <- c(-1,1)
contrasts(dataset$IV2) <- c(-1,1)

# computing the ANOVA
library(car)

model <- aov(dataset$DV ~ dataset$IV1 * dataset$IV2)
Anova(model, type = "III")
summary(model)
```

Report
Report on significance and hypotheses. Report on influence of individual terms in the
    model.

Effect size
```{r}
library(sjstats)
omega_sq(model, partial = TRUE)
```

Report
The ω_p^2 values for each term in the model.

Reporting and meaningfulness
"There was [a significant / no significant] main effect of [IV1] on [DV] (*F* (df1,
    df2) = , *p* =). This effect was of a [...] size (ω_p^2 =). There was [a
    significant / no significant] main effect of [IV2] on [DV] (*F* (df1, df2) = , *p*
     =). This effect was of a [...] size (ω_p^2 =). There was [a significant
    / no significant] interaction effect between [IV1] and [IV2] on [DV] (*F* (df1,
    df2) =, *p* =). This effect was of a [...] size (ω_p^2 =). Specifically,
    the [IV1/IV2] was larger for those participants with a [level 1 / level 2] (*M* =
    , *SD* =) than for those with a [level 2 / level 1] (*M* = , *SD* =) when [...],
     but they [...] when [...]. In the latter case those participants with [level 1 /
    level 2] (*M* = , *SD* =) scored [...] than those with [level 2 / level 1] (*M* =
     , *SD* =)."

Meaningfulness
Sample size? Reliability? Validity? Operationalization?

4.3 Assessing relationships

4.3.1 Correlation

Inserting the data
```{r}
```

Variable types
The dependent variable is [DV], measured on a [...]. The independent variable is [IV],
     measured on a [...].

Choosing a statistical test and defining hypotheses

````
A [Pearson r/Spearman   ] correlation can be used for this type of analysis.

H~0~: There is no significant relationship between [IV] and [DV]. H~a~: There is a significant relationship between [IV] and [DV].


## Scatterplot and assumptions
```{r, fig.cap="**Figure X**: "}
library(pastecs)

# linearity
plot(dataset$DV ~ dataset$IV,
      xlab = "",
      ylab = "")

# normality: Shapiro-Wilk + skewness.2SE and kurtosis.2SE
shapiro.test(dataset$DV)
stat.desc(dataset$DV, norm = TRUE)

shapiro.test(dataset$IV)
stat.desc(dataset$IV, norm = TRUE)
```

```{r, fig.cap="**Figure X**: "}
# optionally: histogram
hist(dataset$DV, probability = TRUE,
      xlab = "",
      ylab = "",
      ylim = c(0,max))
curve(dnorm(x, mean = mean(dataset$DV), sd = sd(dataset$DV)), add=TRUE)
```

```{r, fig.cap="**Figure X**: "}
hist(dataset$IV, probability = TRUE,
      xlab = "",
      ylab = "",
      ylim = c(0,max))
curve(dnorm(x, mean = mean(dataset$IV), sd = sd(dataset$IV)), add=TRUE)
```

### Report
Report on the scatterplot. Report on the assumptions. Report on the direction of effects.

## Computing correlation (Pearson / Spearman)
```{r}
cor.test(dataset$DV, dataset$IV, method = "pearson")
cor.test(dataset$DV, dataset$IV, method = "spearman")
```

### Report
Report on significance and hypotheses. Report on influence of individual terms in the model.

## Effect size
The correlation itself is a measure of the effect size.


## Reporting and meaningfulness
"A Pearson *r* correlational analysis revealed that [IV] and [DV] were [significantly / not significantly] and [positively / negatively] correlated (*r*(df) = , *p* =).
"

###  Meaningfulness
````

```
Sample size? Reliability? Validity? Operationalization?

### Power analysis

It is interesting to check the power of this study, which we can do using the ```pwr
    ``` in the following manner:

```{r}
library(pwr)
pwr.r.test(n = sample size in each group, r = correlation, sig.level = p-value)
pwr.r.test(r = correlation, sig.level = 0.05, power = 0.8)
```

Given the above analysis, it becomes clear that the study had a power of [less/more]
    than 0.80.
```

### 4.3.2 Simple linear regression

```
Inserting the data
```{r}
```

Variable types
The dependent variable is [DV], measured on a [...]. The independent variable is [IV],
     measured on a [...].

Choosing a statistical test and defining hypotheses
A simple linear regression can be used for this type of analysis.

H~0~: There is no significant effect of [IV] on [DV], i.e. its coefficient is 0. H~a~:
     There is a significant effect of [IV] on [DV].

Scatterplot
```{r, fig.cap="**Figure X**: "}
plot(dataset$DV ~ dataset$IV,
      xlab = "",
      ylab = "")
```

Report
Report on the scatterplot. Report on the assumption. Report on the direction of
    effects.

Computing a simple linear regression + assumptions
```{r}
model <- lm(DV~IV, data = dataset)
summary(model)

# normality: Shapiro-Wilk
library(pastecs)
shapiro.test(residuals(model))
```

```{r, fig.cap="**Figure X**: "}
# QQ-plot
qqnorm(residuals(model))
```

```{r}
# linearity and homoscedasticity
plot(fitted(model), residuals(model))
```
```
```

````
### Report
Report on significance and hypotheses. Report on influence of individual terms in the
    model. Report on the assumptions.

## Effect size
Report on the value of R<sup>2</sup>.


## Reporting and meaningfulness
"A simple linear regression model was constructed, modeling [DV] as a function of [IV
    ]. This model was significant (*F* (df1, df2) = ; *p* = ) and was capable
    explaining [...] of the variance in the data (multiple R<sup>2</sup>). Regression
    coefficients can be found in Table X below."


**Table X**:

|              | Estimate  | SE  | t-value   | p-value   |
|-----------   |---------- |---- |---------  |---------  |
| Intercept    |           |     |           |           |
| IV           |           |     |           |           |


###  Meaningfulness
Sample size? Reliability? Validity? Operationalization?

### Power analysis

It is interesting to check the power of this study, which we can do using the ```pwr
    ``` in the following manner:

```{r}
library(pwr)

pwr.f2.test(u = df1, v = df2, f2 = (R^2/(1 - R^2)), sig.level = p-value)
pwr.f2.test(u = df1, f2 = (R^2/(1 - R^2)), sig.level = 0.05, power = 0.8)
```

Given the above analysis, it becomes clear that the study had a power of [less/more]
    than 0.80.
````

4.3.3 Multiple linear regression

````
## Inserting the data
```{r}
dataset <- read.csv(file = "", header = TRUE, sep = ";")
```

## Variable types
The dependent variable is [DV], measured on an interval scale. The independent
    variables are [IV1], measured on [...], and [IV2], which is measured on [...].

## Choosing statistical test and defining hypotheses
To test whether [IV1] and [IV2] can predict [DV], a multiple regression can be used
    with both main effects as well as an interaction effect.

H~0~ (main effect of [IV1]): [IV1] has no influence on [DV]. H~a~: [IV1] has an
    influence on [DV].

H~0~ (main effect of [IV2]): [IV2] has no influence on [DV]. H~a~: [IV2] has an
    influence on [DV].
````
````

````
H~0~ (interaction effect): There is no interaction between [IV1] and [IV2]. H~a~:
    There is an interaction between [IV1] and [IV2].

## Descriptives
```{r, fig.cap="**Figure X**: "}
library(pastecs)
```

```{r}
# DV ~ factorIV -> table
by(dataset$DV, dataset$IV1, stat.desc, norm = TRUE)
```

```{r}
# DV ~ factorIV1 + factorIV2 -> table
by(dataset$DV, list(dataset$factor1, dataset$factor2), stat.desc, norm = TRUE)
```

```{r, fig.cap="**Figure X**: "}
# DV ~ contIV scatterplot
plot(dataset$DV ~ dataset$contIV,
     xlab = "contIV",
     ylab = "DV")
```

```{r, fig.cap="**Figure X**: "}
# DV ~ contIV + contIV scatterplot
pairs(dataset$DV ~ dataset$contIV1 + dataset$contIV2)
```

```{r, fig.cap="**Figure X**: "}
# DV ~ contIV + factorIV
library(ggplot2)
qplot(dataset$DV, dataset$contIV, col = dataset$factorIV) +
      labs(x = "contIV", y = "DV", colour = "factorIV")
```

### Report
Tables + Figures. Distribution of variables. Sub-groups of variables.

## Multiple linear regression computation and assumptions
### Model 1 (main effects) + assumptions

```{r, fig.cap="**Figure X**: "}
model1.mainEffs <- lm(DV ~ IV1 + IV2, data = dataset)
summary(model1.mainEffs)

# linearity and homoscedasticity
plot(fitted(model1.mainEffs), residuals(model1.mainEffs))
```

```{r, fig.cap="**Figure X**: "}
# normality
shapiro.test(residuals(model1.mainEffs))
qqnorm(residuals(model1.mainEffs))
```

```{r}
# multicollinearity
library(car)
vif(model1.mainEffs)
```
````

```
### Model 2 (interaction effect) + assumptions
```{r, fig.cap="**Figure X**: "}
model2.interact <- lm(DV ~ IV1 * IV2, data = dataset)
summary(model2.interact)

# linearity and homoscedasticity
plot(fitted(model2.interact), residuals(model2.interact))
```

```{r, fig.cap="**Figure X**: "}
# normality
shapiro.test(residuals(model2.interact))
qqnorm(residuals(model2.interact))
```

```{r}
# multicollinearity
library(car)
vif(model2.interact)
```

Report
Report on the assumptions. Report on the significance. Report on the direction of the effect and the contribution of predictors. Report on the rejection of hypotheses.

Table X: Summary of Model 1

	Estimate	SE	t-value	p-value
Intercept				
IV1				
IV2				

Table X: Summary of Model 2

	Estimate	SE	t-value	p-value
Intercept				
IV1				
IV2				
IV1 * IV2				

Effect size
The R² of Model 1 is about [...], so [...] of the variance can be explained by [IV1] and [IV2]. It is about [...] for Model 2, so about [...] of the variance can be explained by [IV1] and [IV2] and their interaction. So the added value in explaining the variance of the interaction is [...].

Interpretation
The main effects are [significant/not significant] in Model 1. This can be interpreted as [...]. The main effects are [significant/not significant] in Model 2. The interaction effect in Model 2 is [significant/not significant].

IF APPLICABLE: The difference between the levels of [factorIV]: the same/different direction/size?

```{r, fig.cap="**Figure X**: Subplots for interaction of Model 2"}
library(visreg)
visreg::visreg(model2, xvar = "contIV", by = "factorIV")
```


Reporting and meaningfulness
```

````
! CHOOSE ONE MODEL !

"A multiple linear regression was constructed to model [DV] as a function of [IV1], as well as [IV2]. This model was [significant/not significant] (*F* (df1, df2) = , *p* = ), and explained [R<sup>2</sup>] of the variance in the data (as indicated by adjusted multiple R-squared). Regression coefficients are shown in Table X."

###  Meaningfulness
Sample size? Reliability? Validity? Operationalization?

### Power analysis
It is interesting to check the power of this study, which we can do using the ```pwr``` in the following manner:

```{r}
library(pwr)
pwr.f2.test(u = df1, v = df2, f2 = (R^2/(1 - R^2)), sig.level = p-value)
pwr.f2.test(u = df1, f2 = (R^2/(1 - R^2)), sig.level = 0.05, power = 0.8)
```

Given the above analysis, it becomes clear that the study had a power of [less/more] than 0.80. [Note that desired sample size calculation requires f2 + total number of variables].
````