A Gentle but Critical Introduction to Statistical Inference, Moderation, and Mediation

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Introduction and Reader's Guide

In the years that I have been teaching inferential statistics to bachelor students in Communication Science, I have learned two things. First, it is paramount that students thoroughly understand the principles of statistical inference before they can apply statistical inference correctly themselves. Second, formal notation, manual calculation, and estimation details distract rather than help students understand what they are doing. This book offers a non-technical but thorough introduction to statistical inference. It discusses a minimal set of concepts needed to understand both the possibilities and pitfalls of estimation, null hypothesis testing, moderation, and mediation analysis. It uses a minimum of formal notation.

Intended Audience and Setting

This book is written as reading material for a follow-up course in statistics, in the bachelor of Communication Science at the University of Amsterdam. Students enrolled in this course, have had an introductory course in statistics that explained how to change research questions into variables and associations between variables, how to select and execute the correct analysis or test (in SPSS) to answer their research question, and how to interpret the results in a language that is both comprehensible for the average reader and complying with professional standards (APA6 standard for reporting test results). In addition, they have learned the very basics of inferential statistics: How to decide which null hypothesis to reject based on reported p values, and how to interpret confidence intervals.

This book is meant for use in a flipped-classroom setting. Students should read the text, watch embedded videos, and play with the interactive content before they meet in class. Class meetings are used to answer questions raised by the students, do group work to exercise with the concepts and techniques presented in the text, and do little tests to check understanding.

Interactive Content

The interactive content in this book replaces simulations that used to be demonstrated during lectures. I expect that doing simulations yourself rather than watching them being done by someone else enhances understanding. I have tried to break down the simulations into smaller steps, confronting the student several times with essentially the same simulation, but with added complexity. I hope that this approach enhances understanding and remembrance and, at the same time, avoids frustration caused by complex dashboards offering all options at once.

Most interactive content starts with a question regarding the student's expectations of what is going to happen in the simulation. I strongly recommend that students state their expectations before they start the simulations to see where their intuitions are right and where they are wrong.

With a similar objective, each chapter starts with a *Test your intuition and understanding* Section: interactive content with questions. On first reading, play with the content and use your intuition to answer the questions. Don't worry if you do not know all the answers; the subject matter is explained step by step in the remainder of the chapter. On re-reading and exam preparation, use this section to test your understanding. If you understand the interactive content and know the answers to the questions, you understand the core concepts of the chapter.

Disclaimer

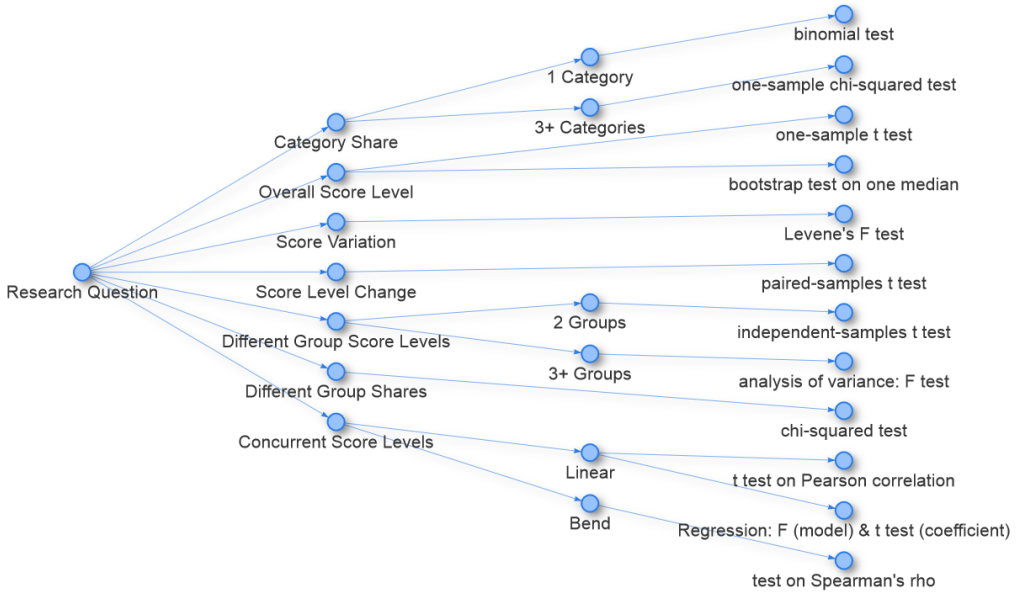
The example data sets have been generated for the purpose of demonstrating statistical techniques. These are not real data and no conclusions should be drawn from the results obtained from the data.

Acknowledgements

Adam Sasiadek developed the more complicated Shiny apps in this book. The College of Communication at the University of Amsterdam generously supported the creation of the apps whereas this university's Grassroots Project for ICT in education refused to support it. Renske van Bronswijk corrected my English. Any remaining errors result from changes and additions that I applied afterwards. My colleague Peter Neijens commented on a draft of this text.

SPSS Tutorial Videos List

Flow chart



Hint: Hover your mouse pointer over a node, click on a dot, drag with your (left) mouse button, and zoom with your mouse wheel.

Chapter 2: Probability Models: How Do I Get a Sampling Distribution?

Figure 2.7: Bootstrapping in SPSS.

Figure 2.8: Interpreting bootstrap results in SPSS.

Figure 2.9: Performing an exact test in SPSS.

Figure 2.10: Interpreting exact test results in SPSS.

Chapter 3: Estimating a Parameter: Which Population Values Are Plausible?

Chapter 4: Testing a Null Hypothesis: Am I Right or Am I Wrong?

Chapter 5: Which Sample Size Do I Need? Power!

Chapter 7: Moderation with Analysis of Variance

Chapter 8: Moderation with Regression Analysis

Chapter 9: Mediation with Regression Analysis

Chapter 1

Sampling Distribution: How Different Could My Sample Have Been?

Key concepts: inferential statistics, generalization, population, random sample, sample statistic, sampling space, random variable, sampling distribution, probability, probability distribution, discrete probability distribution, expected value/expectation, unbiased estimator, parameter, (downward) biased, representative sample, continuous variable, continuous probability distribution, probability density, (left-hand/right-hand) p value.

Summary

Statistical inference is about estimation and null hypothesis testing. We have collected data on a random sample and we want to draw conclusions (make inferences) about the population from which the sample was drawn. From the proportion of yellow candies in our sample bag, for instance, we want to estimate a plausible range of values for the proportion of yellow candies in a factory's stock (confidence interval). Alternatively, we may want to test the null hypothesis that one fifth of the candies in a factory's stock is yellow.

The sample does not offer a perfect miniature image of the population. If we would draw another random sample, it would have different characteristics. For instance, it would contain more or less yellow candies than the previous sample. To make an informed decision on the confidence interval or null hypothesis, we must compare the characteristic of the sample that we have drawn to the characteristics of the samples that we could have drawn.

The characteristics of the samples that we could have draw is called the sampling distribution. Sampling distributions are the central element in estimation and null hypothesis testing.

In this chapter, we simulate sampling distributions to understand what they are. Here, *simulation* means that we let a computer draw many random samples from a population.

In Communication Science, we usually work with samples of human beings, for instance, users of social media, people looking for health information or entertainment, citizens preparing to cast a political vote, and an organization's stakeholders, or samples of media content such as tweets, tv advertisements, or newspaper articles. In the current and two subsequent chapters, however, we avoid the complexities of these samples.

We focus on a very tangible kind of sample, namely a bag of candies, which helps us understand the basic concepts of statistical inference: sampling distributions (the current chapter), probability distributions (Chapter 2), and estimation Chapter 3). Once we thoroughly understand these concepts, we turn to Communication Science examples.

Test your intuition and understanding

Figure 1.1 simulates drawing random samples from a candy factory's stock of candies. We are interested in the colour of the candies in our sample. The histogram shows the distribution of candies according to colour. Draw some samples and have a look at the number of yellow candies in each sample as well as the average number of yellow candies over all samples.

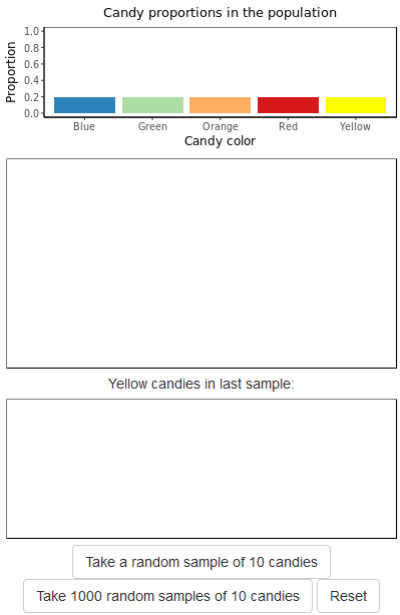


Figure 1.1: A discrete sampling distribution.

1. Figure 1.1 shows a simulated population distribution. What would be the real-world population?

2. Use the button in Figure 1.1 to draw one random sample of ten candies from the population. What do the numbers on the horizontal axis of the bottom histogram represent? What is the statistical name of the variable *Number of yellow candies*? What is the unit of analysis for this characteristic?

3. Which values can the sample characteristic take here and what is the statistical name for this set of values?

4. If you would draw many samples from this population each containing ten candies, what is the number of yellow candies per sample that appears most frequently? Draw 1,000 samples to verify your answer.

5. Is the colour distribution in each sample that you draw representative of the colour distribution in the stock of candies?

6. Why, do you think, is the sample characteristic called a *random variable*?

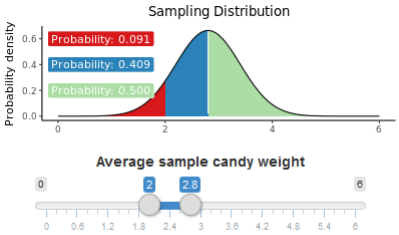


Figure 1.2: A continuous sampling distribution.

7. Use your own words to explain what the sampling distribution in Figure 1.2 represents.

8. What do you think is the average weight of all candies in the population? Justify your answer using the concepts *expected value* and *unbiased estimator*.

9. Use the sliders to find the probability of drawing a sample with average candy weight between 2.0 and 2.9 grams.

10. What, do you expect, is the probability of drawing a sample with average candy weight of exactly 2.9 grams? Use the sliders to check your expectation.

11. Why is this graph an example of a continuous probability distribution?

12. Why is the vertical axis labelled with “Probability density” instead of “Probability”?

On first reading, you may not know all the answers. That is OK. Just try again after you have studied this chapter.

1.1 Statistical Inference: Making the Most of Your Data

Statistics is a tool for scientific research. It offers a range of techniques to check whether statements about the observable world (empirical reality) are supported by data collected from that world. Scientific theories strive for general statements, that is, statements that apply to many situations. Checking these statements requires lots of data covering all situations addressed by theory.

Collecting data, however, is expensive, so we would like to collect as little data as possible and still be able to draw conclusions about a much larger set. The cost and time involved in collecting large sets of data are also relevant to applied research, such as market research. In this context we also like to collect as little data as necessary.

Inferential statistics offers techniques for making statements about a larger set of observations from data collected for a smaller set of observations. The large set of observations about which we want to make a statement is called the *population*. The smaller set is called a *sample*. We want to *generalize* a statement about the sample to a statement about the population from which the sample was drawn.

Traditionally, statistical inference is generalization from the data collected in a *random sample* to the population from which the sample was drawn. This approach is the focus of the present book because it is currently the most widely used type of statistical inference in the social sciences. We will, however, point out other approaches in Chapter 6.

Statistical inference is conceptually complicated and for that reason quite often used incorrectly. We will therefore spend quite some time on the principles of statistical inference. Good understanding of the principles should help you to recognize and avoid incorrect use of statistical inference. In addition, it should help you to understand the controversies surrounding statistical inference and developments in the practice of applying statistical inference that are taking place. Investing time and energy in fully understanding the principles of statistical inference really pays off later.

1.2 A Discrete Random Variable: How Many Yellow Candies in My Bag?

An obvious but key insight in statistical inference is this: If we draw random samples from the same population, we are likely to obtain different samples. No two random samples from the same population need to be identical, even though they can be identical.

1.2.1 Sample statistic

We are usually interested in a particular characteristic of the sample rather than in the exact nature of each observation within the sample. For instance, I happen to be very fond

of yellow candies. If I buy a bag of candies, my first impulse is to tear the bag open and count the number of yellow candies. Am I lucky today? Does my bag contain a lot of yellow candies?

Figure 1.3: How many yellow candies will our sample bag contain?

1. Figure 1.3 shows a population of candies. What do you expect is the number of yellow candies in a random sample of ten candies from this population? Draw several samples and check whether your expectation comes true.

2. What are all the possible outcomes for the number of yellow candies? This collection of all possible outcome scores is called the *sampling space*.

The number of yellow candies in a bag is an example of a *sample statistic*: a number describing a property of the sample. Each bag, that is, each sample, has one outcome score on the sample statistic. For instance, one bag contains four yellow candies, another bag contains seven, and so on.

The sample statistic is called a *random variable*. It is a variable because it assigns an outcome score to a sample and different samples can have different scores. The value of a random variable may vary from sample to sample. It is a random variable because the score depends on chance, namely the chance that particular elements are drawn during random sampling.

1.2.2 Sampling distribution

Some sample statistic outcomes occur more often than other outcomes. We can see this if we draw very many random samples from a population and collect the frequencies of all outcome scores in a table or chart. We call the distribution of the outcome scores of very many samples a *sampling distribution*.

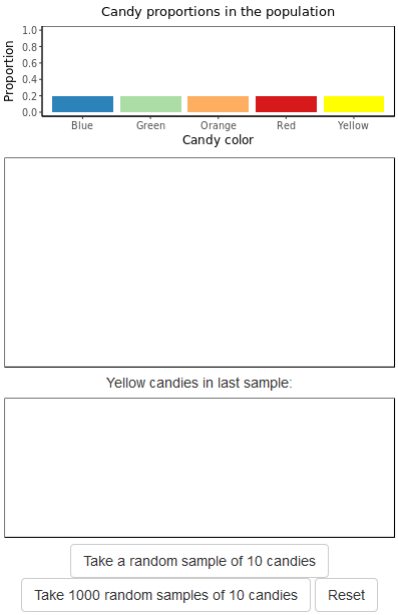


Figure 1.4: What is a sampling distribution?

1. Draw a random sample of ten candies in Figure 1.4. What do the numbers on the horizontal axis of the bottom histograms mean? And what does the vertical axis of this histogram represent?

2. What are the cases (units of analysis) in the three histograms? Hint: There are two different types of cases.

3. Guess the most likely and most unlikely outcome scores for the number of yellow candies in a sample bag containing ten candies in Figure 1.4. Check your intuitions by drawing 1,000 samples.

4. After how many samples does the shape of the sampling distribution stop changing?

1.2.3 Probability and probability distribution

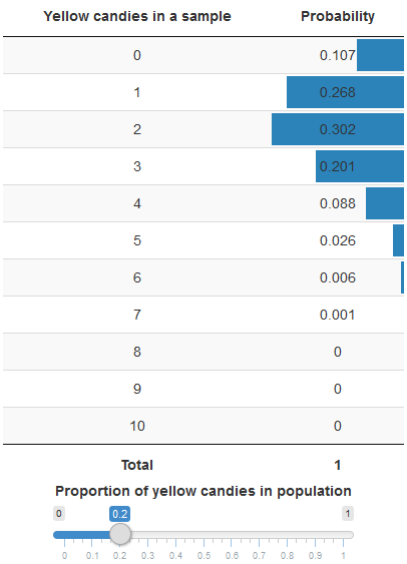


Figure 1.5: How does the probability of drawing a sample bag with two out of ten candies yellow depend on the proportion of yellow candies in the population?

1. In Figure 1.5, what is the sample statistic and what is the sampling space?
2. Which number of yellow candies is most likely to be found in a sample bag of ten candies? How does this relate to the proportion of candies in the population?
3. What is the probability that a sample bag of ten candies contains not more than three yellow candies if the proportion in the population is .2?
4. What do you expect to happen to the probabilities if you increase the proportion of yellow candies in the population (factory stock)? Use the slider to check your answer.
5. What is special about the distribution if the proportion of yellow candies in the population is .5?

What is the probability of buying a bag with exactly five yellow candies? In statistical terminology, what is the probability of drawing a sample with five yellow candies as sample statistic outcome? This probability is the proportion of all possible samples that we could have drawn that happen to contain five yellow candies.

The sampling distribution tells us all possible samples that we could have drawn, that is, if we have drawn very many samples. We can use the distribution of all samples to we can get the the probability of buying a bag with exactly five yellow candies from the sampling distribution: We merely divide the number of samples with five yellow candies by the total number of samples we have drawn.

If we change the (absolute) frequencies in the sampling distribution into proportions (relative frequencies), we obtain the *probability distribution* of the sample statistic: A sampling space with a probability (between 0 and 1) for each outcome of the sample statistic. Because we are usually interested in probabilities, sampling distributions tend to have proportions, that is probabilities, instead of frequencies on the vertical axis. See Figure 1.6 for an example. In this case, the sampling distribution is a probablity distribution.

Figure 1.5 displays the probability distribution of the number of yellow candies per bag of ten candies. This is an example of a *discrete probability distribution* because only a limited number of outcomes are possible. It is feasible to list the probability of each outcome separately.

The sampling distribution as a probability distribution conveys very important information. It tells us which outcomes we can expect, in our example, how many yellow candies we may find in our bag of ten candies. Moreover, it tells us the probability that a particular outcome may occur. If the sample is drawn from a population in which twenty per cent of candies are yellow, we are quite likely to find zero, one, two, three, or four yellow candies in our bag. A bag with five yellow candies would be rare, six or seven candies would be very rare, and a bag with more than seven yellow candies is extremely unlikely even though it is not impossible. If we buy such a bag, we know that we have been extremely lucky.

We may refer to probabilities both as a proportion, that is, a number between 0 and 1, and as a percentage: a number between 0% and 100%. Proportions are commonly considered to be the correct way to express probabilities. When we talk about probabilities, however, we tend to use percentages; we may, for example, say that the probabilities are fifty-fifty.

1.2.4 Expected value or expectation

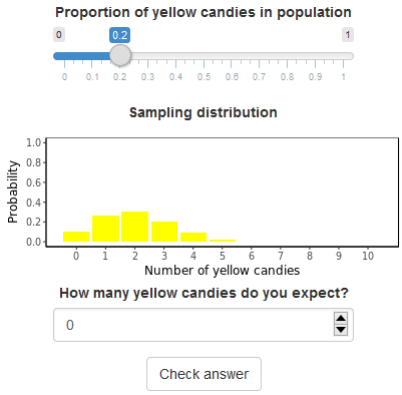


Figure 1.6: What is the expected value of a probability distribution?

1. In Figure 1.6, which number of yellow candies is most likely to occur in a sample bag of ten candies? How does this number change if you change the proportion of yellow candies in the population?

2. How does the mean of the sampling distribution relate to the expected value? Experiment with different values for the population proportion.
3. How does the mean of the sampling distribution relate to the population proportion? Experiment with different values for the population proportion.

We haven't yet thought about the value that we are most likely to encounter in the sample that we are going to draw. Intuitively, it must be related to the distribution of colours in the population of candies from which the sample was drawn. In other words, the share of yellow candies in the factory's stock from which the bag was filled or in the machine that produces the candies, seems to be relevant to what we may expect to find in our sample.

If the share of yellow candies in the population is 0.20 (or 20%), we expect one out of each five candies in a bag (sample) to be yellow. In a bag with 10 candies, we would expect two candies to be yellow: one out of each five candies or the population proportion times the total number of candies in the sample = 0.20 * 10 = 2.0. This is the expected value.

The expected value of the proportion of yellow candies in the sample is equal to the proportion of yellow candies in the population. If you carefully inspect a sampling distribution (Figure 1.6), you will see that the expected value also equals the mean of the sampling distribution. This makes sense: Excess yellow candies in some bags must be compensated for by a shortage in other bags.

Thus we arrive at the definition of the *expected value* of a random variable:

> The expected value is the average of the sampling distribution of a random variable.

In our example, the random variable is a sample statistic, more sepcifically, the number of yellow candies in a sample.

The sampling distribution is an example of a probability distribution, so, more generally, the expected value is the average of a probability distribution. The expected value is also called the *expectation* of a probability distribution.

1.2.5 Unbiased estimator

Note that the expected value of the proportion of yellow candies in the bag (sample statistic) equals the true proportion of yellow candies in the candy factory (population statistic). This is always, that is, by definition, true for all sample statistics that are *unbiased estimators* of the population statistic. By the way, we usually refer to the population statistic as a *parameter*.

Most but not all sample statistics are unbiased estimators of the population statistic. Think, for instance, of the actual number of yellow candies in the sample. This is certainly not an unbiased estimator of the number of yellow candies in the population. Because the population is so much larger than the sample, the population must contain many more yellow candies than the sample. If we were to estimate the number in the population (the parameter) from the number in the sample—for instance, we estimate that there are two yellow candies in the population of all candies because we have two in our sample of ten—we

are going to vastly underestimate the number in the population. This estimate is *downward biased*: It is too low.

In contrast, the proportion in the sample is an unbiased estimator of the population proportion. That is why we do not use the number of yellow candies to generalize from our sample to the population. Instead, we use the proportion of yellow candies. You probably already did this intuitively.

Sometimes, we have to adjust the way in which we calculate a sample statistic to get an unbiased estimator. For instance, we must calculate the standard deviation and variance in the sample in a special way to obtain an unbiased estimate of the population standard deviation and variance. The exact calculation need not bother us, because our statistical software will take care of that.

1.2.6 Representative sample

Because the share of yellow candies in the population represents the probability of drawing a yellow candy, we also expect 20% of the candies in our bag to be yellow. For the same reason we expect the shares of all other colours in our sample bag to be equal to their shares in the population. As a consequence, we expect a random sample to resemble the population from which it is drawn.

A sample is *representative* of a population if variables in the sample are distributed in the same way as in the population. Of course, we know that a random sample is likely to differ from the population due to chance, so the actual sample that we have drawn is usually not representative of the population.

But we should expect it to be representative, so we say that it is *in principle representative* of the population. We can use probability theory to account for the misrepresentation in the actual sample that we draw. This is what we do when we use statistical inference to construct confidence intervals and test null hypotheses.

1.3 A Continuous Random Variable: Overweight And Underweight.

Let us now look at another variable: the weight of candies in a bag. The weight of candies is perhaps more interesting to the average consumer because it is related to the number of calories that a candy contains.

1.3.1 Continuous variable

Weight is a *continuous variable* because we can always think of a new weight between two other weights. For instance, consider two candy weights: 2.8 and 2.81 gram. It is easy to see that there can be a weight in between these two values, for instance, 2.803 gram. Between

2.8 and 2.803 we can discern an intermediate value such as 2.802. In principle, we could continue doing this endlessly, e.g., find a weight between 2.80195661 and 2.80195662 gram even if our scales may not be sufficiently precise to measure any further differences. It is the principle that counts. If we can always think of a new value in between two values, the variable is continuous.

1.3.2 Continuous sample statistic

We are not interested in the weight of a single candy. If a relatively light candy is compensated for by a relatively heavy candy in the same bag, we still get the calories that we want. We are interested in the average weight of all candies in our sample bag, so average candy weight in our sample bag is our key sample statistic. We want to use this sample statistic to say something about average candy weight in the population of all candies. Can we do that?

The sample mean is an unbiased estimator of the population mean, so the average weight of all candies in the population (at the factory) is the average of the (candy weights in the) sampling distribution. And this is the average weight that we expect in a sample drawn from this population (the expected value or expectation). So far, everything is the same as in the case of the proportion of yellow candies, which was a discrete random variable because it could take only a limited set of values: yellow, blue, green, red, and orange.

1.3.3 Continuous probabilities

When we turn to the probabilities of getting samples with a particular average candy weight, we run into problems with a continuous sample statistic. If we would want to know the probability of drawing a sample bag with an average candy weight of 2.8 gram, we should exclude sample bags with an average candy weight of 2.81 gram, or 2.801 gram, or 2.8000000001 gram, and so on. In fact, we are very unlikely to draw a sample bag with an average candy weight of exactly 2.8 gram, that is, with an infinite number of zeros trailing 2.8. In other words, the probability of such a sample bag is for all practical purposes zero and negligible.

This applies to every average candy weight, so all probabilities are virtually zero. As a consequence, we cannot construct a probability distribution of the sampling space, that is, of all possible outcomes. By the way, note that this is also impossible because we have an infinite number of possible outcomes. After all, we can always find a new weight between two selected weights.

1.3.4 p Values

We can solve this problem by looking at a range of values instead of a single value. We can meaningfully talk about the probability of having a sample bag with an average candy weight of at least 2.8 gram or at most 2.8 gram. We choose a threshold, in this example 2.8 gram, and determine the probability of values above or below this threshold. We can also use two thresholds, for example the probability of an average candy weight between 2.75

and 2.85 gram. This is probably what you were thinking of when I referred to a bag with 2.8 gram as average candy weight.

If we cannot determine the probability of a single value, which we used to depict on the vertical axis, and we have to link probabilities to a range of values on the x axis, for example, average candy weight above/below 2.8 gram, how can we display probabilities? We have to display a probability as an area between the horizontal axis and a curve. This curve is called a *probability density function*, so if there is a label to the vertical axis of a continuous probability distribution, it usually is "Probability density" instead of "Probability".

Figure 1.7 shows an example of a continuous probability distribution for the average weight of candies in a sample bag. This is the familiar normal distribution so we could say that the normal function is the probability density function here. The total area under this curve is set to one, so the area belonging to a range of sample outcomes (average candy weight) is 1 or less, as probabilities should be.

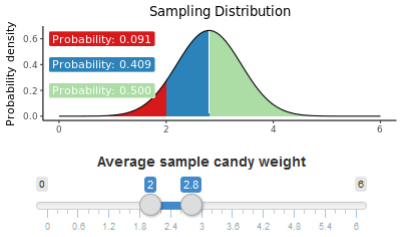


Figure 1.7: How do we display probabilities in a continuous sampling distribution?

1. In Figure 1.7, what is the probability of buying a bag with average candy weight of 2.8 gram or more?
2. Is this a left-hand probability, a right-hand probability, or neither?
3. Use the sliders to find the probability of buying a bag with average candy weight between 2.6 and 3.7 gram. Is this a left-hand probability, a right-hand probability, or neither?
4. What is the minimum average weight of the 10% heaviest candy bags?

The probability of values up to (and including) the threshold value or the threshold value and higher are called *p values*. The probability of values up to (and including) the threshold value is known as the *left-hand p value* and the probability of values above (and including) the threshold value is called the *right-hand p value*.

Why did I put *(and including)* between parentheses? It does not really matter whether we add the exact boundary value (2.8 gram) to the probability on the left or on the right because the probability of getting a bag with average candy weight at exactly 2.8 gram (with a very long trail of zero decimals) is negligible.

Are you struggling with the idea of areas instead of heights (values on the vertical axis) as probabilities? Just consider the idea that we could use the area of a bar in a histogram instead of the height as indication of the probability in discrete probability distrbutions, for example, Figure 1.6. After all, the bars in a histogram are all equally wide, so differences between bar areas are proportional to differences in bar height.

1.3.5 Probabilities always sum to 1

While you were playing with Figure 1.7, you may have noticed that displayed probabilities always add up to one. This is true for every probability distribution as you have learned before. In addition, you may have realized that the probabilities can also be interpreted as proportions or percentages. The probability that a sample bag contains candies with average weight over 2.9 gram is equal to the proportion of samples in the sampling distribution with average candy weight over 2.9 gram. Thus, we can use probabilities to find the threshold values that separate the top ten per cent or the bottom five per cent in a distribution.

1.4 Concluding Remarks

A communication scientist wants to know whether children are sufficiently aware of the dangers of media use. On a media literacy scale from one to ten, an average score of 5.5 or higher is assumed to be sufficient.

If we translate this to the simple candy bag example, we realize that the outcome in our sample need not be the true population value. After all, we could very well draw a bag with less or more than twenty per cent yellow candies.

Average media literacy, then, can exceed 5.5 in our sample of children, even if average media literacy is below 5.5 in the population or the other way around. How we decide on this is discussed in later chapters.

1.4.1 Samples characteristics as observations

Perhaps the most confusing aspect of sampling distributions is the fact that samples are our cases (units of analysis) and sample characterstics are our observations. We are accustomed to think of observations as measurements on empirical *things* such as people or candies. We perceive each person or each candy as a case and we observe a characteristic that may change across cases (a variable), for instance the colour of a candy or the weight of a candy.

In a sampling distribution, however, we observe samples (cases) and measure a sample statistic as the (random) variable. Each sample adds one observation to the sampling distribution and its sample statistic value is the value added to the sampling distribution.

1.4.2 Means at three levels

In our first example, the sample statistic is a proportion, namely the proportion of candies that are yellow. The horizontal axis of the sampling distribution represents the proportion of yellow candies. This is fully in line with our research question. If we want to know whether all colours are equally distributed, we are interested in sample proportions, not in properties of individual candies.

Things become a little confusing if we are interested in a sample mean, such as the average weight of candies in a sample bag. Now we have means at three levels: the population, the sampling distribution, and the sample.

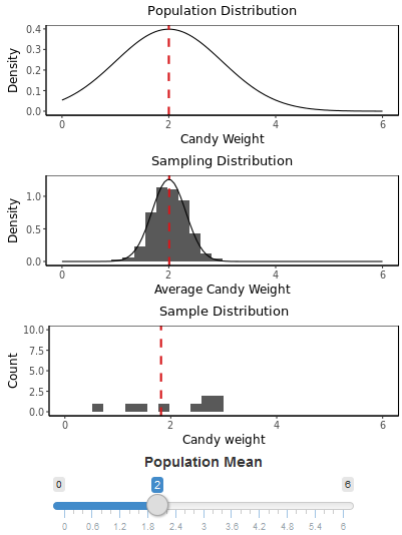


Figure 1.8: What is the relation between the three distributions?

1. In Figure 1.8, explain the meaning of the three means (dotted red lines). Which mean is a mean of means?
2. Is it a coincidence that the mean of the population and sampling distribution are the same? Use a slider to check if these means are the same.
3. How does the sample mean relate to the population mean and the mean of the sampling distribution?

The sampling distribution, here, is a distribution of sample means but the sampling distribution itself also has a mean, which is called the expected value or expectation of the sampling distribution. Don't get confused about this. The mean of the sampling distribution is the average of the average weight of candies across all possible samples. This mean of means has the same value as our first mean, namely the average weight of the candies in the population because a sample mean is an unbiased estimator of the population mean.

Think of the three distributions as a hamburger. The top and bottom part of a hamburger are both made of bread. They represent the population and the sample, which consist if the same substance: candies and their weight in our example. The middle part of the hamburger, however, is a completely different type of food. The meat holds the two halves of the bun together. In a similar way, the sampling distribution connects the population to the sample but it is of a very different substance. It consists of samples, for instance, bags of candies instead of single candies.

The sampling distribution sticks to the population because the population statistic (parameter), for example, the average weight of all candies, is equal to the mean of the sampling distribution. The sampling distribution sticks to the sample because it tells us which sample means we will find with what probabilities. The sampling distribution is the vital link connecting the sample to the population. We need it to make statements about the population based on our sample.

1.5 Take-Home Points

- Values of a sample statistic vary across random samples from the same population. But some values are more probable than other values.
- The sampling distribution of a sample statistic tells us the probability of drawing a sample with a particular value of the sample statistic or a particular minimum/maximum value.
- If a sample statistic is an unbiased estimator of a parameter, the parameter value is the average of the sampling distribution, which is called the expected value or expectation.
- For discrete sample statistics, the sampling distribution tells us the probability of individual sample outcomes. For continuous sample statistics, it tells us the p value: the probability of drawing a sample with an outcome that is at least or at most a particular value.

Chapter 2

Probability Models: How Do I Get a Sampling Distribution?

Key concepts: bootstrapping/bootstrap sample, sampling with replacement, exact approach, approximation with a theoretical probability distribution, binomial distribution, (standard) normal distribution, (Student) t distribution, F distribution, chi-squared distribution, condition checks for theoretical probability distributions, sample size, equal population variances, expected values, independent samples, dependent/paired samples.

Summary

In the previous chapter, we drew a large number of samples from a population to obtain the sampling distribution of a sample statistic, for instance, the proportion of yellow candies or average candy weight in the sample. The procedure is quite simple: Draw a sample, calculate the desired sample statistic, add the sample statistic value to the sampling distribution, and repeat this thousands of times.

Although this procedure is simple, it is not practical. In a research project, we would have to draw thousands of samples and administer a survey to each sample or collect data on the sample in some other way. This requires too much time and money to be of any practical value. So how do we create a sampling distribution, if we only collect data for a single sample? This chapter presents three ways of doing this: bootstrapping, exact approaches, and theoretical approximations.

Test your intuition and understanding

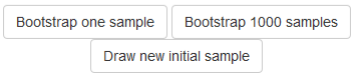


Figure 2.1: How do we bootstrap a sampling distribution?

1. Why does Figure 2.1 not show a population?
2. Which type of sampling is better here: with or without replacement? Justify your answer.
3. Draw a new initial sample in Figure 2.1. Is the bootstrapped sampling distribution going to resemble the true sampling distribution? Note that twenty per cent of the candies in the population are yellow. Motivate your answer. Draw 1,000 bootstrap samples to check your answer.

Table 2.1: Number of heads for a toss of three coins.

Number of heads	Combination
0	tail-tail-tail
1	tail-tail-head
1	head-tail-tail
1	head-tail-tail
2	head-head-tail
2	head-tail-head
2	tail-head-head
3	head-head-head
Total	8

4. Calculate the exact probability distribution of the number of heads in a toss of three

fair coins (Table 2.1).

5. In which situations can we use exact probabilities as a sampling distribution?

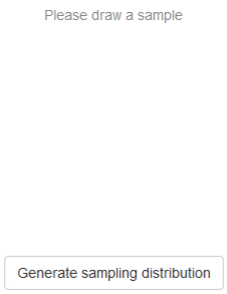


Figure 2.2: How do we approximate a sampling distribution with a theoretical probability distribution?

6. Generate a sampling distribution of average sample candy weight in Figure 2.2. Try to explain in your own words why the sampling distribution of a sample mean has a bell shape.

7. Which part of the graph in Figure 2.2 represents the theoretical probability distribution?

8. Can we always use this theoretical probability distribution if we are interested in sample means? See if the general outline of the theoretical probability distribution matches the histogram of average sample candy weight observed in a large number of samples. Pay special attention to the lowest (red) and highest (green) 2.5% of observed sample means.

On first reading, you may not know all answers. Try again after you have studied this chapter.

2.1 The Bootstrap Approximation of the Sampling Distribution

The first way to obtain a sampling distribution is still based on the idea of drawing a large number of samples. However, we only draw one sample from the population for which we collect data. As a next step, we draw a large number of samples from our initial sample. The samples drawn in the second step are called *bootstrap samples*. The technique was developed by Bradley Efron (1979; 1987). For each bootstrap sample, we calculate the sample statistic of interest and we collect these as our sampling distribution. We usually want about 5,000 bootstrap samples for our sampling distribution.

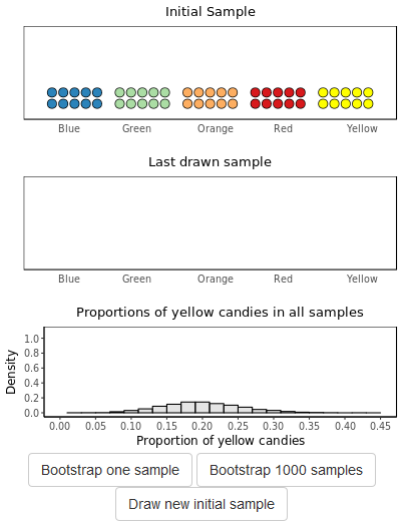


Figure 2.3: How do we create a sampling distribution with bootstrapping?

In Figure 2.3, an initial sample has been drawn from a population containing five candy colours in equal proportions.

1. How large is a bootstrap sample in Figure 2.3? Formulate and motivate your answer before you check it with the *Bootstrap one sample* button.

2. What element in Figure 2.3 represents the true sampling distribution in this example? If in doubt, see Figure 1.5.

3. Does the bootstrap sampling distribution resemble the true sampling distribution? Use the "Bootstrap 1000 samples" button and justify your answer.

4. Draw a new initial sample. This sample is probably less representative of the distribution of candy colour in the population. What happens to the bootstrap samples and the bootstrap sampling distribution?

The *bootstrap* concept refers to the story in which Baron von Münchhausen saves himself by pulling himself and his horse by his bootstraps (or hair) out of a swamp. In a similar miraculous way, the bootstrap samples resemble the sampling distribution even though they are drawn from a sample instead of the population. This miracle requires some explanation and it need not work always, as we will discuss in the remainder of this section.

[htbp] 

Figure 2.4: Baron von Münchhausen pulls himself and his horse out of a swamp.

2.1.1 Sampling with and without replacement

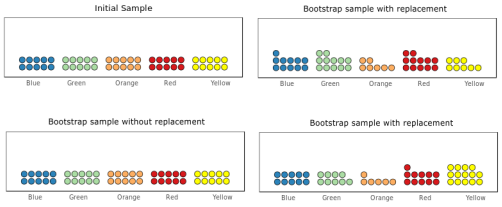
[htbp] 

Figure 2.5: Sampling with and without replacement.

1. What are the differences between sampling with and without replacement (Figure 2.5)?

As we will see in a later chapter, the size of a sample is very important to the shape of the sampling distribution. The sampling distribution of samples with twenty cases can be very different from the sampling distribution of samples with forty cases. To construct a sampling distribution from bootstrap samples, the bootstrap samples must be exactly as large as the original sample.

How can we draw many different bootstrap samples from the original sample if each bootstrap sample must contain the same number of cases as the original sample? If we allow every case in the original sample to be sampled only once, each bootstrap sample contains all cases of the original sample, so it is an exact copy of the original sample. Thus, we cannot create different bootstrap samples.

By the way, we often use the type of sampling described above, which is called *sampling without replacement*. If a person is (randomly) chosen for our sample, we do not put this person back into the population so she or he can be chosen again. We want our respondents to fill out our questionnaire only once or participate in our experiment only once.

If we do allow the same person to be chosen more than once, we sample *with replacement*. The same person can occur more than once in a sample. Bootstrap samples that are sampled with replacement from the original sample can vary because they need not contain all cases in the original sample. Some cases may not be sampled while other cases are sampled several times. You probably have noticed this in Figure 2.5. Sampling with replacement allows us to obtain different bootstrap samples from the original sample, and still have bootstrap samples of the same size as the original sample.

2.1.2 Calculating probabilities with replacement

You may wonder whether it is OK to sample with replacement. The short answer is: Yes it is. We usually calculate probabilities as if we sampled with replacement. Suppose we want to calculate the probability of picking two yellow candies from a population in which 20% of the candies are yellow. The probability of picking two yellow candies is then calculated as .200 * .200: twice the probability of drawing a yellow candy.

In this calculation, we assume that the probability to draw a yellow candy remains the same while we are sampling. The probability of sampling a yellow candy is assumed to be .200 whether we sample the first or the second candy. We act as if the proportion of yellow candies in the population remains the same, namely 20%. This assumption is very convenient because it simplifies the calculation of probabilities.

2.1.3 Calculating probabilities without replacement

However, the number of yellow candies is reduced by one after we have drawn the first yellow candy unless it is immediately replaced by a new yellow candy in the factory. The probability of drawing a second yellow candy should then be less than 20%. If the population is large, the decrease in the probability is too small to be in any way relevant. For instance, if we have a population of one million candies and 20% is yellow, the probability of drawing the first yellow candy is 200,000 / 1,000,000 = .200. The probability of drawing the second yellow candy would be 199,999 / 999,999 = 0.1999992 ; the difference between the two probabilities (0,0000008) is negligible.

So is it OK to sample with replacement? From the point of view of probabilities, it is OK because we usually calculate probabilities as if we sampled with replacement. In practice, however, we never want the same respondent to participate twice in our research because this does not yield new information.

In contrast, when is it *not* OK to sample without replacement as we normally do in research? It is OK to sample without replacement as long as the population is much larger than the sample. If the population is much larger, the probabilities more or less remain the same during the sampling process, so calculating probabilities as if the probabilities do not change is not a problem.

2.1.4 Limitations to bootstrapping

Figure 2.6: How is bootstrapping influenced by sample size?

1. When does the bootstrap sampling distribution (yellow histogram) reflect the true sampling distribution (grey histogram) better: at small or large sample sizes? Play with sample size in Figure 2.6 to check your answer.
2. How does sample size relate to representativeness of the sample? Twenty per cent of the candies in the population are yellow.
3. If you use a very small sample size, it may happen that there is no yellow histogram in the bottom graph. What is the matter if that happens?

We can create a sampling distribution by sampling from our original sample with replacement. It is hardly a miracle that we obtain different samples with different sample statistics if we sample with replacement. Much more miraculous, however, is that this bootstrap distribution resembles the true sampling distribution that we would get if we draw lots of samples directly from the population.

Does this miracle always happen? No, it need not happen. First, the original sample that we have drawn from the population must not be too small. We cannot draw many different samples from a small sample. For this reason, the bootstrap distribution cannot resemble the true sampling distribution, in this situation.

Second, the original sample must be more or less representative of the population. The variables of interest in the sample should be distributed more or less the same as in the population. If this is not the case, the sampling distribution may be biased, giving a distorted view of the true sampling distribution.

A sample is more likely to be representative of the population if the sample is drawn in a truly random fashion and if the sample is larger. But we can never be sure. There always is a chance that we have drawn a sample that does not reflect the population well. This is the main problem with the bootstrap approach to sampling distributions.

2.1.5 Any sample statistic can be bootstrapped

The big advantage of the bootstrap approach (*bootstrapping*), however, is that we can get a sampling distribution for any sample statistic that we are interested in. Every statistic that we can calculate for our original sample can also be calculated for each bootstrap sample. The sampling distribution is just the collection of the sample statistics calculated for all bootstrap samples.

Bootstrapping is more or less the only way to get a sampling distribution for the sample median, for instance, the median weight of candies in a sample bag. We may create sampling distributions for the wildest and weirdest sample statistics, for instance the difference between sample mean and sample median squared. I would not know why you would be interested in the squared difference of sample mean and median, but there are very interesting statistics that we can only get at through bootstrapping. A case in point is the strength of an indirect effect in a mediation model (Chapter 9).

2.2 Bootstrapping in SPSS

2.2.1 Instructions

Figure 2.7: Bootstrapping in SPSS.

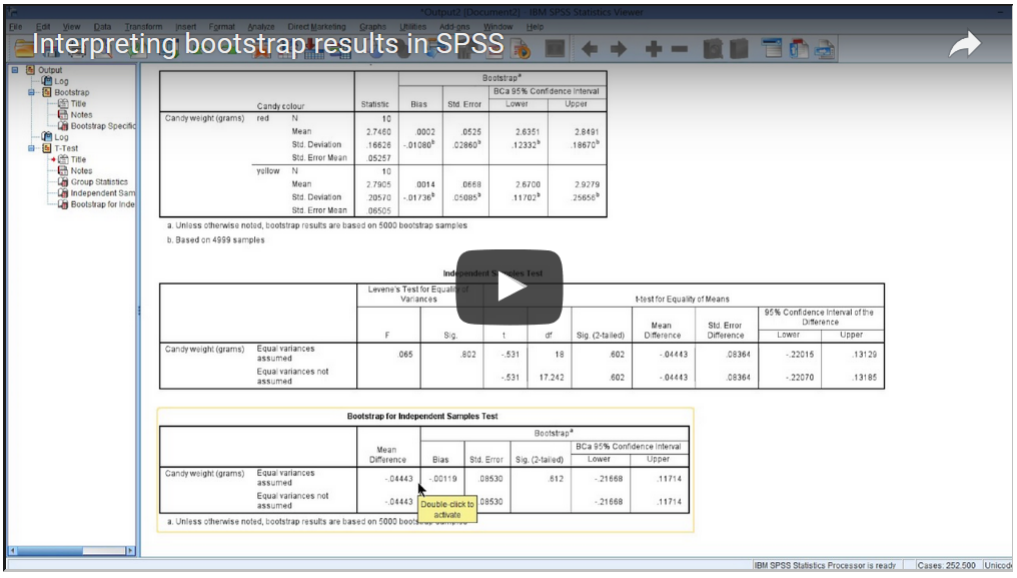


Figure 2.8: Interpreting bootstrap results in SPSS.

In principle, any sample statistic can be bootstrapped. SPSS, however, does not bootstrap all sample statistics. For example, SPSS does not bootstrap the minimum value, maximum value or the range between minimum and maximum value of a variable.

2.2.2 Exercises

1. Download the data set candies.sav and use SPSS to bootstrap the t test on average weight of yellow and red candies (the example above). The test is available in the *Analyze>Compare Means* menu.
2. Use the same data set to bootstrap the median of candy weight. Remember that measures of central tendency can be obtained with the *Frequencies>Statistics* command in the *Analyze>Descriptive Statistics* menu.

2.3 Exact Approaches to the Sampling Distribution

Table 2.2: Number of heads for a toss of three coins.

Outcome	Combination	Probability
0	tail-tail-tail	1/8 = .125
1	tail-tail-head	
1	head-tail-tail	
1	head-tail-tail	3/8 = .375
2	head-head-tail	
2	head-tail-head	
2	tail-head-head	3/8 = .375
3	head-head-head	1/8 = .125
Total	8	1.000

1. Explain the meaning of the entries in the column **Combinations** and how they relate to the entries in the **Outcomes** columns.
2. Explain how the combinations relate to the probabilities.

A second approach to constructing a sampling distribution has implicitly been demonstrated in the preceding section on bootstrapping (Section 2.1) and the section on probability distributions (Section 1.2.3). In these sections, we calculated the true sampling distribution of the proportion of yellow candies in a sample from the probabilities of the colours. If we know or think we know the proportion of yellow candies in the population, we can exactly calculate the probability that a sample of ten candies includes one, two, three, or ten yellow candies. See the section on discrete random variables for details.

The calculated probabilities of all possible sample statistic outcomes give us an exact approach to the sampling distribution. Note that I use the word *approach* instead of *approximation*

here because the obtained sampling distribution is no longer an approximation, that is, more or less similar to the true sampling distribution. No, it is the true sampling distribution itself.

2.3.1 Exact approaches for categorical data

An exact approach lists and counts all possible combinations. This can only be done if we work with discrete or categorical variables. For an unlimited number of categories, we cannot list all possible combinations.

A proportion is based on frequencies and frequencies are discrete (integer values), so we can use an exact approach to create a sampling distribution for one proportion such as the proportion of yellow candies in the example above. The exact approach uses the binomial probability formula to calculate probabilities. Consult the internet if you want to know this formula; we are not going to use it here.

Exact approaches are also available for the association between two categorical (nominal or ordinal) variables in a contingency table: Do some combinations of values for the two variables occur relatively frequently? For example, are yellow candies more often sticky than red candies? If candies are either sticky or not sticky and they have one out of a limited set of colours, we have two categorical variables. We can create an exact probability distribution for the combination of colour and stickiness. The *Fisher-exact test* is an example of an exact approach to the sampling distribution of the association between two categorical variables.

2.3.2 Computer-intensive

The exact approach can be applied to discrete variables because they have a limited number of values. Discrete variables are usually measured at the nominal or ordinal level. If the number of categories becomes large, a lot of computing time can be needed to calculate the probabilities of all possible sample statistic outcomes. Exact approaches are said to be *computer-intensive*.

It is usually wise to set a limit to the time you allow your computer to work on an exact sampling distribution because otherwise the problem may keep your computer occupied for hours or days.

2.4 Exact Approaches in SPSS

2.4.1 Instructions

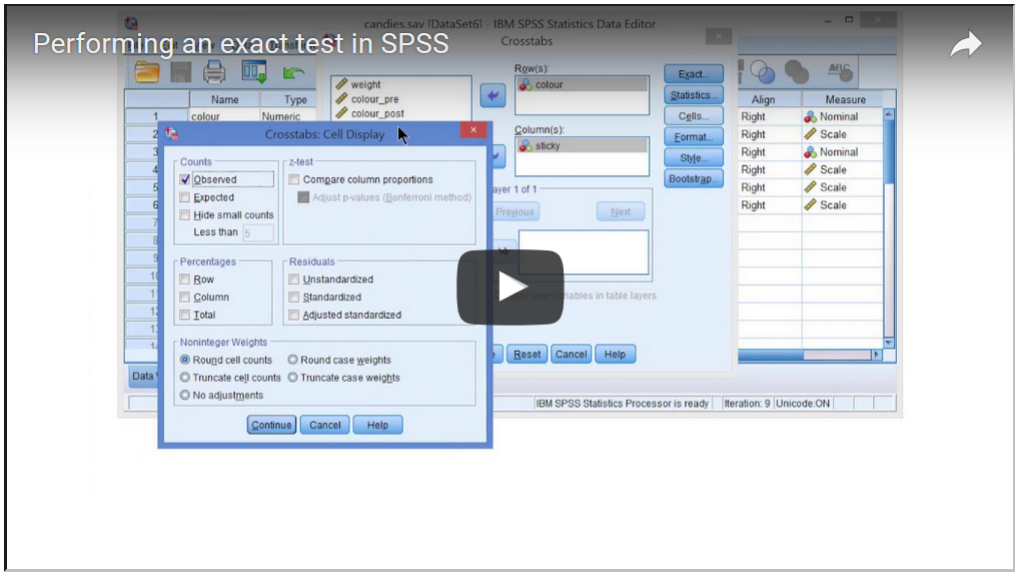


Figure 2.9: Performing an exact test in SPSS.

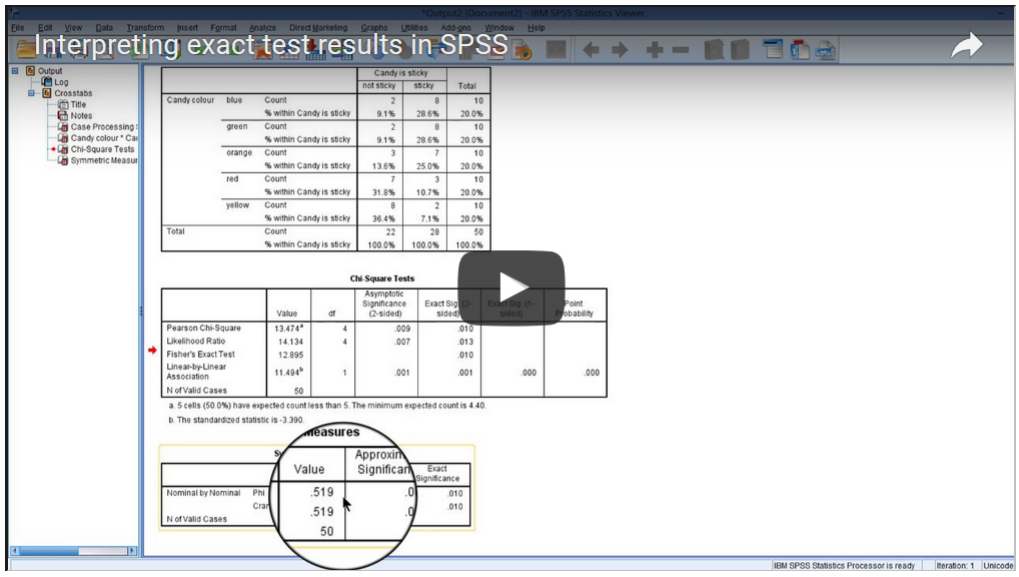


Figure 2.10: Interpreting exact test results in SPSS.

2.4.2 Exercises

1. Download the data set candies.sav and use SPSS to apply a Fisher-exact test to the association between candy colour and candy stickiness.
2. With the same data, apply a Fisher-exact test to the association between candy colour and candy spottiness.

2.5 Theoretical Approximations of the Sampling Distribution

Because bootstrapping and exact approaches to the sampling distribution require quite a lot of computing power, these methods were not practical in the not so very distant pre-computer age. In those days, mathematicians and statisticians discovered that many sampling distributions look a lot like known mathematical functions. For example, the sampling distribution of the sample mean can be quite similar to the well-known bell-shape of the *normal distribution* or the closely related *(Student) t distribution*. The mathematical functions are called *theoretical probability distributions*.

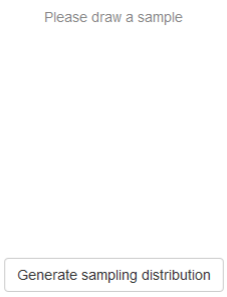


Figure 2.11: Normal function as theoretical approximation of a sampling distribution.

1. In Figure 2.11, generate a sampling distribution of sample means (the computer draws many random samples from a candy population). Check if the normal function (curve) is a good approximation of the sampling distribution.
2. While checking the distribution, pay special attention to the tails because these are used for significance tests (see Chapter 4). The red and green bars represent the 2.5 per cent samples with minimum or maximum average weight. The vertical lines mark the outer 2.5 per cent according to the normal function.
3. Generate some new sampling distributions to see if the normal function always yields a good approximation. What changes in the distribution: the mean, the standard deviation, or both?

The normal distribution is a mathematical function linking continuous scores, e.g., a sample statistic such as the average weight in the sample, to p values, that is, to the probability

of finding at least, or at most, this score. Such a function is called a *probability density function*, Section 1.3.

We like to use a theoretical probability distribution as an approximation of the sampling distribution because it is convenient. The computer can calculate probabilities from the mathematical function very quickly. We also like theoretical probability distributions because they usually offer plausible argumentation about chance and probabilities.

2.5.1 Reasons for a bell-shaped probability distribution

The bell shape of the normal distribution, for instance, makes sense. Our sample of candies is just as likely to be too heavy, as it is too light, so the sampling distribution of the sample mean should be symmetrical. A normal distribution is symmetrical.

In addition, it is more likely that our sample bag has an average weight that is near the true average candy weight in the population than an average weight that is much heavier or much lighter than the true average. Bags with on average extremely heavy or extremely light candies may occur, but they are extremely rare (we are very lucky or very unlucky). From these intuitions we would expect a bell shape for the sampling distribution.

From this argumentation, we conclude that the normal distribution is a reasonable model for the probability distribution of sample means. Actually, it has been proven that the normal distribution exactly represents the sampling distribution in particular cases, for instance the sampling distribution of the mean of a large sample.

As a model, the theoretical probability distribution may actually give a better approximation of the sampling distribution than a sampling distribution created by drawing many samples from the population (as you have done in Figure 2.11), or from the initial sample as in bootstrapping. Sampling is always subject to chance, so we may have accidentally drawn samples that do not cover the sampling distribution well.

2.5.2 Conditions for the use of theoretical probability distributions

Theoretical probability distributions, then, are plausible models for sampling distributions. They are known or likely to have the same shape as the true sampling distributions under particular circumstances or conditions.

If we use a theoretical probability distribution, we must assume that the conditions for its use are met. We have to check the conditions and decide whether they are close enough to the ideal conditions. *Close enough* is of course a matter of judgement. In practice, rules of thumb have been developed to decide if the theoretical probability distribution can be used.

Figure 2.12 shows an example in which the normal distribution is a good approximation for the sampling distribution of a proportion in some situations, but not in all situations.

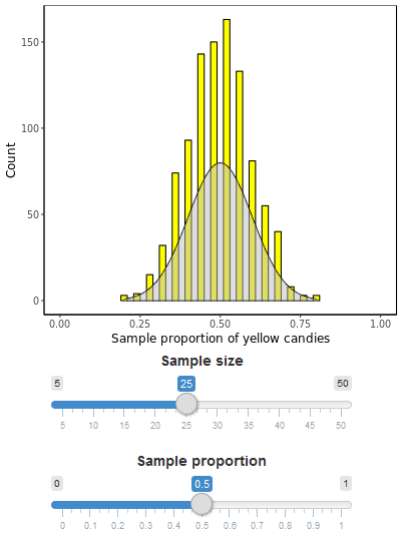


Figure 2.12: How does the shape of the distribution of sample proportions change with sample size and proportion value?

1. How do you expect that sample size affects the shape of the sampling distribution? State your expectation and then check it in the interactive content by changing sample size.

2. How do you expect that the value of the proportion in the population affects the shape of the sampling distribution? State your expectation and then check it in the interactive content by changing the population proportion.

Do theoretical probability distributions fit the true sampling distribution? As you may have noticed from the interactive content, this is not always the case. In general, theoretical probability distributions fit sampling distributions better if the sample is larger. In addition, the value of the parameter may be relevant to the fit of the theoretical probability distribution. The sampling distribution of a sample proportion is more symmetrical, like the normal distribution, if the proportion in the population is nearer .5.

This illustrates that we often have several conditions for a theoretical probability distribution to fit the sampling distribution that we should evaluate together. In the example of proportions, a large sample is less important if the true proportion is closer to .5 but it is more important for true proportions that are more distant from .5.

The rule of thumb for using the normal distribution as the sampling distribution of a sample proportion combines the two aspects by multiplying them and requiring the resulting product to be larger than five. If the probability of drawing a yellow candy is .2 and our sample size is 30, the product is .2 * 30 = 6, which is larger than five. So we may use the normal distribution as approximation of the sampling distribution.

Note that this rule of thumb uses one minus the probability, if the probability is larger

Table 2.3: Rules of thumb for using theoretical probability distributions.

Distribution	Sample statistic	Minimum sample size	Other requirements
Binomial distribution	proportion	-	-
(Standard) normal distribution	proportion	>= 5 divided by test proportion (<= .5)	-
(Standard) normal distribution	one or two means	> 100	OR variable is normally distributed in the population and population standard deviation is known (for each group)
t distribution	one or two means	> 30	OR variable is normally distributed in each group's population
t distribution	(Pearson) correlation coefficient	-	variables are normally distributed in the population
t distribution	(Spearman) rank correlation coefficient	> 30	-
t distribution	regression coefficient	20+ per predictor variable	See Chapter 8.
F distribution	3+ means	all groups are more or less of equal size	OR all groups have the same population variance
F distribution	two variances	-	no conditions for Levene's F test
chi-squared distribution	row or cell frequencies	expected frequency >= 1 and 80% >= 5	contingency table: 3+ rows or 3+ columns

than .5. In other words, it uses the smaller of two probabilities: the probability that an observation has the characteristic and the probability that it has not. For example, if we want to test the probability of drawing a candy that is not yellow, the probability is .8 and we use 1 - 0.8 = 0.2, which is then multiplied by the sample size.

Apart from the normal distribution, there are several other theoretical probability distributions. We have the *binomial distribution* for a proportion, the *t distribution* for one or two sample means, regression coefficients, and correlation coefficients, the *F distribution* for comparison of variances and comparing means for three or more groups (analysis of variance, ANOVA), and the *chi-squared distribution* for frequency tables and contingency tables.

For most of these theoretical probability distributions, sample size is important. The larger the sample, the better. There are additional conditions that must be satisfied such as the distribution of the variable in the population. The rules of thumb are summarized in Table 2.3. Bootstrapping and exact tests can be used if conditions for theoretical probability distributions have not been met. Special conditions apply to regression analysis (see Chapter 8, Section 8.1.5).

2.5.3 Checking conditions

Rules of thumb about sample size are easy to check once we have collected our sample. By contrast, rules of thumb that concern the scores in the population cannot be easily checked, because we do not have information on the population. If we already know what we want to know about the population, why would we draw a sample and do the research in the first place?

We can only use the data in our sample to make an educated guess about the distribution of a variable in the population. For example, if the scores in our sample are clearly normally distributed, it is plausible that the scores in the population are normally distributed.

In this situation, we do not *know* that the population distribution is normal but we *assume* it is. If the sample distribution is clearly not normally distributed, we had better not

assume that the population is normally distributed. In short, we sometimes have to make assumptions when we decide on using a theoretical probability distribution.

We could use a histogram of the scores in our sample with a normal distribution curve added to evaluate whether a normal distribution applies. Sometimes, we have statistical tests to draw inferences about the population from a sample that we can use to check the conditions. We discuss these tests in a later chapter.

2.5.4 More complicated sample statistics: differences

Up to this point, we have focused on rather simple sample statistics such as the proportion of yellow candies or the average weight of candies in a sample. Table 2.3, however, contains more complicated sample statistics.

If we compare two groups, for instance, the average weight of yellow and red candies, the sample statistic for which we want to have a sampling distribution must take into account both the average weight of yellow candies and the average weight of red candies. The sample statistic that we are interested in is the difference between the averages of the two samples.

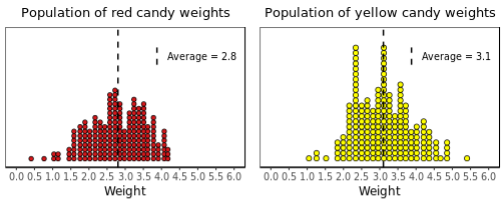


Figure 2.13: How do we obtain a sampling distribution for the mean difference of two independent samples?

1. Click on the button once. Why are these samples called independent?
2. Click on the button several times. What exactly is the sample statistic in the histogram at the bottom of the app?

3. Click on the button to draw one thousand samples once or more often. Does the sampling distribution look familiar to you?

4. What, do you expect, is the mean of the sampling distribution?

If we draw a sample from both the yellow and the red candies in the population, we may calculate the means for both samples and the difference between the two means. For example, the average weight of yellow candies in the sample bag is 2.76 gram and the average for red candies is 2.82 gram. For this pair of samples, the statistic of interest is 2.76 - 2.82 = -0.06, that is, the difference in average weight. If we repeat this many, many times and collect all differences between means in a distribution, we obtain the sampling distribution that we need.

The sampling distribution of the difference between two means is similar to a t-distribution, so we may use the latter to approximate the former. Of course, the conditions for using the t distribution must be met.

It is important to note that we do not create separate sampling distributions for the average weight of yellow candies and for the average weight of red candies and then look at the difference between the two sampling distributions. Instead, we create *one sampling distribution for the statistic of interest*, namely the difference between means. We cannot combine different sampling distributions into a new sampling distribution. We will see the importance of this when we discuss mediation (Chapter 9).

2.5.5 Independent samples

If we compare two means, there are two fundamentally different situations that are sometimes difficult to distinguish. When comparing the average weight of yellow candies to the average weight of red candies, we are comparing two samples that are *statistically independent* (see Figure 2.13), which means that we could have drawn the samples separately.

In principle, we could distinguish between a population of yellow candies and a population of red candies, and sample yellow candies from the first population and separately sample red candies from the other population. Whether we sampled the colours separately or not does not matter. The fact that we could have done so implies that the sample of red candies is not affected by the sample of yellow candies or the other way around. The samples are statistically independent.

This is important for the way in which probabilities are calculated. Just think of the simple example of flipping two coins. The probability of having heads twice in a row is .5 times .5 that is .25 if the coins are unbiased and the result of the second coin does not depend on the result of the first coin. The second flip is not affected by the first flip.

Imagine that a magnetic field is activated if the first coin lands with heads up and that this magnetic field increases the odds that the second coin will also be heads. Now, the second toss is not independent of the first toss and the probability of getting heads twice is larger than .25.

2.5.6 Dependent samples

The example of a manipulated second toss is applicable to repeated measurements. If we want to know how quickly the yellow colour fades when yellow candies are exposed to sun light, we may draw a sample of yellow candies once and measure the colourfulness of each candy at least twice: at the start and after some time interval. Subsequently, we compare the average colourfulness of the second set of measurements to the average in the first set of measurements.

Figure 2.14: Dependent samples.

1. In Figure 2.14, use the **Sample 1 case** button repeatedly to draw a sample of five observations. What is the precise meaning of the numbers on the horizontal axis in the sample histogram?
2. Why is the sample called dependent or paired?
3. Draw 1,000 samples to obtain a sampling distribution. What is the precise meaning of the numbers on the horizontal axis in the histogram of the sampling distribution?

In this example, we are comparing two means, just like the yellow versus red candy weight example, but now the samples for both measurements are the same. It is impossible to draw the sample for the second measurement independently from the sample for the first measurement if we want to compare repeated measurements. Here, the second sample is fixed once we have drawn the first sample. The samples are *statistically dependent*; they create *paired samples*. Even if the second sample depends only partly upon the first sample, the samples are statistically dependent.

With dependent samples, probabilities have to be calculated in a different way, so we need

a special sampling distribution. In the interactive content above, you may have noticed a relatively simple solution for two repeated measurements. We just calculate the difference between the two measurements for each candy in the sample and use the mean of this new difference variable as the sample statistic that we are interested in. The t-distribution, again, offers a good approximation of the sampling distribution of dependent samples if the samples are not too small.

For other applications, the actual sampling distributions can become quite complicated but we need not worry about that. If we choose the right technique, our statistical software will take care of this. Of course, we should check whether the conditions are met for approximating the sampling distribution with a theoretical probability distribution.

2.6 SPSS and Theoretical Approximation of the Sampling Distribution

By default, SPSS uses a theoretical probability distribution to approximate the sampling distribution. It chooses the correct theoretical distribution but you yourself should check if the conditions for using this distribution are met. Is the sample size large enough or is it plausible that the variable is normally distributed in the population?

In one case, SPSS automatically selects an exact approach if the conditions for a theoretical approximation are not met: If you do a chi-squared test to a contingency table in SPSS, SPSS will automatically apply Fisher's exact test if the table has two rows and two columns. In all other cases, you have to select a bootstrapping or exact approach yourself if the conditions for a theoretical approximation are not met.

We are not going to practice with theoretical approximations in SPSS, now. Because theoretical approximation is the default approach in SPSS, we will encounter it in the exercises in later chapters.

2.7 Take-Home Points

- We may create an exact sampling distribution or simulate a bootstrap sampling distribution in simple situations or if we have a lot of computing power.
- For a bootstrap sampling distribution, we need about 5,000 bootstrap samples from our original sample.
- We can often approximate the sampling distribution of a sample statistic with a known theoretical probability distribution.
- Approximations only work well under conditions, which we have to check.
- Conditions usually involve the size of the sample, sample type (independent vs. dependent/paired), and the shape or variance of the population distribution.

- Samples are independent if, in principle, we can draw a sample for one group without taking into account the sample for another group of cases. Otherwise, the samples are dependent or paired.

Chapter 3

Estimating a Parameter: Which Population Values Are Plausible?

Key concepts: point estimate, interval estimate, confidence (level), precision, standard error, critical value, degrees of freedom, confidence interval, uncertainty.

Summary

In this chapter, we set out to make educated guesses of a population value (parameter, often called "the true value") based on our sample. This type of guessing is called *estimation*. Our first guess will be a single value for the population value. We merely guess that the population value is equal to the value of the sample statistic. This guess is the most precise guess that we can make, but it is most likely to be wrong.

Our second guess uses the sampling distribution to make a statement about the approximate population value. More precisely, we calculate an interval for which we are confident that it includes the population value. The wider the interval, the more confident we are that it contains the true population value but, at the same time, the less precise our guess.

Test your intuition and understanding

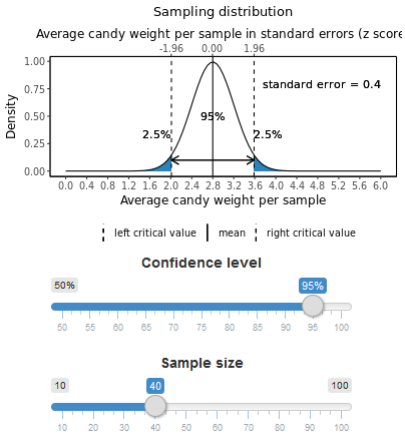


Figure 3.1: Point and interval estimates, confidence intervals.

Figure 3.1 shows the sampling distribution of average candy weight in a sample bag, which is a normal distribution.

1. What is most likely estimate for average candy weight in the population?
2. The percentage in between the two vertical lines can be interpreted as a probability. A probability of what?
3. The double arrow represents an interval of sample means, in this example, average candy weight. What happens if you change the confidence level? Explain why this makes sense.
4. What happens to the graph if you change sample size?
5. What happens to the standard error if you change sample size? How are sample size and standard error linked? What characteristic of the sampling distribution is expressed by the standard error?
6. The values of the interval limits—average candy weights in this example—on the scale in standard errors are called critical values. What happens to the critical values if you change sample size?
7. What happens to the critical values if you change the confidence level?
8. If 2.8 is average candy weight in the sample but not necessarily true average candy weight in the population, the interval marked by the arrows is called a *confidence interval*. In this example, a confidence interval for what? And what is the point estimate?

On first reading, you may not know all answers. That is OK. Just try again after you have studied this chapter.

3.1 Point Estimate

If we have to name one value for the population value, our best guess is the value of the sample statistic. For example, if 18% of the candies in our sample bag are yellow, our best guess of the proportion of yellow candies in the population of all candies from which this bag was filled, is .18. What other number can we give if we only have our sample? This type of guess is called a *point estimate* and we use it a lot.

The sample statistic is the best estimate of the population value only if the sample statistic is an unbiased estimator of the population value. As we have learned in Section 1.2.5, the true population value is equal to the mean of the sampling distribution for an unbiased estimator. The mean of the sampling distribution is the expected value for the sample.

In other words, an unbiased estimator neither systematically overestimates the population value, nor does it systematically underestimate the population value. With an unbiased estimator, then, there is no reason to prefer a value higher or lower than the sample value as our estimate of the population value.

Even though the value of the statistic in the sample is our best guess, it is very unlikely that our sample statistic is exactly equal to the population value (parameter). The recurrent theme in our discussion of random samples is that a random sample differs from the population because of chance during the sampling process. The precise population value is highly unlikely to actually appear in our sample.

The sample statistic value is our best point estimate but it is nearly certain to be wrong. It may be slightly or strongly off the mark but it will hardly ever be spot on. For this reason, it is better to estimate a range within which the population value falls. Let us turn to this in the next section.

3.2 Interval Estimate for the Sample Statistic

The sampling distribution of a continuous sample statistic tells us the probability of finding a range of scores for the sample statistic in a random sample. For example, the average weight of candies in a sample bag is a continuous random variable. The sampling distribution tells us the probability of drawing a sample with average candy weight between 2.0 and 3.6 gram. We can use this range as our *interval estimate*.

Remember that the average or expected value of a sampling distribution is equal to the population value if the estimator is unbiased. For example, the mean weight of yellow candies averaged over a large number of samples is equal to the mean weight of yellow candies in the population. For an interval estimate, we now select the sample statistic values that are closest to the average of the sampling distribution.

Between which boundaries are the sample statistic values situated that are closest to the population value? Of course, we have to specify what we mean by "closest". Which part of all samples do we want to include? A popular proportion is 95%, so we want to know the boundary values that include 95% of all samples that are closest to the population value. For example, between which boundaries is the average candy weight situated for 95% of all samples that are closest to the average candy weight in the population?

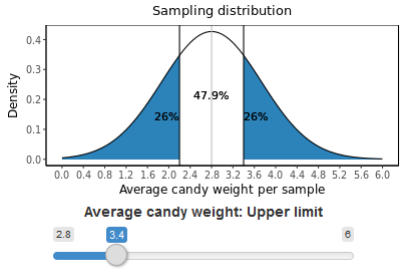


Figure 3.2: Within which interval do we find the sample results that are closest to the population value?

Figure 3.2 shows the sampling distribution of average sample candy weight.

1. What is the average candy weight in the population of candies?

2. Move the slider until you have found the interval containing 95% of all samples that are closest to the (true) population value. What are the upper and lower limits of the interval that contains these samples?

Say, for instance, that 95% of all possible samples in the middle of the sampling distribution have an average candy weight ranging from 1.6 to 4.0 gram. The proportion .95 can be interpreted as a probability. Our sampling distribution tells us that we have 95% probability that the average weight of yellow candies lies between 1.6 and 4.0 gram in a random sample that we draw from this population.

We now have boundary values, that is, a range of sample statistic values, and a probability of drawing a sample with a statistic falling within this range. The probability shows our *confidence* in the estimate. It is called the *confidence level* of an interval estimate.

3.3 Precision, Standard Error, and Sample Size

The width of the estimated interval represents the *precision* of our estimate. The wider the interval, the less precise our estimate. With a less precise interval estimate, we we will have to reckon with a wider variety of outcomes in our sample.

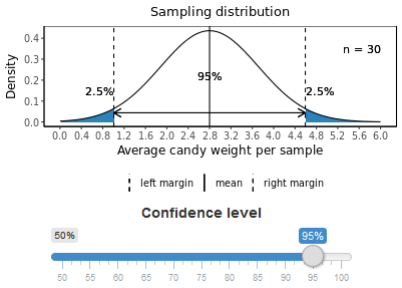


Figure 3.3: How does the confidence level affect the precision of an interval estimate?

1. How, do you think, does the precision (width) of the interval estimate (represented by the double-sided arrow) change if you change the confidence level? First write down what you expect, and why you expect that. Then check what happens if you change the confidence level slider in Figure 3.3.

2. What happens if we want to be 100% certain that our interval contains the true population value?

If we want to predict something, however, we value precision. We rather conclude that the average weight of candies in the next sample we draw lies between 2.0 and 3.6 gram than between 1.6 and 4.0 gram. If we would be satisfied with a very imprecise estimate, we need not do any research at all. With relatively little knowledge about the candies that we are investigating, we could straightaway predict that the average candy weight is between zero and ten gram. The goal of our research is to find a more precise estimation.

There are several ways to increase the precision of our interval estimate, that is, to obtain a narrower interval for our estimate. The easiest and least useful way is to decrease the probability that our estimate is correct. If we lower the probability that we are right, we can discard a large number of other possible sample statistic outcomes and focus on a narrower range of sample outcomes around the true population value.

This method is not useful because we sacrifice our confidence that the range includes the outcome in the sample that we are going to draw. What is the use of a more precise estimate if we are less certain that it predicts correctly? Therefore, we usually do not change the confidence level and leave it at 95% or thereabouts (90%, 99%). We think it important to be quite sure that our prediction will be right.

3.3.1 Sample size

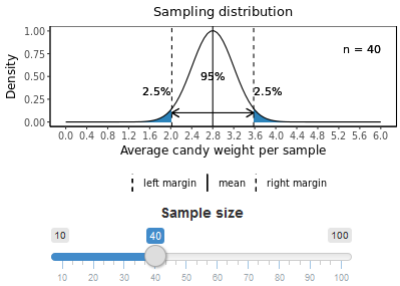


Figure 3.4: How does sample size affect the precision of an interval estimate?

Figure 3.4 shows a sampling distribution of average candy weight in candy sample bags. The horizontal arrow indicates the precision of the interval estimate.

1. How does the precision of the interval estimate change if you change the size of the sample? First write down what you expect, and why you expect that. Then, check what happens if you change the sample size slider.

2. How does the shape of the sampling distribution change if you change sample size? Explain what this means for the values of the sample statistic.

A less practical but very useful method of narrowing the interval estimate is increasing sample size. As you may have noticed while playing with Figure 3.4, a larger sample yields a narrower, that is, more precise interval. You may have expected intuitively that larger samples give more precise estimates because they offer more information. This intuition is correct.

In a larger sample, an observation above the mean is more likely to be compensated by an observation below the mean. Just because there are more observations, it is less likely that we sample relatively high scores but no or considerably fewer scores that are relatively low.

In other words, the larger the sample, the more the distribution of scores for a variable in the sample will resemble the distribution of scores for this variable in the population. As a consequence, a sample statistic value will be closer to the population value for this statistic.

Larger samples resemble the population more closely, and therefore large samples drawn from the same population are also closer to one another. The result is that the sample statistic values in the sampling distribution are less varied and more similar. They are more concentrated around the true population value, which is the average of the sampling distribution. The sampling distribution is more peaked, so the middle 95% of all sample statistic values are closer to the centre.

3.3.2 Standard error

The concentration of sample statistic values, such as average candy weight in a sample bag, is expressed by the standard deviation of the sampling distribution. Hitherto, we have only paid attention to the centre of the sampling distribution, its mean, because it is the expected value in a sample and it is equal to the population value if the estimator is unbiased.

Now, we start looking at the standard deviation of the sampling distribution as well, because it tells us how precise our interval estimate is going to be. The sampling distribution's standard deviation is so important that it has received a special name: the *standard error*.

Figure 3.5: The standard error: How wrong are point estimates?

1. Draw a single sample by pressing the button *Take single sample* in Figure 3.5. Explain why we can interpret the red arrow in the sample plot as error.
2. Use the button **Take single sample** several times. What is the meaning of the double-sided red arrow that appears in the sampling distribution?
3. Use the button **Take 100 samples** once or repeatedly. What happens to the length of the double-sided red arrow in the sampling distribution?

The word *error* reminds us that the standard error tells us the size of the error that we are likely to make (on average under many repetitions) if we use the value of the sample statistic as a point estimate for the population value.

Let us assume, for instance, that the standard error of the average weight of candies in a sample bag is 0.6. Loosely stated, this means that the average difference between true average candy weight and average candy weight in a sample is 0.6 if we draw a very large number of samples from the same population.

By the way, the standard deviation does not give us the ordinary average difference but it gives us the square root of the average of squared differences. But this detail is irrelevant to

how we interpret the standard error.

The smaller the standard error, the more the sample statistic values resemble the true population value, and the more precise our interval estimate with a given confidence level, for instance, 95%. Because we like more precise interval estimates, we prefer small standard errors over high standard errors.

In theory, it is easy to obtain smaller standard errors: just increase sample size. See Figure 3.4: larger samples yield more peaked sampling distributions. In a peaked distribution, values are closer to the mean. In our example, average candy weight in sample bags are closer to the average candy weight in the population. Imagine a horizontal arrow showing the width of the distribution: It becomes smaller for a more peaked distribution, so the standard error is lower.

In practice, however, it is both time-consuming and expensive to draw a very large sample. Usually, we want to settle on the optimal size of the sample, namely a sample that is large enough to have interval estimates at the confidence level and precision that we need but as small as possible to save on time and expenses. We return to this matter in Chapter 5.

3.4 Critical Values

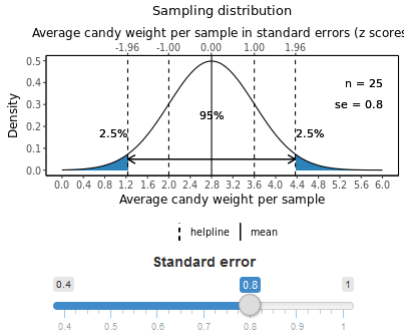


Figure 3.6: How do critical values relate to the standard error in a normal distribution?

Figure 3.6 shows the sampling distribution of average candy weight per sample bag. It contains two horizontal axes, one with average candy weight in grams (bottom) and one with average candy weight in standard errors, also called z scores (top).

1. How do the two horizontal axes tell you the size of the standard error in grams?
2. How do you expect the location of the vertical lines on the two horizontal axes to change if you change the size of the standard error? Check your expectation by using the slider.

In Figure 3.6, we approximate the sampling distribution with a theoretical probability distribution, namely the normal distribution. The theoretical probability distribution links

probabilities (areas under the curve) to sample statistic outcome values (scores on the horizontal axis). For example, we have 2.5% probability to draw a sample bag with average candy weight below 1.2 gram or 2.5% probability to draw a sample bag with average candy weight over 4.4 gram.

3.4.1 Standardization and *z* scores

The average candy weights that are associated with 2.5% and 97.5% probabilities in Figure 3.6 depend on the sample that we have drawn. As you will have noticed while playing with Figure 3.4, changing the size of the sample also changes the avergae candy weights that mark the 2.5% and 97.5% probabilities.

We can simplify the situation if we *standardize* the sampling distribution: Subtract the average of the sampling distribution from each sample mean in this distribution, and divide the result by the standard error. Thus, we transform the sampling distribution into a distribution of standardized scores. The mean of the new standardized variable is always zero.

If we use the normal distribution for standardized scores, which is called the *standard-normal distribution* or *z distribution*, there is a single z value that marks the boundary between the top 2.5% and the bottom 97.5% of any sample. This z value is 1.96. If we combine this value with -1.96, separating the bottom 2.5% of all samples from the rest, we obtain an interval [-1.96, 1.96] containing 95% of all samples that are closest to the mean of the sampling distribution. This is part of the *empirical rule* for the normal distribution.

In a standard-normal or z distribution, 1.96 is called a *critical value*. Together wih its negative (-1.96), it separates the 95% sample statistic outcomes that are closest to the parameter, hence that are most likely to appear, from the 5% that are furthest away and least likely to appear. There are also critical z values for other probabilities, for instance, 1.64 for the middle 90% of all samples and 2.58 for the middle 99%.

3.4.2 Interval estimates from critical values and standard errors

Critical values in a theoretical probability distribution tell us the boundaries, or range, of the interval estimate expressed in standard errors. In a normal distribution, 95% of all sample means are situated no more than 1.96 standard errors from the population mean.

If the standard error is 0.5 and the population mean is 2.8 gram, we have 95% probability that the mean candy weight in a sample that we draw from this population lies between 1.82 gram (this is 1.96 times 0.5 subtracted from 2.8) and 3.78 gram.

Critical values make it easy to calculate an interval estimate if we know the standard error. Just take the population value and add the critical value times the standard error to obtain the upper limit of the interval estimate. Subtract the critical value times the standard error from the population value to obtain the lower limit.

Normal distributions make life easier for us, because there is a fixed critical value for each probability, such as 1.96 for 95% probability, which is well-worth memorizing.

3.4.3 Degrees of freedom (*df*)

For other theoretical probability distributions, the situation is slightly more complicated because we have different critical values for the same confidence level. Small samples usually require higher critical values than large samples. More generally, critical values depend on the *degrees of freedom* in the sample.

We need not be concerned with the exact meaning of degrees of freedom, or how the degrees of freedom are calculated for a sample, if we want to use a theoretical probability distribution. Our statistical software takes care of this for us. We must, however, report the degrees of freedom in accordance with the APA6 standard.

3.5 Confidence Interval for a Parameter

Working through the preceding sections, it may have occurred to you that it is all very well to be able to estimate the value of a statistic in a new sample with a particular precision and probability, but that this is not what we are primarily interested in. Instead, we want to estimate the value of the statistic in the population.

For example, we don't care much about the average weight of candies in our sample bag or in the next sample bag that we may buy. We want to say something about the average weight of candies in the population. How can we do this?

In addition, you may have realized that, if we know the sampling distribution, we also know the precise population value, for instance, average candy weight. After all, the average of the sampling distribution is equal to the population mean for an unbiased estimator. In the preceding paragraphs, we acted as if we knew the sampling distribution. If we know the sampling distribution, and it then follows that we also know the population value, why would we even care about estimating an interval?

Our problem is this: We want to estimate a population value using probabilities. For probabilities we need the sampling distribution but for the sampling distribution, we must know the population. A vicious circle.

In the exact approach to the sampling distribution of the proportion of yellow candies in a sample bag, for instance, we must know the proportion of yellow candies in the population. If we know the population proportion, we can exactly calculate the probability of getting a sample bag with a particular proportion of yellow candies. But we don't know the population proportion of yellow candies; we want to estimate it.

A theoretical probability distribution can only be used as an approximation of a sampling distribution if we know some characteristics of the population. We know that the sampling distribution of sample means always has the bell shape of a normal (z) distribution or

t distribution. However, knowing the shape is not sufficient for using the theoretical distribution as an approximation of the sampling distribution.

We must also know the population mean because it specifies where the centre of the sampling distribution is located. So, we must know the population mean to use a theoretical probability distribution to estimate the population mean. This sounds like a problem that only Baron von Münchhausen can solve. How can we drag ourselves by the hair out of this swamp?

By the way, we also need the standard error to know how peaked or flat the bell shape is. The standard error can usually be estimated from the data in our sample. But let us not worry about how the standard error is being estimated and focus on estimating the population mean now.

3.5.1 Imaginary population values

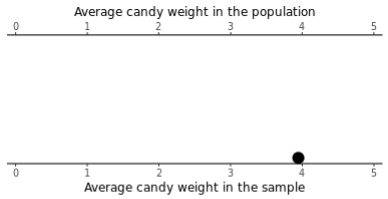


Figure 3.7: For which population means is our sample mean plausible?

Figure 3.7 shows average candy weight in a random sample (lower scale). Click somewhere under the top axis to select a possible value for the population mean. The app will then display the interval of most plausible sample means (green if it contains the actual sample means, red otherwise) and the actual sample mean's z value if this would have been the true population value.

1. Click repeatedly on Figure 3.7 to find the highest and lowest value of the population mean for which the sample mean is in the interval of sample means that have 95% probability to occur.
2. How does the z value of the sample mean help you to minimize the number of clicks you need?
3. How does the depicted interval estimate help you to minimize the number of clicks you need?
4. What is the most efficient strategy (minimum number of clicks) to determine the lower and upper limits of the population means for which the sample mean is among the 95% most likely samples? Explain why this is the most efficient strategy.

How do we solve the Münchhausen problem that we must know the population mean to estimate the population mean? The solution is that we select a lot of imaginary population means. For each imaginary population mean, we calculate the interval within which the sample mean is expected to fall if this imaginary mean would be the true population mean. We use a fixed confidence level, usually a probability of 95 per cent.

As a next step, we check if the mean of the sample that we have actually drawn falls within this interval. If it does, we conclude that this (imaginary) population mean is not at odds with the sample that we have drawn. In contrast, if our sample mean falls outside the interval, we conclude that this population mean is not plausible because our sample is too unlikely to be drawn from a population with this mean.

In this way, we can find all population means that are *consistent* with our sample. If the true population mean is any of these imaginary means, we are sufficiently likely (95% probability) to draw a sample with our actual sample mean.

While playing with Figure 3.7, you may have noticed the z values of the sample mean for the lowest and highest population means for which the sample mean is still within the interval. When you hit the lower bound of the population means, the sample mean has a z value of about 1.96 while it has a z value of about -1.96 for the highest population mean in the range.

It is not a coincidence that we find the critical values of the standard-normal distribution when we reach the minimum and maximum population means that are plausible. We are using the standard-normal distribution to approximate the sampling distribution of the sample mean. The critical z value 1.96 marks the upper limit of the interval containing 95% of all samples with means closest to the population mean and -1.96 marks the lower limit. A distance of 1.96 standard errors, then, is the maximum distance between a population mean and a sample mean that belongs to the 95% sample means closest to the population mean.

As a consequence, we could simply have calculated the range of plausible population values by adding and subtracting 1.96 standard errors from the sample mean. This can be illustrated with an example: If the average candy weight in our sample is 2.8 gram and the standard error is 0.5, the lower and upper boundary for plausible population means are 1.82 gram (this is 2.8 minus 1.96 times 0.5) and 3.78 gram (2.8 plus 1.96 times 0.5).

Haven't we seen this calculation before? Yes we did, in Section 3.4.2, where we estimated the interval for sample means. We now simply reverse the calculation, using the sample mean to estimate an interval of plausible population means instead of the other way around.

Jerzy Neyman introduced the concept of a confidence interval in 1937:

"In what follows, we shall consider in full detail the problem of estimation by interval. We shall show that it can be solved entirely on the ground of the theory of probability as adopted in this paper, without appealing to any new principles or measures of uncertainty in our judgements". (Jerzy Neyman, 1937: 347)

[htbp] 

Figure 3.8: Jerzy Neyman

3.5.2 Confidence interval

The upper and lower bounds for the population mean or, more generally, the parameter that we want to estimate, yield an interval for the parameter. We use this as the interval estimate of the parameter.

This interval is linked to a probability, for instance, 95%. However, it is very important that we understand that this is NOT the probability that the parameter has a particular value, or that it falls within the interval. The parameter is *not* a random variable because it is not affected by the random sample that we draw. In our example, it will be clear that the sample that we draw does not and cannot change the average weight of all candies.

The parameter has one value, which is either within or outside the interval that we have constructed. We just don't know. But we do know that our sample is more likely for population values within the interval.

We use the term *confidence* instead of probability when we use this interval to estimate a parameter. We say that we are 95% confident that the parameter falls within the interval. The interval is called a *confidence interval* and we usually add the confidence level, for instance, the 95% confidence interval (abbreviated: 95%CI) of the average weight of candies in the population ranges from 2.4 to 3.2 gram. An average candy weight between 2.4 and 3.2 gram is plausible given the sample that we have drawn. In our reports, we say that:

> We are 95% confident that the average candy weight in the population is between 2.4 and 3.2 gram.

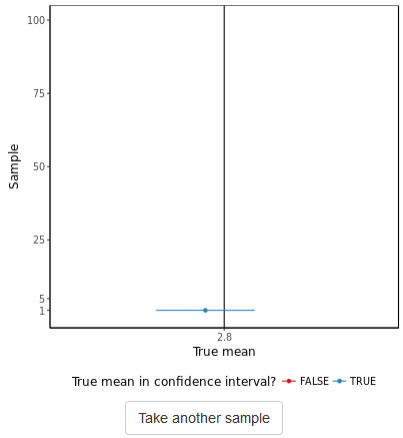


Figure 3.9: How often does a confidence interval include the true population value?

Figure 3.9 shows a 95% confidence interval for average candy weight in the population based on a sample of candies. The vertical line indicates the true average candy weight in the population.

1. Does the (first) confidence interval include the true average candy weight in the population?
2. What does the dot in the middle of the confidence interval represent?
3. If you would draw a hundred random samples from the same population and calculate the 95% confidence interval for the mean of each sample, how many confidence intervals do you expect to contain the true population mean? Press the **New Sample** button until there are one hundred confidence intervals. Does your expectation come true? If not, why not?

The more precise meaning of a confidence interval is rather complicated. If we draw a very large number of samples from the same population, 95% of the sample means would differ less from the population mean than the critical value times the standard error. This is just the definition of critical value.

Because the critical value times the standard error also defines the width of the confidence interval, we can reverse the statement. The population mean would be within the 95% confidence interval of 95% of all sample means. In other words, if we construct the 95% confidence interval for each sample mean, 95% of all samples will have confidence intervals that contain the true population mean.

Our confidence interval is a random variable because it depends on the sample that we draw. After all, we construct the interval around the sample statistic outcome, for instance, average candy weight in our sample (the point estimate), which may change from sample to sample. So we may say that the confidence level is the *probability that our confidence interval includes the true population value*. But we avoid this interpretation because it is easily misread as the probability that the true population value is in the interval. The latter

reading is wrong from the perspective that the population value is not a random variable, so it does not have a probability.

Unfortunately, we have no clue whether or not our single sample belongs to the 95 per cent of 'lucky' samples with confidence intervals containing the true population value. We can only hope and be confident that this is the case.

3.5.3 Confidence intervals with bootstrapping

If we approximate the sampling distribution with a theoretical probability distribution such as the normal (z) or t distribution, critical values and the standard error are used to calculate the confidence interval (see Section 3.5.1).

There are theoretical probability distributions that do not work with a standard error, such as the F distribution or chi-squared distribution. If we use those distributions to approximate the sampling distribution of a continuous sample statistic, for instance, the quotient of two variances, we must use bootstrapping to obtain a confidence interval.

As you probably remember from Section 2.1, we simulate an entire sampling distribution if we bootstrap a statistic, for instance the median candy weight in a sample bag. This simulated sampling distribution can be used to estimate the standard error, which is by definition the standard deviation of the sampling distribution. This standard error can then be combined with critical values to calculate the confidence interval.

As an alternative, we can just take the values separating the bottom 2.5% and the top 2.5% of all samples in the bootstrapped sampling distribution as the lower and upper limits of the 95% confidence interval. This is known as the percentile approach.

It is also possible to construct the entire sampling distribution in exact approaches to the sampling distribution. Both the standard error and percentiles can be used to create confidence intervals. This can be very demanding in terms of computer time, so exact approaches to the sampling distribution usually only report p values, not confidence intervals.

3.6 Confidence Intervals in SPSS

3.6.1 Instruction

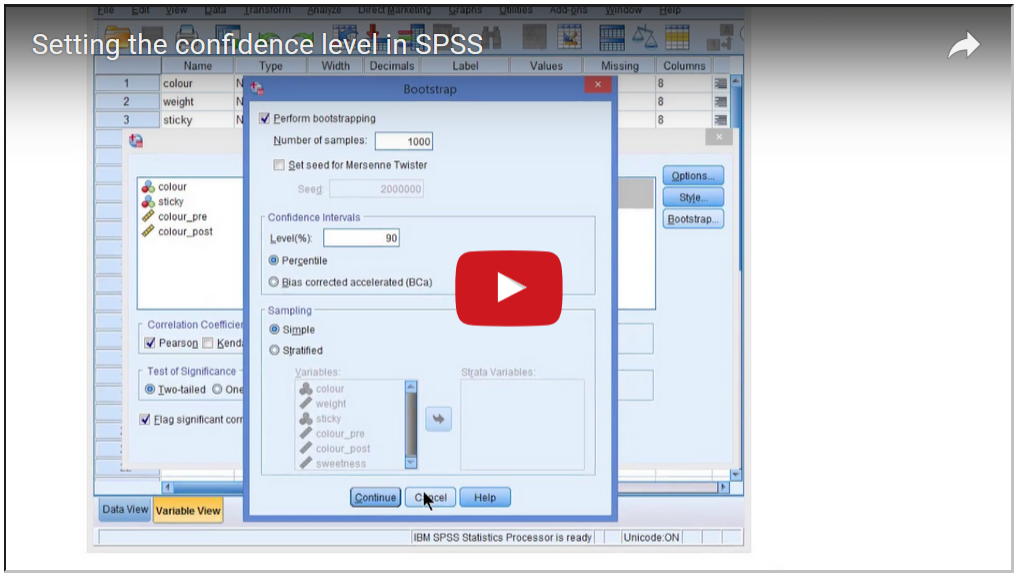


Figure 3.10: Setting the confidence level in SPSS.

3.6.2 Exercises

1. Download the data set candies.sav and use SPSS to calculate the 95% and 99% confidence intervals of average candy weight.

   Hint: Use the *Analyze* > *Compare Means* > *One-Sample T Test* command and leave the test value at zero.

   Interpret the results and explain why the 99% confidence interval is wider than the 95% confidence interval.

2. Let SPSS calculate the 95% confidence interval for median candy weight. Interpret the result. The data are in "candies.sav".

   Remember the SPSS exercises in Chapter 2.

3. Use SPSS to determine the 95% confidence interval for a paired-samples t test on candy colour fading under sunlight (variables colour_pre and colour_post in "candies.sav"). In your interpretation of the confidence interval, clarify the meaning of the statistic for which the confidence interval was calculated.

   The paired-samples t test is available in SPSS under *Analyze* > *Compare Means*.

4. Use SPSS to determine if candy colourfulness after exposure to sunlight (colour_post) depends on candy weight and candy sweetness. Interpret the 95% confidence intervals for both effects.

   Hint: Use regression analysis, which is available under *Analyze > Regression > Linear* in SPSS.

3.7 Take-Home Points

- If a sample statistic is an unbiased estimator, we can use it as a point estimate for the value of the statistic in the population.
- A point estimate may come close to the population value but it is most certainly not correct.
- A 95% confidence interval is an interval estimate of the population value: We are 95% confident that the population value lies within this interval. Note that confidence is not a probability!
- A larger sample or a lower confidence level yields a narrower, that is, a more precise confidence interval. The sample statistic is more likely to be closer to the population value. We have less uncertainty in our results.
- A larger sample yields a smaller standard error, which yields a more precise confidence interval because the limits of a confidence interval fall one standard error times the critical value below and above the value of the sample statistic.

Chapter 4

Testing a Null Hypothesis: Am I Right or Am I Wrong?

Key concepts: research hypothesis, statistical null and alternative hypothesis, nil hypothesis, test statistic, p value, significance level (Type I error rate), Type I error, inflated Type I error, capitalization on chance, one-sided and two-sided tests and tests to which this distinction does not apply, rejection region.

Summary

In the preceding chapter, we have learned that a confidence interval contains the population values that are plausible, given the sample that we have drawn. In the current chapter, we narrow this down to the question whether the expectation of the researcher about the population is plausible.

The expectation is usually called a (research) hypothesis and it must be translated into statistical hypotheses about a population value (parameter): a null hypothesis and an alternative hypothesis.

We test the null hypothesis in the following way. We construct a sampling distribution in one of the ways we have learned in Chapter 2 using the value specified in the null hypothesis as the imaginary population value. In other words, we act as if the null hypothesis is true.

Then, we calculate the probability of drawing a sample such as the one we have drawn or a sample that differs even more from a population for which the null hypothesis is true. If this p value is very low, say, below 5%, we reject the null hypothesis because our sample would be too unlikely if the null hypothesis is true. In this case, the test is statistically significant. The probability threshold that we use is called the significance level of the test.

Test your intuition and understanding

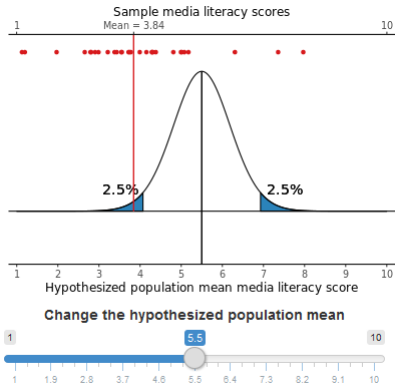


Figure 4.1: Testing null hypotheses.

Figure 4.1 displays a random sample of media literacy scores (red) and a sampling distribution if the null hypothesis is true.

1. What are the null and alternative hypotheses in Figure 4.1? Is the null hypothesis a nil hypothesis here?
2. What represents the p value of the sample mean that we have found in Figure 4.1? Does the p value depend on the type of null hypothesis: one-sided or two-sided?
3. What represents the significance level and rejection region in Figure 4.1?
4. Is the test statistically significant? How do you decide?
5. What happens if you change the hypothesized population mean? Check your answer by using the slider.
6. Is it OK to change your null hypothesis when you know your sample mean? Why is it OK or not OK?

Return to these question after studying this chapter.

4.1 A Binary Decision

The overall goal of statistical inference is to increase our knowledge about a population, when we only have a random sample from that population. In Chapter 3, we estimated population values that are plausible considering the sample that we drew. For instance, we looked for all plausible average weights of candies in the population using information about the weight of candies in our sample bag. This is what we do when we estimate a population value.

Estimation is one of two types of statistical inference, the other being null hypothesis testing. When we estimate a population value, we do not use our previous knowledge about the world of candies or whatever other subject we are investigating. We can be completely ignorant about the phenomenon that we are investigating. This approach is not entirely in line with the conceptualisation of scientific progress as an *empirical cycle*, in which scientists develop theories about the empirical world, test these theories against data collected from this world, and improve their theories if they are contradicted by the data.

Hypothesis testing, however, is more in line with a conceptualisation of scientific progress. It requires the researcher to formulate an expectation about the population, usually called a *hypothesis*. If the hypothesis is based on theory and previous research, the scientist uses previous knowledge. As a next step, the researcher tests the hypothesis against data collected for this purpose. If the data contradict the hypothesis, the hypothesis is rejected and the researcher has to improve the theory. If the data does not contradict the hypothesis, it is not rejected and, for the time being, the researcher need not change their theory.

Hypothesis testing, then, amounts to choosing one of two options: reject or not reject the hypothesis. This is a binary decision between believing that the population is as it is described in the hypothesis, or believing that it is not. This is quite a different approach from estimating a confidence interval as a range of plausible population values. Nevertheless, hypothesis testing and confidence intervals are tightly related as we will see later on in this chapter (Section 4.8).

4.2 Formulating Statistical Hypotheses

A *research hypothesis* is a statement about the empirical world that can be tested against data. Communication scientists, for instance, may hypothesize that:

- a television station reaches half of all households in a country,
- media literacy is below a particular standard (for instance, 5.5 on a 10-point scale) among children,
- opinions about immigrants are not equally polarized among young and old voters,
- the celebrity endorsing a fundraising campaign makes a difference to people's willingness to donate,
- more exposure to brand advertisements increases brand awareness,
- and so on.

As these examples illustrate, research hypotheses seldom refer to statistics such as means, proportions, variances, or correlations. Still, we need statistics to test a hypothesis. The researcher must translate the hypothesis into a new hypothesis specifying a statistic in the population, for example, the population mean. The new hypothesis is called a *statistical hypothesis*.

Translating the research hypothesis into a statistical hypothesis is perhaps the most creative part of statistical analysis, which is just a fancy way of saying that it is difficult to give

general guidelines stating which statistic fits which research hypothesis. All we can do is give some hints.

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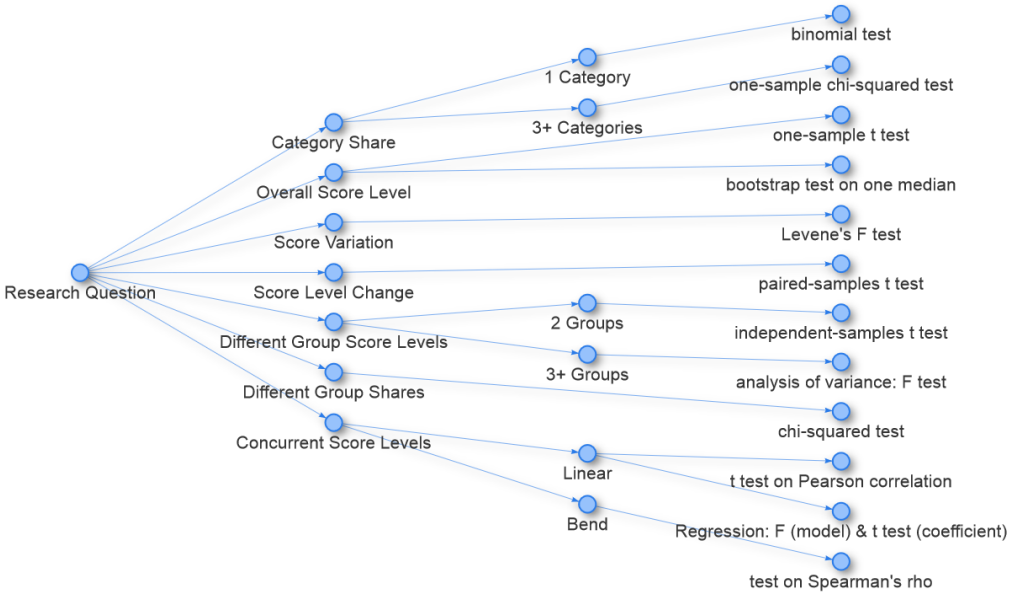


Figure 4.2: Flow chart for selecting the appropriate statistical test.

1. For each of the research hypothesis examples (above), find the appropriate statistical test using Figure 4.2. Hint: Hover your mouse pointer over a node, click on a dot, drag with your (left) mouse button, and zoom with your mouse wheel.

4.2.1 Proportions: shares

This book covers tests for four types of statistics: proportions, means, variance/standard deviations, and associations. A proportion is the statistic best suited to test research hypotheses addressing the share of a category or entity in the population. The hypothesis that a television station reaches half of all households in a country provides an example. All households in the country constitute the population. The share of the television station is the proportion or percentage of all households watching this television station.

If we want to use a statistic, we need to know the variable and cases for which the statistic must be calculated. In this example, a household does or does not watch the television statement, so our variable is a dichotomy with the two categories (“No, does not watch this station”, “Yes, watches this station”) usually coded as 0 versus 1 or 1 versus 2.

Each household provides an observation, namely either the score 0 or the score 1 on this

Table 4.1: Statistical hypothesis about four proportions as a frequency table.

Region	Hypothesized Proportion
North	0.5
East	0.5
South	0.5
West	0.5

variable or no score if there are missing values. To test the research hypothesis that a television station reaches half of all households in a country, we have to formulate a statistical hypothesis about the proportion—of households viewing this television station—in the population—all households in this country. For example, the researcher's statistical hypothesis could be that the proportion in the population is 0.5.

We can also be interested in more than two categories, for instance, does the television station reach half of all households in the north, east, south, and west of the country? This translates into a statistical hypothesis containing three or more proportions in the population: The proportion of households viewing this station is 0.5 in the north, it is 0.5 in the east, it is 0.5 in the south, and it is 0.5 in the west. Our statistical hypothesis is actually a relative frequency distribution, such as, for instance, in Table 4.1.

A test for this type of statistical hypothesis is called a one-sample chi-squared test. It is up to the researcher to specify the hypothesized proportions for all categories. This is not a simple task: What reasons do you have to expect particular values, say a reach of fifty per cent of all households instead of sixty per cent?

The test is mainly used if the researcher has information on the proportions of the categories in the population. If we draw a sample from all citizens of a country, we usually know the frequency distribution of sex, age, educational level, and so on of all citizens from the national bureau of statistics. With the bureau's information, we can test if the respondents in our sample have the same distribution with respect to sex, age, or educational level as the population; just use the population proportions in the hypothesis. If they do, the sample is *representative* (see Section 1.2.6) of the population with respect to sex, age, or educational level. This is an important check on the representativeness of our sample.

4.2.2 Testing proportions in SPSS

4.2.2.1 Instructions

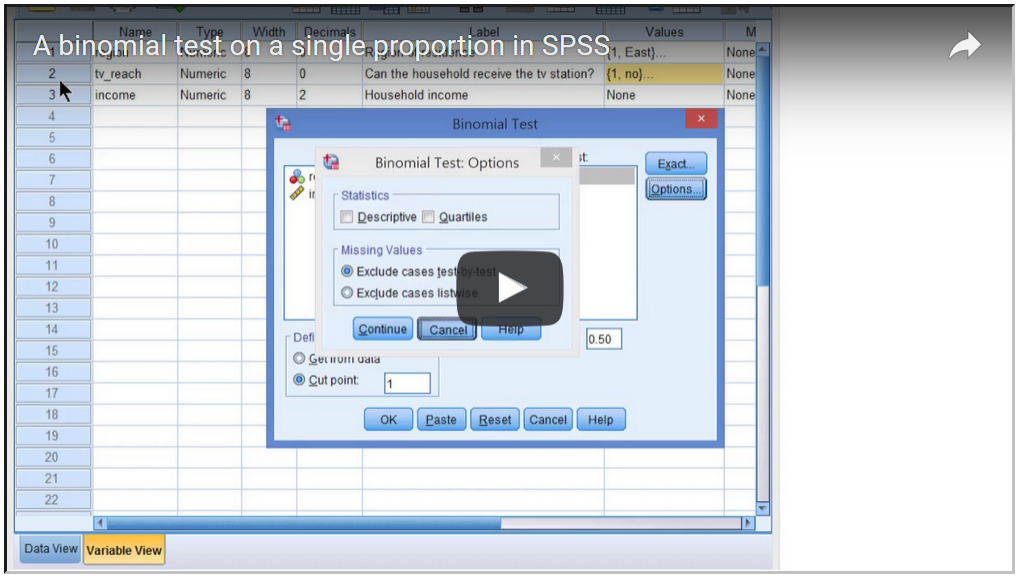


Figure 4.3: A binomial test on a single proportion in SPSS.

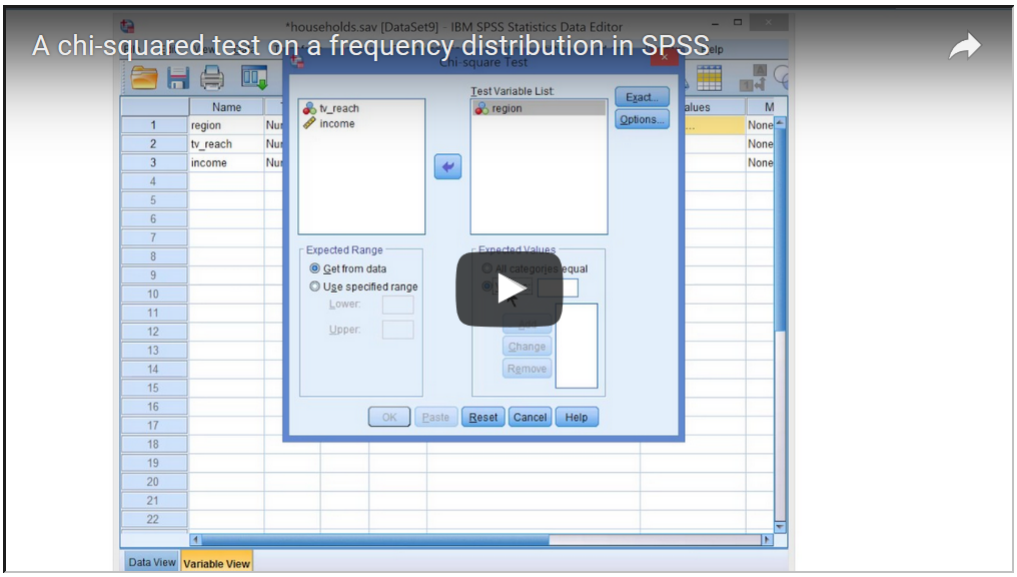


Figure 4.4: A chi-squared test on a frequency distribution in SPSS.

4.2.2.2 Exercises

1. Use the data set households.sav to test the hypothesis that the TV station does not reach 40 per cent of all households in the population.
2. Test the hypothesis that the TV station reaches 55 per cent of all households in the population.
3. Does half of the households have an income of at most 40,000?
4. According information from the National Bureau of Statistics, 20 per cent of all households have incomes up to 30,000, 50 per cent have incomes between 30,000 and 50,000, and 30 per cent has incomes over 50,000. Use a test to decide if our sample is representative with respect to income. Hint: recode income first.

4.2.3 Mean and median: level

Research hypotheses that focus on the level of scores are usually best tested with the mean or another measure of central tendency such as the median value. For example, the hypothesis that media literacy is below a particular standard (e.g., 5.5 on a 10-point scale) among children refers to a level: the level of media literacy scores.

The hypothesis probably does not argue that all children have a media literacy score below 5.5. Instead, it means to say that the overall level is below this standard. The centre of the distribution offers a good indication of the general score level.

For a numeric (interval or ratio measurement level) variable such as the 10-point scale in the example, the mean is a good measure of the distribution's centre. In this example, our statistical hypothesis would be that average media literacy score of all children in the population is (below) 5.5.

4.2.4 Testing one mean in SPSS

4.2.4.1 Instructions

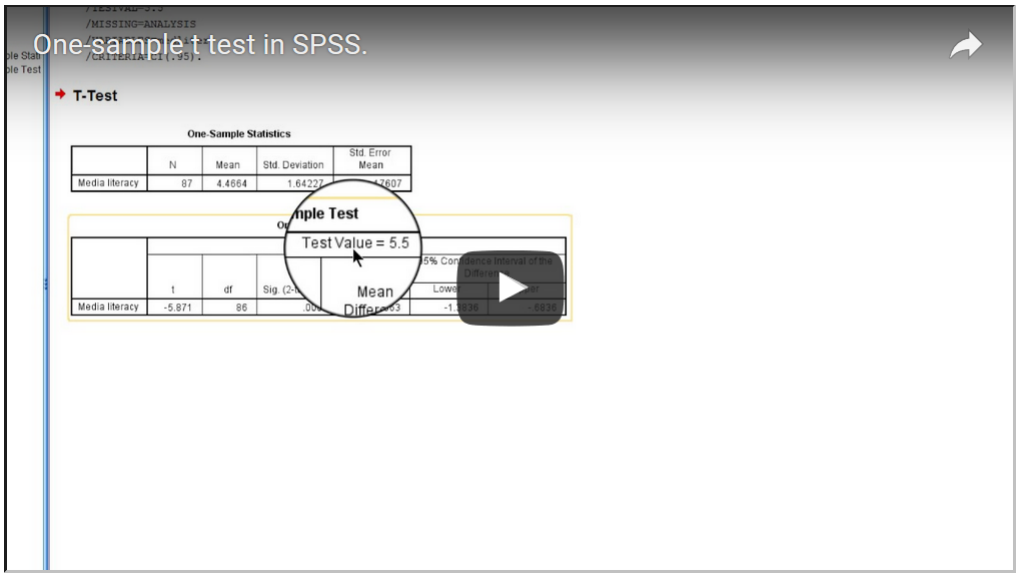


Figure 4.5: A one-sample t test in SPSS.

4.2.4.2 Exercises

1. Use the data set children.sav to test the hypothesis that average parental supervision of the child's media use is 5.5 (on a scale from 1 to 10) in the population.
2. Have a look at the confidence interval reported for Exercise 1. If you would test the hypothesis that average media literacy in the population is 4.5, would the test be statistically significant? Check your answer by carrying out this test.

4.2.5 Variance: (dis)agreement

Although rare, research hypotheses may focus on the variation in scores rather than on score level. The hypothesis about polarization provides an example. Polarization means that we have scores well above the centre and well below the centre rather than all scores

concentrated in the middle. If voters' opinions about immigrants are strongly polarized, we have a lot of voters strongly in favour of admitting immigrants as well as many voters strongly opposed to admitting immigrants.

For a numeric variable, the variance or standard deviation—the latter is just the square root of the former—is the appropriate statistic to test a hypothesis about polarization. The research hypothesis concerns the variation of scores in two groups, for instance, young versus old voters. The statistical hypothesis would be that the variance in opinions in the population of young voters is different from the variance in the population of old voters.

4.2.6 Testing two variances in SPSS

4.2.6.1 Instructions

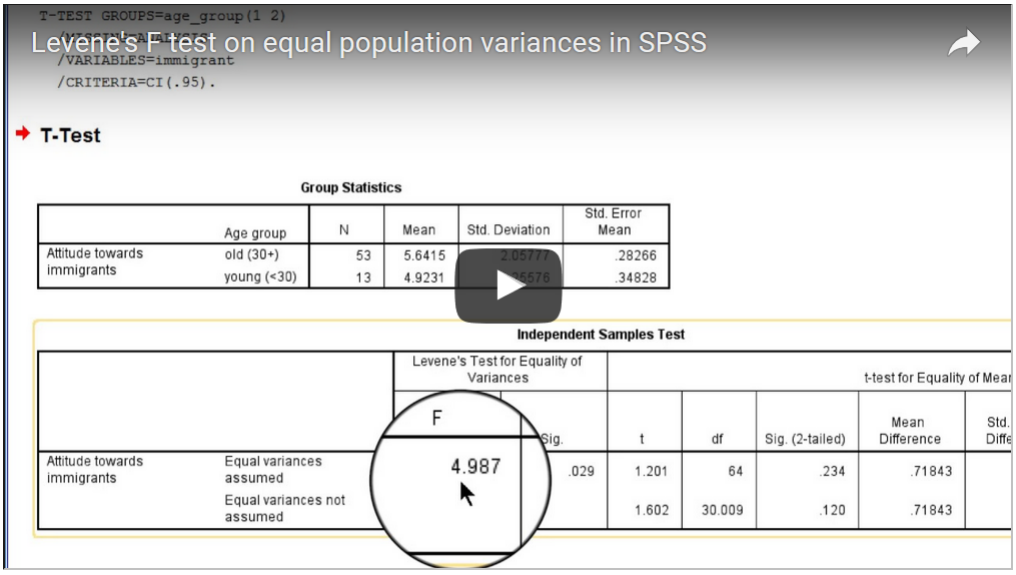


Figure 4.6: Levene's F test on equal population variances in SPSS.

4.2.6.2 Exercises

1. Data set voters.sav contains information about the age and attitude towards immigration among a random sample of voters. Is the attitude towards immigrants equally polarized among young (under 30) and old (30+) voters? Justify your answer with a statistical test.
2. Use the data of Exercise 1. Create a new variable grouping voter's age with classes 18-35, 36-65, and 66+ years. Is the attitude towards immigrants equally polarized among these three age groups in the population? Justify your answer with a statistical test.

4.2.7 Association: relations between characteristics

Finally, research hypotheses may address the relation between two or more variables. Relations between variables are at stake if the research hypothesis states or implies that one (type of) characteristic is related to another (type of) characteristic. The statistical name for a relation between variables is *association*.

For example, if the identity of the endorser makes a difference to the willingness to donate, the endorser to whom a person is exposed (one characteristic) is related to this person's willingness to donate (another characteristic). Another example: If exposure to the campaign increases willingness to donate, a person's willingness to donate is positively related to this person's exposure to the campaign.

4.2.8 Score level differences

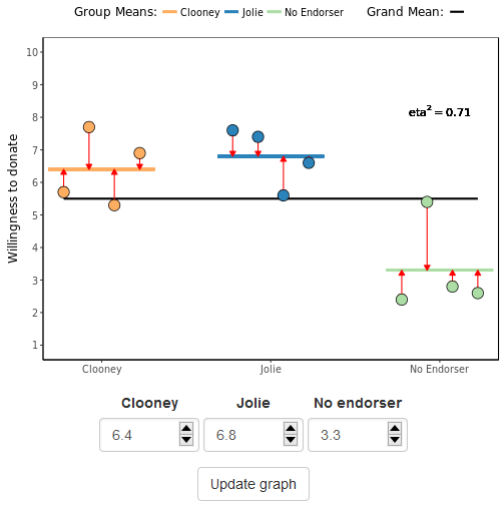


Figure 4.7: How do group level differences express association?

1. Figure 4.7 shows the willingness to donate for twelve respondents and the celebrity they saw endorsing the fund-raising campaign. Do you think that the willingness to donate is associated with the endorsing celebrity? Motivate your answer.
2. Can you create or remove an association between willingness to donate and endorsing celebrity by changing the group averages? Change the group averages to check your expectations.

Association comes in two related flavours: a difference in score level between groups or the predominance of particular combinations of scores on different variables.

The relation between the endorser's identity and willingness to donate is an example of

the first flavour. All people are confronted with one of the celebrities as endorser of the fund-raising campaign. This is captured by a categorical variable: the endorsing celebrity.

The categorical variable clusters people into groups: One group is confronted with Celebrity A, another group with Celebrity B, and so on. If the celebrity matters to the willingness to donate, the general level of donation willingness should be higher in the group exposed to one celebrity than in the group exposed to another celebrity.

Thus, we return to statistics needed to test research hypotheses about score levels, namely measures of central tendency. If willingness to donate is a numeric variable, we can use group means to test the association between endorsing celebrity (grouping variable) and willingness to donate (score variable). The statistical hypothesis would then be that group means are not equal in the population of all people.

If you closely inspect Figure 4.2, you will see that we prefer to use a t distribution if we compare two different groups (independent-samples t test) or two repeated observations for the same group (paired-samples t test). By contrast, if we have three or more groups, we use analysis of variance with an F distribution.

4.2.9 Comparing means in SPSS

4.2.9.1 Instructions

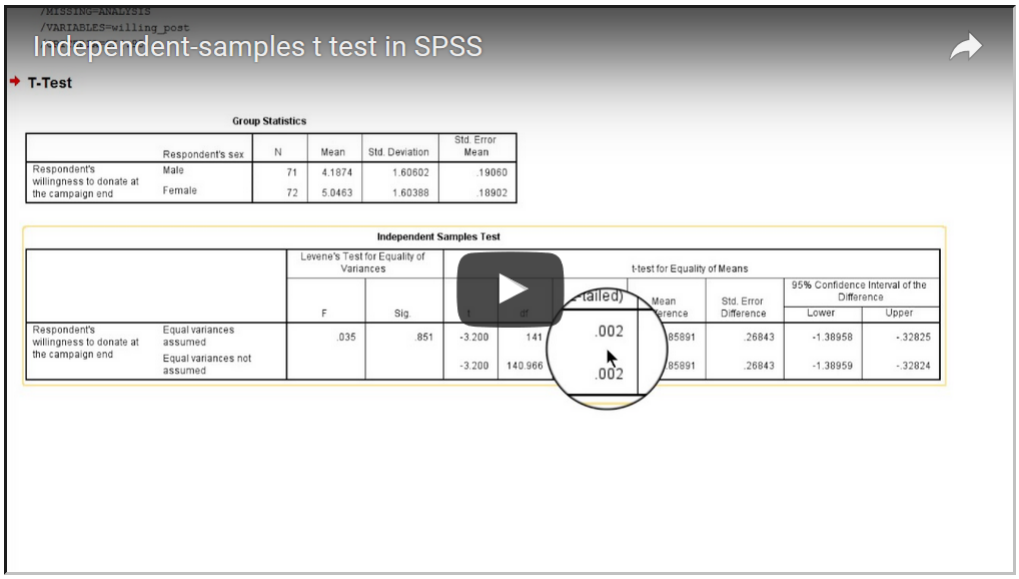


Figure 4.8: An independent-samples t test in SPSS.

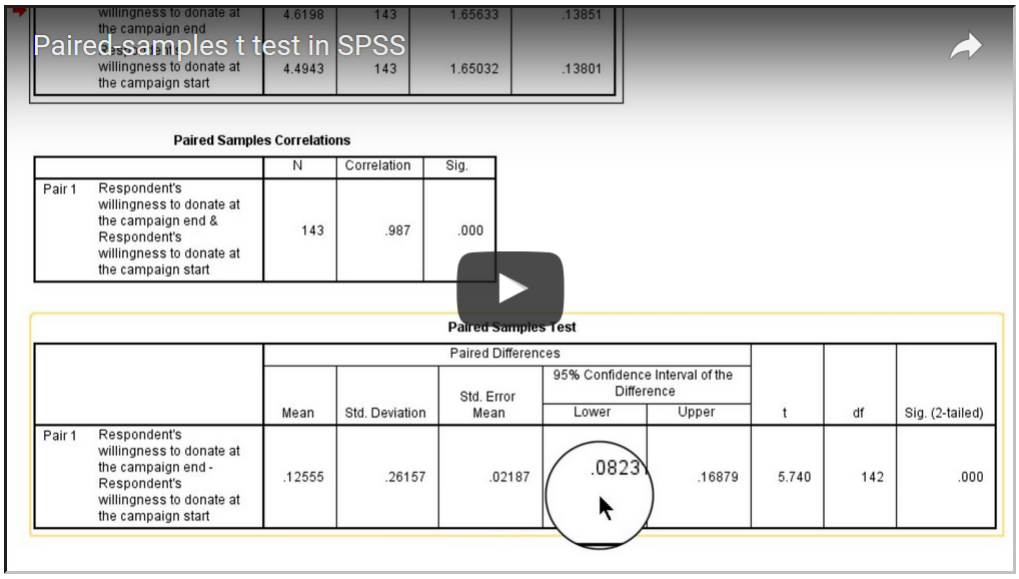


Figure 4.9: A paired-samples t test in SPSS.

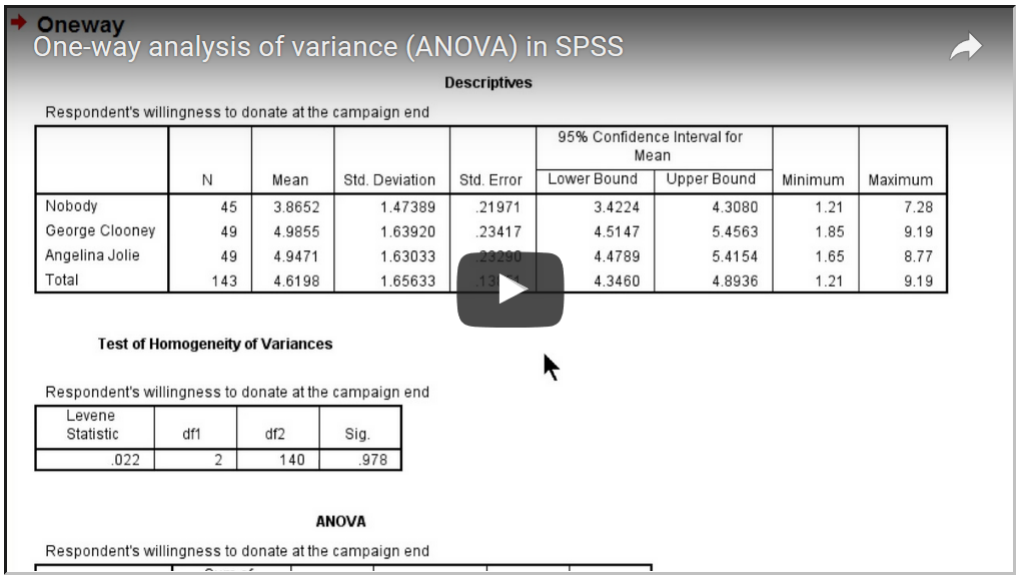


Figure 4.10: One-way analysis of variance (ANOVA) in SPSS.

4.2.9.2 Exercises

1. Use donors.sav to test if people's willingness to donate at the end of the campaign depends on the celebrity endorsing the campaign.

2. Is willingness to donate at the end of the campaign higher for those who remember the campaign than for those who do not remember it?

3. Did willingness to donate increase in the population between the start and the end of the campaign?

4.2.10 Combinations of scores

The other flavour of association represents situations in which some combinations of scores on different variables are much more common than other combinations of scores.

Think of the hypothesis that brand awareness is related to exposure to advertisements for that brand. If the hypothesis is true, people with high exposure and high brand awareness should occur much more often than people with high exposure and low brand awareness or low exposure and high brand awareness.

The two variables here are exposure and brand awareness. One combination of scores on the two variables is high exposure combined with high brand awareness. This combination should be more common than high exposure combined with low brand awareness.

Measures of association are statistics that put a number to the pattern of group-score levels or combinations of scores. The exact statistic that we use depends on the measurement level of the variables. For numerical variables, measured at the interval or ratio level, we use Pearson's correlation coefficient or the regression coefficient. For ordinal variables with quite a lot of different scores, we use Spearman's rank correlation.

For categorical variables, measured at the nominal or ordinal level, chi-squared indicates whether variables are statistically associated. The larger chi-squared, the less probable it is that the variables are not associated in the population. If variables are not associated, they are said to be *statistically independent*.

Several measures exist that express the strength of the association between two categorical variables. We use Phi and Cramer's V (two nominal variables, symmetric association), Goodman & Kruskals tau (two nominal variables, asymmetric association), Kendalls tau-b (two categorical ordinal variables, symmetric association), and Somers' d (two categorical ordinal variables, symmetric association).

4.2.11 Testing associations in SPSS

4.2.11.1 Instructions

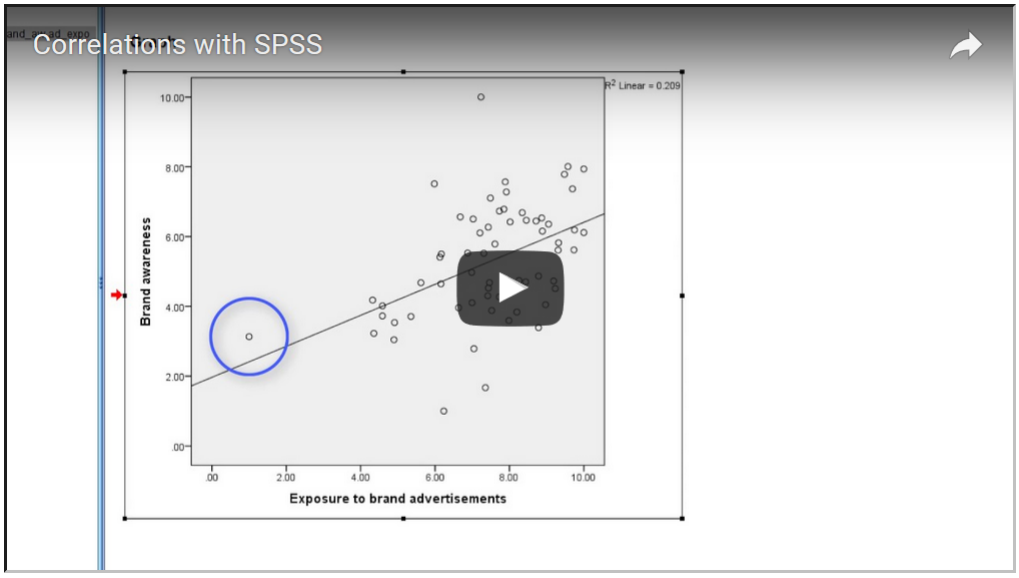


Figure 4.11: Correlations with SPSS.

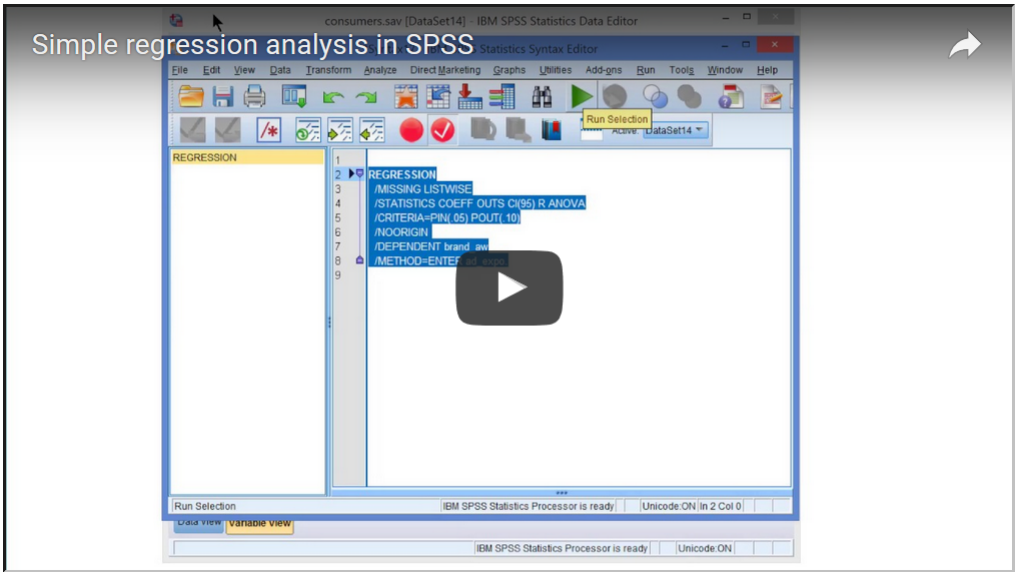


Figure 4.12: Simple regression analysis in SPSS.

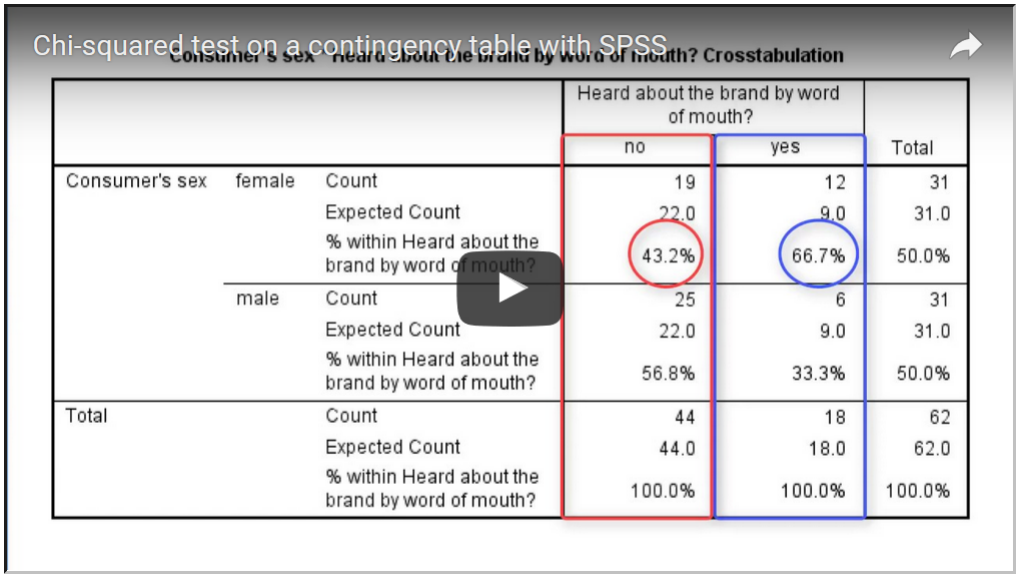


Figure 4.13: Chi-squared test on a contingency table with SPSS.

4.2.11.2 Exercises

1. In the population of all consumers, is brand awareness linked to exposure to advertisements for the brand? Use consumers.sav to answer this question.
2. How well can we predict brand awareness with ad exposure?
3. Does word of mouth involve women rather than men? Interpret the contents, strength, and statistical significance of the association. Have a look at Section 2.4 if you forgot which p value to interpret.

4.3 The Null and Alternative Hypothesis

In the preceding section, I referred to statistical hypotheses without further qualification. There are, however, at least two different statistical hypotheses: the null hypothesis (H_0) and the alternative hypothesis (H_1 or H_A).

For reasons that will be explained in Section 4.5.1, the *null hypothesis* must equate the test statistic to a single value. For example, the statistical hypothesis that the proportion of all households in the population reached by a television station is .5 equates the population proportion to .5.

In contrast, the statistical hypothesis that the average media literacy score of all children in the population is below 5.5 does not equate the population mean to one particular value. It is hypothesized to be smaller than 5.5 but it can be any number below 5.5.

4.3.1 Alternative hypothesis

If the research hypothesis is not the null hypothesis, it is the *alternative hypothesis*. The alternative hypothesis covers all situations not covered by the null hypothesis and the other way round. The null hypothesis stating that the proportion of all households in the population reached by the television station is .5 is linked to the alternative hypothesis that states the proportion is not .5. Thus, we cover all possible outcomes.

The research hypothesis stating that the average media literacy score of all children in the population is below 5.5, is an example of an alternative hypothesis. Most of the research hypothesis examples in the previous section are alternative hypotheses because they do not equate the statistic with a particular value:

- If opinions about immigrants are hypothesized to be different for younger and older voters, the variances are hypothesized to be unequal in the population. But the research hypothesis does not state how unequal.
- If the celebrity endorsing a fundraising campaign makes a difference to the willingness of people to donate, the average willingness is not hypothesized to be equal for all groups but, again, the size of the difference is not specified.

- If we hypothesize that more exposure to brand advertisements increases brand awareness, we expect the correlation or regression coefficient to be positive, that is, larger than zero. But we have not hypothesized a particular value, so the research hypothesis represents the alternative hypothesis.

4.3.2 Research hypotheses tend to be alternative hypotheses

It is not a coincidence that most of the research hypotheses in the examples are alternative hypotheses instead of null hypotheses. This is very common in social research, even though it is not necessarily always the case, as some statistics textbooks would have us believe. Often, our theories tell us to expect differences or changes but not the size of differences or changes.

If the research hypothesis is the alternative hypothesis, we have to formulate the null hypothesis ourselves. This is very important, because it is this hypothesis that is actually tested as we will see in a later section. Some examples:

- A research hypothesis stating that average media literacy of children is below 5.5 is an alternative hypothesis. The associated null hypothesis would be that average media literacy is at least 5.5.
- If the alternative hypothesis states that variances or group means are unequal in the population, the null hypothesis would be that they are equal in the population.
- An alternative hypothesis expecting a correlation between exposure and brand awareness requires the null hypothesis to state that there is no such association in the population.

4.3.3 Nil hypothesis

Null hypotheses are quite often stating that there is no difference or no association in the population. They equate the population statistic to zero. This type of null hypothesis is called a *nil hypothesis* or just plainly *the nil*.

A null hypothesis on association in the population usually is a nil hypothesis, assigning the value zero to the measure of association in the population. For example, Spearman's rho or Pearson's correlation between exposure and brand awareness are hypothesized to be zero in the population. For a measure of association, zero always means that there is no association.

This also applies to the regression coefficient (b or b^* in the regression equation): If it is zero, the predictor variable is useless for predicting the outcome variable. In these cases, the null hypothesis is the nil. If statistical software does not report the null hypothesis that is being tested, you may assume that it equates the parameter of interest to zero.

4.4 One-Sided and Two-Sided Tests

The research hypothesis stating that average media literacy is below 5.5 in the population represents the alternative hypothesis because it does not fix the hypothesized population value to one number. The accompanying null hypothesis must state that the population mean is 5.5 or higher.

This null hypothesis is slightly different from the ones we have encountered so far, which equated the population value to a single value, usually zero. If the null hypothesis equates a parameter to a single value, the null hypothesis can be rejected if the sample statistic is either too high or too low. There are two ways of rejecting the null hypothesis, so this type of hypothesis is called *two-sided* or two-tailed.

By contrast, the null hypothesis stating that the population mean is 5.5 or higher is a *one-sided* or one-tailed hypothesis. It can only be rejected if the sample statistic is at one side of the spectrum: only below (left-sided) or only above (right-sided) a particular value. A test of a one-sided null hypothesis is called a *one-sided test*.

In a left-sided test of the media literacy hypothesis, the researcher is not interested in demonstrating that average media literacy among children can be larger than 5.5. Usually, she is not interested because she rules out the possibility. For instance, she beliefs that average media literacy among children cannot be substantially higher than 5.5. The researcher brings prior knowledge about the world to bear that has convinced her that average media literacy among children can only be lower than 5.5 on average in the population.

If there is a possibility that the score may also be higher than 5.5 and it is deemed important to note values well over 5.5 and values well below 5.5, the research and null hypotheses should be two-sided. Then, a sample average well above 5.5 would also have resulted in a rejection of the null hypothesis. In a left-sided test, however, a high sample outcome cannot reject the null hypothesis.

4.4.1 Boundary value as hypothesized population value

You may wonder how a one-sided null hypothesis equates the parameter of interest with one value as it should. The special value here is 5.5. If we can reject the null hypothesis stating that the population mean is 5.5 because our sample mean is sufficiently lower than 5.5, we can also reject any hypothesis involving population means higher than 5.5.

A population average over 5.5 differs even more from the sample average than a population average of 5.5, if our sample average is below 5.5. If the smaller difference between population average and sample average is statistically significant, the larger difference for population averages over 5.5 are necessarily also statistically significant. Therefore, we use the boundary value of a one-sided null hypothesis as the value for a one-sided test.

4.4.2 One-sided – two-sided distinction is not always relevant

Note that the difference between one-sided and two-sided tests is only useful if we test a statistic against a particular value or if we test the difference between two groups. In the first situation, we may rule out the possibility that the population value is higher (or lower) than the hypothesized value if we have good reasons to believe that it can only be lower (or higher). In the second situation, we may expect that one group can only score higher than the other group and not the other way around.

In contrast, we cannot meaningfully formulate a one-sided null hypothesis if we are comparing three groups or more. Even if we expect that Group A can only score higher than Group B and Group C, what about the difference between Group B and Group C? If we can't have meaningful one-sided null hypotheses, we cannot meaningfully distinguish between one-sided and two-sided null hypotheses.

4.4.3 Formulate statistical hypotheses in advance

Statistical hypotheses are important because they specify the statistic that we use in our test and they determine whether we do a two-sided or one-sided test. We have to formulate our statistical hypotheses before we have a look at our sample. After all, we want to give the sample data a fair chance to prove our hypothesis wrong. A statistical test is useless if we already know the result in the sample and adjust our hypotheses to this information.

Finally, you should note that scientific papers usually report the research hypothesis but not the statistical hypotheses. The statistical hypotheses of a test are supposed to be known to all researchers. Make sure you know them, as well.

4.5 p Value and Significance Level (α)

The purpose of formulating a null hypothesis is that we can use the value specified in the null hypothesis as a hypothetical population value. This saves us the trouble of looking for plausible population values, which we do if we estimate a confidence interval.

When testing a null hypothesis, we just act as if the null hypothesis is true. We pretend that the value specified in the null hypothesis is the true population value. This allows us to create one sampling distribution that will tell us how plausible our sample is if the null hypothesis would be true. For this reason, the null hypothesis must equate the parameter to one value.

Let us assume that average media literacy is 3.9 in our sample. According to our null hypothesis, the population average is (at least) 5.5. If average media literacy of children in the population would really be 5.5, how plausible is it to draw a sample with 3.9 (or less) as average media literacy? We can use a hypothetical sampling distribution with 5.5 as mean value to answer this question.

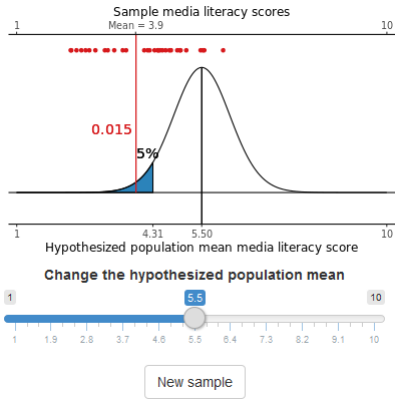


Figure 4.14: Sampling distribution of average media literacy.

1. Figure 4.14 shows the hypothesized population mean, the associated sampling distribution, and the sample scores (red dots) with their mean. What does the red number directly to the left of the sample mean line mean?
2. The significance level is 5% here. Why is it marked by the blue tail in Figure 4.14?
3. How low must the sample mean be to have a p value below 5% (a statistically significant test result)?
4. What happens to the p value of our initial sample mean (3.9) if we change the value of our null hypothesis? Is it always possible to formulate a null hypothesis such that the sample mean is statistically significant? Take some new samples to check your answer.

4.5.1 p Value

If our sample statistic is a continuous variable, for instance, average media literacy, we know that it does not make sense to calculate the probability of finding the exact sample mean that we obtained. In Section 1.3, we have learned that we work with p values in this situation. For example, we use the probability of finding our sample mean or a mean that is even more distant from the hypothesized population mean.

The question now is: How large must the difference be between the value that we expect according to our null hypothesis (the hypothesized population value), and the value that we observe in our sample, before we stop believing that the null hypothesis is true? If our null hypothesis expects the average media literacy of all children to be (at least) 5.5, how small should the sample mean be before we reject the null hypothesis?

The answer is that the difference should be so large that it is very improbable that we would draw a sample with the observed mean from a population with the hypothesized mean. In statistical terms, the p value of our sample outcome must be very low if the null hypothesis is true. With a very low p value, our sample is too improbable to sustain our belief that the null hypothesis is true.

4.5.2 Statistical significance and rejection region

How low should we go? A commonly accepted threshold value is .05 (5%). If the p value is .05 or less, we decide that our sample is too improbable and implausible to be drawn from a population for which the null hypothesis is true. Therefore, we reject the null hypothesis and we say that the test is *statistically significant*.

The decision about the null hypothesis is simple if you have the p value. If the reported p value is lower than the significance level, we reject the null hypothesis. Otherwise, we do not reject the null hypothesis.

> If p is low, the null must go and the test is statistically significant.

This is the golden rule of null hypothesis testing (although some argue that the gold of this rule is fool's gold, see Chapter 6).

The values for the sample statistic for which the test is statistically significant, so that the null hypothesis is rejected, is called the *rejection region*. If the sample statistic is in the rejection region of a test, we reject the null hypothesis, and the test is statistically significant.

However, we usually do not know the rejection region in terms of the sample statistic, so we ordinarily use p values to determine if a test is statistically significant. SPSS reports p values, which are sometimes referred to as *significance* or *Sig.*.

4.5.3 Conditional probability

It is important to remember that the p value that we calculate is a probability **under the assumption that the null hypothesis is true**. Therefore, it is a *conditional probability*.

Compare it to the probability that we throw sixes with a dice. This probability is one out of six under the assumption that the dice is unbiased. Probabilities always rest on assumptions. If the assumptions are violated, we cannot calculate probabilities.

If the dice is biased, we don't know the probability of throwing sixes. In the same way, we have no clue whatsoever of the probability of drawing a sample like the one we have if the null hypothesis is not true in the population. This is why specifying a null hypothesis is so important.

4.5.4 Significance level and Type I error

The threshold value, conventionally .05, is called the *significance level* of the test. If the null hypothesis—for instance, average media literacy is 5.5 in the population—is true, but we accidentally draw a sample with a mean well below 5.5, our p value is smaller than the significance level and we reject the null hypothesis.

We have to reject the null hypothesis in this situation; those are the rules of the game. However, in concluding that the null hypothesis is wrong, we made a mistake. We don't

know and don't believe that we make this error, but we still do. This error is called a *Type I error*: rejecting a hypothesis that is actually true.

We cannot entirely avoid this error because samples can be very different from the population from which they are drawn, as we learned in Chapter 1. Thankfully, however, we know the probability that we make this error. This probability is the significance level.

You should understand the exact meaning of probabilities. A significance level of .05 allows five per cent of all possible samples to be so different from the population that we reject the null hypothesis if it is true.

In other words, if we draw a lot of samples and decide on the null hypothesis for each sample, we would reject a true null hypothesis in five per cent of our decisions. So we have a five per cent chance of making a Type I error.

We decide on that probability when we select the confidence level of the test and we think that .05 is an acceptable probability for making this type of error. However, we do not know whether our sample belongs to the five per cent.

4.5.5 p Values in one-sided tests

In the example of average media literacy, we have only taken into account the left tail of the sampling distribution to calculate the p value. If we expect that average media literacy is below 5.5, we only consider the chance that the sample mean is below 5.5, so we do a one-sided test.

In this case, it makes sense to care only for the left tail of the sampling distribution. The entire probability of rejecting the null hypothesis while it is actually true is located in the left tail of the sampling distribution.

Of course, a one-sided test may also focus solely on the right tail of the sampling distribution. For example, if we hypothesize that exposure to advertisements increases brand awareness among consumers, we expect a positive correlation or regression coefficient. Our null hypothesis specifies that the correlation or regression coefficient is at most zero and we only reject it if the sample value is well above zero.

4.5.6 Significance level in two-sided tests

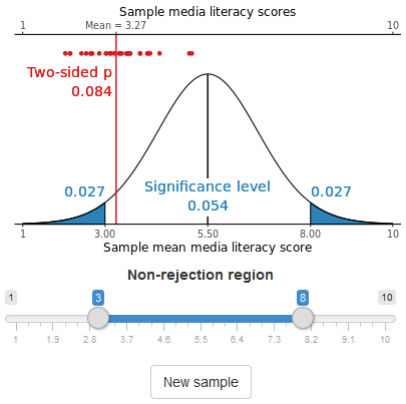


Figure 4.15: How do we obtain two-sided significance evels and p values?

1. In Figure 4.15, use the *Non-rejection region* slider to determine the rejection region for a two-sided test at 5% significance level. Hint: Click a handle and then use the left and right arrow keys on your keyboard to make tiny changes to the handle's value.
2. what is the significance level of a one-sided test using the rejection area in the right tail that you have just determined? To check your answer, change one of the slider handles such that you obtain a one-sided rejection region and read out the p value.
3. When does Figure 4.15 indicate that a significance level is not applicable? Why is that so?
4. When is the two-sided p value largest and when is a one-sided p value largest? Draw several samples and inspect the p values to check your answer.
5. What is special about a significance level of .05?

What is the situation in a two-sided test, for instance, if we hypothesize that average media literacy is not 5.5 in the population? Now, there are two ways in which we may reject the null hypothesis of 5.5 average media literacy: If the sample average media literacy is sufficiently larger than 5.5 or if it is sufficiently smaller. Each way of rejecting the null hypothesis has an associated probability if the null hypothesis is true (Type I error). Their sum is the significance level.

In practice, we divide the significance level by two and use half of the probability for the left tail and the other half for the right tail of the sampling distribution. If our significance level is .05, as it usually is, we use .025 as the maximum probability of finding a sample with a statistic that is so low that we would reject a null hypothesis that is true. We use the other .025 probability for drawing a sample with a statistic that is so high that we reject the null hypothesis.

4.5.7 p Values in two-sided tests

Just like the significance level, the p value in a two-sided test has to take into account that we may reject the null hypothesis in two different ways.

A p value gives us the probability of drawing a sample with the value for the sample statistic that we have found in our current sample or a more extreme value. In other words, it is the probability of drawing a sample with a statistic that is at least as distant from the hypothesized population value as our current sample result.

In a two-sided test, the distance can go in two directions: larger than the hypothesized value or smaller. As a consequence, the p value must cover samples at opposite sides of the sampling distribution. Because we assume equal p values at both sides, we can double the one-sided p value to obtain the two-sided p value. And we can halve a two-tailed p value to obtain the one-sided p value.

You do not need to worry about this if your statistics software reports the type of p value that you need: one-sided or two-sided. If there is no choice between one- and two-sided tests, the reported p value is always correct.

However, if your software reports a one-sided p value but you need a two-sided p value, you have to double the reported p value. In contrast, if the software reports a two-sided p value while you need a one-sided p value, you have to divide the reported p value by two yourself because you do not want to take the probability in the other tail into account. Statistical software usually reports two-sided p values, so this situation may occur.

4.5.8 Unfounded one-sided null hypotheses

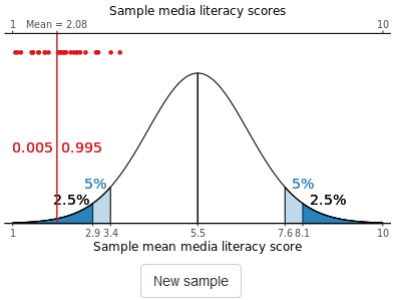


Figure 4.16: Is the test statistically significant?

1. Practice recognizing significant test results in Figure 4.16. Draw some samples and decide if a two-sided, right-sided, and left-sided test is statistically significant at 5% significance level.
2. In which situation is a one-sided test not statistically significant whereas a two-sided test is statistically significant at the 5% significance level?

Be careful, however. If your left-sided test hypothesizes that average media literacy is below 5.5 but your sample mean is above 5.5, your left-sided test can never be significant. After all, your sample result is fully in line with the null hypothesis.

In this situation, the two-sided p value can be significant but you should never use the two-sided p value if your null hypothesis was one-sided. Changing your null hypothesis during the analysis, even from one-sided to two-sided, is cheating (see Section 4.9) because you must formulate the null hypothesis before you know the sample result. If you test the significance of null hypotheses, you have to live with the fact that you excluded outcomes from your one-sided test that perhaps should not have been excluded.

4.6 Test Statistic and Degrees of Freedom

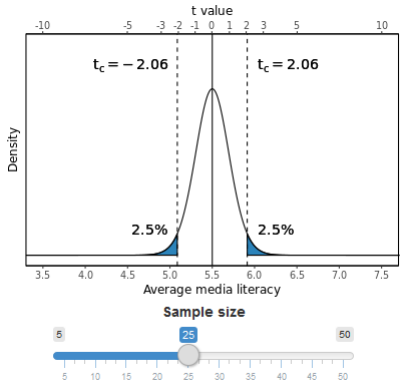


Figure 4.17: Sample size and critical values in a one-sample t test.

Figure 4.17 uses the t distribution to approximate the sampling distribution of average media literacy in a random sample of children.

1. What is the meaning of the coloured tails?
2. What is the meaning of t_c?
3. Why does the distribution become more pointed when sample size increases?
4. Is there a fixed relation between the t values and the values for average sample media literacy? Change the sample size to find the answer.
5. What is the relation between sample size and critical t values?

A theoretical probability distribution links sample outcomes such as a sample mean to probabilities by means of a *test statistic*. A test statistic is named after the theoretical probability distribution to which it belongs: z for the standard-normal or z distribution,

t for the t distribution, F for the F distribution and, you guessed it, chi-squared for the chi-squared distribution.

A test statistic is calculated from the sample statistic that we want to test, for instance, the sample proportion, mean, variance, or association, but it uses the null hypothesis as well. A test statistic more or less standardizes the difference between the sample statistic and the population value that we expect under the null hypothesis.

The exact formula and calculation of a test statistic is not important to us. Just note that the larger the difference between observation (sample outcome) and expectation (hypothesized population value), the more extreme the value of the test statistic, the less likely (lower p value) it is that we draw a sample with the observed outcome or an outcome even more different from the hypothesized value, and, finally, the more likely we are to reject the null hypothesis.

Actually, we reject the null hypothesis if the test statistic is in the *rejection region*. The value of the test statistic where the rejection region starts, is called the *critical value*. In Section 3.4, we learned that 1.96 is the critical value of z for a two-sided test at 5% significance level in a standard-normal distribution. In a z test, then, a sample z value above 1.96 or below -1.96 indicates a significant test result.

Except for the normal distribution, the probability distributions that we use depend on the degrees of freedom of the test. The degrees of freedom can depend on sample size, the number of groups that we compare, or the number of rows and columns in a contingency table. We don't need to worry about this.

The t distribution depends on the degrees of freedom of the test, for example. The degrees of freedom are determined by sample size: a larger sample yields slightly lower critical values in a t distribution. For samples that are not too small, however, the critical values of t are near 2. You may have noticed this in Figure 4.17.

APA6 requires us to report the degrees of freedom. If SPSS reports the degrees of freedom, usually in a column with the header "df". You should include it between brackets after the name of the test statistic, for instance: t (18) = 0.63 (see Figure **??**). Note that the F test statistic has two degrees of freedom, both of which should be reported (separated by a comma).

4.7 Test Recipe and Rules for Reporting

Testing a null hypothesis consists of several steps, which are summarized below, much like a recipe in a cookbook.

1. Specify the statistical hypotheses.

In the first step, translate the research hypothesis into a null and alternative hypothesis. This requires choosing the right statistics for testing the research hypothesis (Section 4.2) and choosing between a one-sided or two-sided test if applicable (Section 4.4).

2. Select the significance level of the test.

Before we execute the test, we have to choose the maximum probability of rejecting the null hypothesis if it is actually true. This, as we know now, is the significance level. We almost always select .05 (5%) as the significance level. If we have a very large sample, e.g., several thousands of cases, we may select a lower significance level, for instance, 0.01. See Chapter 5 for more details.

3. Select how the sampling distribution is going to be created.

Are you going to use bootstrapping, an exact approach, or a theoretical probability distribution? Theoretical probability distributions are the most common choice and we focus on these, here. We have to know which theoretical probability distribution can be used for which test. If you are working with statistical software, you automatically select the correct probability distribution (e.g. the t distribution), by selecting the correct test (in this example, a test on the means of two independent samples).

4. Execute the test.

Let your statistical software calculate the p value of the test and/or the value of the test statistic. It is important that this step comes after the first three steps. The first three steps should be made without knowledge of the results in the sample.

5. Decide on the null hypothesis.

Reject the null hypothesis if the p value is lower than the significance level.

6. Report the test results.

The ultimate goal of the test is to increase our knowledge. To this end, we have to communicate our results both to fellow scientists and to the general reader who is interested in the subject of our research.

4.7.1 Reporting to fellow scientists

Fellow scientists need to be able to see the exact statistical test results. According to APA6, we should report the test statistic, the associated degrees of freedom (if any), the value of the test statistic, the p value of the test statistic, and the confidence interval (if any). The APA6 requires a particular format for presenting statistical results and it demands that the results are included at the end of a sentence.

The statistical results for a t test on one mean, for example, would be:

t (67) = 2.73, p = .004, 95%CI[4.13, 4.87]

- The degrees of freedom are between parentheses directly after the name of the test statistic. Chi-squared tests add sample size to the degrees of freedom, for instance: chi-squared (12, N = 89) = 23.14, p = .027.
- The value of the test statistic is 2.73 in this example.
- The p value is .004. Note that we report all results with two decimal places except probabilities, which are reported with three decimals. We are usually interested in small probabilities—less than .05—so we need the third decimal here.

- The 95% confidence interval is 4.13 to 4.87, so with 95% confidence we state that the population mean is between 4.13 and 4.87.

Not all tests produce all results reported in the example above. For example, a z test does not have degrees of freedom and F or chi-squared tests do not have confidence intervals. Exact tests or bootstrap tests usually do not have a test statistic. Just report the items that your statistical software produces, and give them in the correct format.

4.7.2 Reporting to the general reader

For fellow scientists and especially for the general reader, it is important to read an interpretation of the results that clarifies both the subject of the test and the test results. Make sure that you tell your reader who or what the test is about:

- What is the population that you investigate?
- What are the variables?
- What are the relevant sample statistics?
- Which comparison(s) do you make?
- Are the results statistically significant and, if so, what are the estimates for the population?
- If the results are significant, how large are the differences or associations?

A test on one proportion, for instance, the proportion of all households reached by a television station, could be reported as follows:

> "The television station reaches significantly and substantially ($p = .61$) more than half of all households in Greece, $z = 4.01$, $p < .001$."

The interpretation of this test tells us the population ("all households in Greece"), the variable ("reaching a household") and the sample statistic of interest (p for proportion). It tells us that the result is statistically significant, which a fellow scientist can check with the reported p value.

Note that the actual p value is well below .001. If we would round it to three decimals, it would become .000. This suggests that the probability is zero but there is always some probability of rejecting the null hypothesis if it is true. For this reason, APA6 wants us to report $p < .001$ instead of $p = .000$.

Finally, the interpretation tells us that the difference from .5 is substantial. Sometimes, we can express the difference in a number, which is called the *effect size*, and give a more precise interpretation (see Chapter 5 for more information).

If you have the value of the test statistic but not the p value, you may report the significance level of the test instead of the p value. In this case, you either report "$p < .05$" if the test is significant or "n.s." if the test is not significant.

4.8 Relation Between Null-Hypothesis Test and Confidence Interval

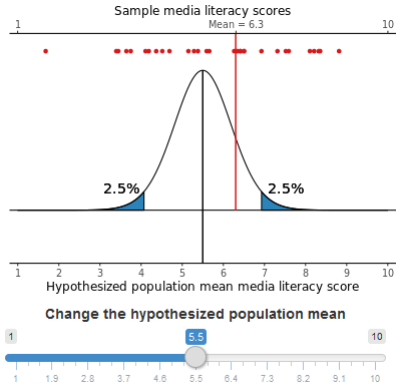


Figure 4.18: How does null hypothesis significance relate to confidence intervals?

The top of Figure 4.18 shows media literacy scores in a random sample of children and their average media literacy score (red). The hypothesized average media literacy in the population of children is shown on the bottom axis. The curve represents the sampling distribution if the null hypothesis is true. The coloured areas under the curve represent 2.5% of the total area each.

1. Would you reject the current null hypothesis with this sample?
2. What are the lowest and highest sample means for which the null hypothesis is *not* rejected?
3. Why does the sampling distribution (curve) move horizontally if you change the hypothesized population mean?
4. Use the slider to find the 95% confidence interval for the population mean given the sample mean.

Null-hypothesis testing and confidence-interval estimation are related. The long and the short of it is that a 95% confidence interval contains all null hypotheses that would *not* be rejected with the current sample at the 5% significance level, two-sided.

Remember that the probability involved in a 95% confidence interval is not the probability that the population value is within the interval. The population value is a fixed number, not a random variable with a probability distribution (at least, not in the approach to statistical inference that we follow here). For this reason, we say that we are 95% confident that the parameter lies within the 95% confidence interval but not that the population value is included in the interval with 95% probability.

The probability refers to the sample that we have drawn. If the population value would

have a value within the interval, our sample result is among the 95% samples that are most plausible to be drawn. However, this is just another way of saying that a null hypothesis with this value for the parameter is sufficiently plausible (at a 5% significance level) considering the sample that we have drawn. So we do *not* reject the null hypothesis if it specifies any of the parameter values included in the 95% confidence interval.

4.8.1 Testing a null hypothesis with a confidence interval

It is easy to execute a null hypothesis test if you know the confidence interval. If the population value specified in the null hypothesis is within the confidence interval, do not reject the null hypothesis. Otherwise, reject the null hypothesis.

Let us imagine, for instance, that the 95% confidence interval for average media literacy among children is 4.11 to 4.87. Our initial null hypothesis states that the average is at least 5.5. An average of 5.5 is clearly outside this 95% confidence interval, so this sample rejects the null hypothesis at the 5% significance level.

We have already encountered this result in a previous section. Note, however, that our original test was one-sided but a confidence interval corresponds always to a two-sided test because it allows the parameter to be both smaller and larger than the sample value.

It is also clear that any null hypothesis specifying a population mean above 5.5 would be rejected. We could already infer that from our one-sided null hypothesis test. What we could not see there, however, is that a hypothesis specifying a population mean of 4.9 or 4.0 would also have been rejected in a two-sided test at the 5% level. A confidence interval gives more information than a single null hypothesis test because it shows us test results for a range of null hypotheses.

4.8.2 Testing a null hypothesis with bootstrapping

Using the confidence interval is the easiest and sometimes the only way of testing a null hypothesis if we create the sampling distribution with bootstrapping. for instance, we may use the median as the preferred measure of central tendency rather than the mean, if the distribution of scores is quite skewed and the sample is not very large. In this situation, a theoretical probability distribution for the sample median is not known, so we resort to bootstrapping.

Bootstrapping creates an empirical sampling distribution: a lot of samples with a median calculated for each sample. A confidence interval can be created from this sampling distribution (see Section 3.5.3). If our null hypothesis about the population median is included in the 95% confidence interval, we do not reject the null hypothesis. Otherwise, we reject it.

4.9 Capitalization on Chance

The relation between null hypothesis testing and confidence intervals may have given the impression that one could test a range of null hypotheses using just one sample and one confidence interval. for instance, we could simultaneously test the null hypotheses that average media literacy among children is 5.5, 4.5, or 3.5. Just check if these values are inside or outside the confidence interval and you are done?

This impression is wrong. The probabilities that we calculate using one sample assume that we only apply one test to the data. If we test the original null hypothesis that average media literacy is 5.5, we run a risk of five per cent to reject the null hypothesis if the null hypothesis is true.

If we apply a second test to the same sample, for example, testing the null hypothesis that average media literacy is 4.5, we again run this risk of five per cent. But the risk of rejecting at least one true null hypothesis increases dramatically if we do two tests. This risk is 9.75 per cent, namely one minus the risk of rejecting no true null hypothesis, which is 1 - .95 * .95 = .0975.

The situation becomes even worse if we do three or more tests on the same sample. The total level of rejecting at least one null hypothesis that is true increases well above the significance level that we want to maintain, namely five per cent.

The phenomenon that we are dealing with probabilities of making Type I errors that are higher (*inflated Type I errors*) than the significance level that we want to use, is referred to as *capitalization on chance*. Applying more than one test to the same data is one way to capitalize on chance. If you do a lot of tests on the same data, it is very rare not to find some statistically significant results even if all null hypotheses are true.

4.9.1 Capitalization on chance in post-hoc tests

This type of capitalization on chance may occur, for example, in an analysis of variance. To test the research hypothesis that the celebrity endorsing a fundraising campaign makes a difference to people's willingness to donate, we may organize an experiment using four versions of a video clip as the treatment, each clip featuring a different celebrity endorsing the campaign. This results in four groups of participants, each group having an average score on their willingness to donate. As a first step, we test the null hypothesis that all groups have equal population means using an F test (analysis of variance).

If this test is statistically significant, we reject the null hypothesis and conclude that at least two groups have different population means. The next question is: Which groups, that is, endorsement by which celebrities, display a different willingness to donate? To answer this question, we must do post-hoc t tests on pairs of groups. With four groups, we have six pairs of groups, so we have six t tests on independent means. The probability of rejecting at least one true null hypothesis of no difference is much higher than five per cent if we use a significance level of five per cent for each single t test.

4.9.2 Correcting for capitalization on chance

We can correct in several ways for this type of capitalization on chance; one such way is by applying the Bonferroni correction. This correction merely divides the significance level that we use for each test by the number of tests that we do. In our example, we do six t tests, so we divide the significance level of five per cent by six. The resulting significance level for each t test is .008. If a t test's p value is below .008, we reject the null hypothesis, but we do not reject it otherwise.

The Bonferroni correction is a rather coarse correction, which is not entirely accurate. However, it has a simple logic that directly links to the problem of capitalization on chance. Therefore, it is a good technique to help understand the problem, which is the main goal we want to attain, here. We will skip better but more complicated alternatives to Bonferroni correction.

Note that we need not apply a correction if we specify a hypothesis beforehand about the two groups that we expect to differ. In the example of celebrity endorsement, we would not have to apply the Bonferroni correction to the t test on the mean difference between participants confronted to Celebrity A and Celebrity C if we had hypothesized that the willingness to donate differs here. Of course, we could have skipped the analysis of variance and gone straight to the t test with such a hypothesis.

4.9.3 Specifying hypotheses afterwards

Capitalization on chance occurs if we apply different tests to the same variables in the same sample. This occurs in exploratory research in which we do not specify hypotheses beforehand but try out different predictors or different outcome variables.

It occurs more strongly if we first have a look at our sample data and then formulate an hypothesis. Knowing the sample outcome, it is easy to specify a null hypothesis that will be rejected. This is plain cheating and it should be avoided at all times.

4.9.4 Advantages of using confidence intervals

If we cannot use the confidence interval to test a range of null hypotheses, what, then, is the added value of a confidence interval over a single null hypothesis test? The confidence interval tells us the plausible values of the parameter rather than whether or not it is one particular value. Putting it simply, we just know more from a confidence interval than from a null hypothesis test.

We could use the additional information, if we were to do a new null hypothesis test on a new sample. We would have a better idea of plausible null hypotheses. We could, for instance, test whether media literacy is 4.49, the middle of the confidence interval in our previous research project. A confidence interval helps us to be more specific in the next study addressing our topic, whether this study is carried out by ourselves or by our colleagues.

4.10 Take-Home Points

- We use a statistical test if we want to decide on a null hypothesis: reject or not reject? Usually, this boils down to the question: "Is there or is there not an effect (difference, association) in the population?"
- The decision rules should be specified beforehand: decide on the directionality of the test (one-sided or two-sided) and the significance level.
- The null and alternative hypotheses always concern a population statistic. Together they cover all possible outcomes for the statistic. The null hypothesis always specifies one (boundary) value for the population statistic.
- We reject the null hypothesis if a test is statistically significant. This means that the probability of drawing a sample with the current or a more extreme outcome (even more inconsistent with the null hypothesis) for the test statistic is below the significance level.
- The 95% confidence interval includes all null hypotheses that would *not* be rejected in a two-sided test at 5% significance level. It contains the population values that are not sufficiently contradicted by the data.
- The calculated p value is only correct if the same data is used for no more than one null hypothesis test and the null hypothesis was formulated beforehand.
- If the same data is used for more null hypotheses tests, the probability of a Type I error increases. We obtain too many significant results, which is called capitalization on chance.

Chapter 5

Which Sample Size Do I Need? Power!

Key concepts: minimum sample size, (unstandardized) effect size, practically significant, standardized effect size, Cohen's d (for means), Type I error, Type II error, test power.

Summary

At the start of a quantitative research project, we are confronted with a seemingly simple practical question: How large should our sample be? In some cases, the statistical test that we plan to use gives us rules of thumb for the minimum size that we need for this test.

This may tell us the minimum sample size but not necessarily the optimal sample size. Even if we can apply the statistical test technically, sample size need not be sufficient for the test to signal the population differences or associations, for short, the effect sizes, that we are interested in.

If we want to know the minimum sample size that we need to signal important effects in our data, things become rather complicated. We have to decide on the size of effects that we deem interesting. We also have to decide on the minimum probability that the statistical test will actually be significant if the true effect in the population is of this size.

This probability is the power of a test: the probability to reject a null hypothesis of no effect if the effect in the population is of a size interesting to us. If we do not reject a false null hypothesis, we make a Type II error.

Thinking about sample size thus confronts us with a problem that we have hitherto neglected, namely the problem of not rejecting a false null hypothesis. This problem is very important if the null hypothesis represents our research hypothesis. If the null hypothesis represents

our research hypothesis, our expectations are confirmed if we do *not* succeed in rejecting the null hypothesis.

However, if we do *not* reject the null hypothesis, we cannot make a Type I error, namely rejecting a false null hypothesis. As a consequence, the significance level of our test, which is the maximum probability of making a Type I error, is meaningless. We must know the probability of *not* rejecting a false null hypothesis—the power of the test—to express our confidence that our research hypothesis is true.

Test your intuition and understanding

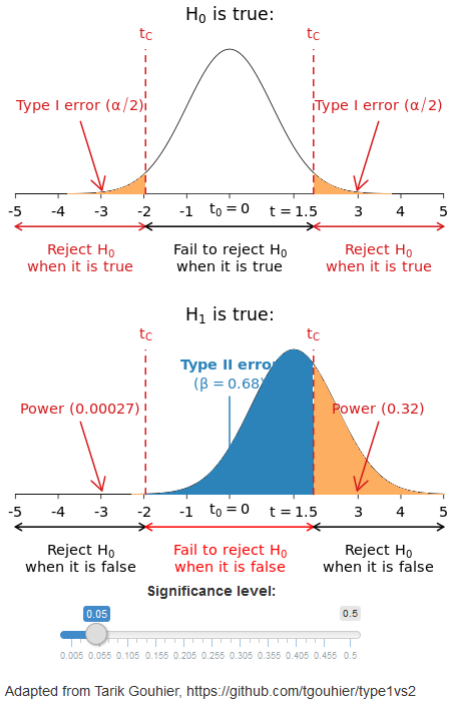


Figure 5.1: Effect size, power, Type I and Type II error.

Figure 5.1 shows sampling distributions for two worlds. Both sampling distributions are approximated with a t distribution. At the top is the hypothetical world of the researcher. In this hypothetical world, the researcher's null hypothesis is true, namely that average candy weight is 2.8 gram in the population. At the bottom is the real world in which average candy weight is 2.9 gram. The standard deviation of candy weights is 0.5.

1. What do the values on the horizontal axes mean?

Table 5.1: Rules of thumb for minimum sample sizes.

Distribution	Sample statistic	Minimum sample size
Binomial distribution	proportion	-
(Standard) normal distribution	proportion	>= 5 divided by test proportion (<= .5)
(Standard) normal distribution	one or two means	> 100
t distribution	one or two means	> 30
t distribution	(Spearman) rank correlation coefficient	> 30
t distribution	regression coefficient	20+ per predictor variable
F distribution	3+ means	all groups are more or less of equal size
chi-squared distribution	row or cell frequencies	expected frequency >= 1 and 80% >= 5

2. What does t_c mean?
3. Why are the t values and $t_c$values exactly the same on both horizontal axes?
4. What is the unstandardized and standardized effect size if average candy weight is 2.83 gram in our sample?
5. What do the double-sided horizontal red arrows represent in the top graph?
6. Why are the double-sided horizontal arrows red in the top graph and black in the bottom graph and the other way around?
7. Why are the orange sections in the top graph labelled Type I error?
8. What happens to the probability of Type II error (the blue section in the bottom graph) if you change the significance level with the slider?
9. What does *Type II error* mean in the bottom graph?

Didn't you know all answers? Return to these question after studying this chapter.

5.1 Sample Size and Test Requirements

Table 2.3 in Chapter 2 shows the conditions that must be satisfied if we want to use a theoretical probability distribution to approximate a sampling distribution. Only if the conditions are met, the theoretical probability distribution resembles the sampling distribution sufficiently for using the theoretical probability distribution.

Conditions often include sample size (Table 5.1 reproduces the sie requirements from Table 2.3). If you plan to do a t-test, either on its own or in post-hoc tests after analysis of variance, each group should contain more than thirty cases. So if you plan on doing t-tests, recruit more than thirty participants for each experimental group or more than thirty respondents

for each group in your survey and you are fine. Well, if you have to reckon with non-response, that is, sampled participants or respondents unwilling to participate in your research, you should recruit more participants or respondents to have more than thirty observations in the end.

Chi-squared tests require a minimum of five expected frequencies per category in a frequency distribution or cell in a contingency table. Your sample size should be at least the number of categories or cells times five to come even near this requirement. Regression analysis requires at least 20 cases per predictor variable in the regression model.

The variation of sample size across groups is important to the analysis of variance. If the number of cases is more or less the same across all groups, we need not worry about the variances of the outcome variable in the population for the groups. To be on the safe side, then, it is recommended to design your sampling strategy in such a way that you end up with more or less equal group sizes if you plan to use analysis of variance (ANOVA).

5.2 Effect Size

We have learned that larger samples have smaller standard errors (Section 3.3.1). Smaller standard errors yield (absolutely) larger test statistic values and larger test statistics have smaller p values. In other words, a test on a larger sample is more often statistically significant.

A larger sample offers more precision, so we will more often be convinced that the difference between our sample outcome and the hypothesized value is sufficient to reject the null hypothesis. For example, we would reject the null hypothesis that average candy weight is 2.8 gram in the population if the average weight in our sample bag is 2.75 gram and our sample bag is very big. But we may not reject the null hypothesis if we have the same outcome in a small sample bag.

Of course, the size of the difference between our sample outcome and the hypothesized value matters as well. If average candy weight in our sample bag deviates more from the average weight that we expect according to the null hypothesis, we are more likely to reject the latter. If we think of our statistical test as a security metal detector, our test will pick up smaller amounts of metal if the sample is larger.

[htbp] 

Figure 5.2: Security metal detector

The probability to reject a null hypothesis, then, depends both on sample size and the difference between what we expect null hypothesis) and what we find (sample outcome). This difference is called *effect size*. With a larger sample, we need a smaller difference between outcome and expectation (effect size) to reject the null hypothesis.

Deciding on our sample size, we should ask ourselves this question: What effect size should produce a significant test result? In the security metal detector example, at what minimum quantity of metal should the alert sound? To answer this question, we should consider the practical aims and context of our research.

5.2.1 Practical significance

Investigating the effects of a new medicine on a person's health, we may require some minimum level of health improvement to make the new medicine worthwhile medically or economically. If a particular level of improvement is clinically important, it is *practically significant*.

If we have decided on a minimum level of improvement that is relevant to us, we want our test to be statistically significant if the average true health improvement in the population is at least of this size. We want to reject the null hypothesis of no improvement in this situation.

For media interventions such as health, political, or advertisement campaigns, one could think of a minimum change of attitude affected by the campaign in relation to campaign costs. A choice between different campaigns could be based on their efficiency in terms of attitudinal change per cost unit.

Note the important difference between practical significance and statistical significance. Practical significance is what we are interested in. If the new medicine is sufficiently effective, we want our statistical test to signal it. In the security metal detector example: If a person carries too much metal, we want the detector to signal it.

Statistical significance is just a tool that we use to signal practically significant effects. Statistical significance is not meaningful in itself. For example, we do not want to have a security detector responding to a minimal quantity of metal in a person's dental filling. Statistical significance is important only if it signals practical significance. We will return to this topic in Chapter 6.

5.2.2 Unstandardized and standardized effect sizes

The difference between our sample outcome and the hypothesized value is the _ unstandardized effect size_. If we test a mean, the unstandardized effect size is just the difference between our sample mean and the hypothesized population mean. For example, if we hypothesized that average candy weight in the population is 2.8 gram and we find an average candy weight in our sample bag of 2.75 gram, the unstandardized effect size is -0.05 gram.

Unstandardized effect sizes depend on the scale on which we measure the sample outcome. The unstandardized effect size of average candy weight changes if we measure candy weight in grams, micro grams, kilograms, or ounces. Of course, changing the scale does not affect the meaning of the effect size but the number that we are looking at is very different: 0.05 gram, 50 micro gram, 0.00005 kilo, or 0.00176 ounce. The unstandardized effect size value, then, does not tell us whether the effect size is large or small.

5.2.3 Cohen's d

In scientific research, we rarely have precise norms for differences that are practically significant and differences that are not. Instead, we tend to think of small and large effects as differences that are large or small in comparison to the scores that we encounter.

If candy weights vary a lot, we will not be very impressed by a relatively small difference between observed and expected (hypothesized) average candy weight. In contrast, if candy weight is quite constant, a small average difference is important.

For this reason, standardized effect sizes for sample means divide the difference between the sample mean and the hypothesized population mean by the standard deviation in the sample. Thus, we take into account the variation in scores. This standardized effect size for tests on means is known as *Cohen's d*.

The sample outcome can be a single mean, for instance the average weight of candies, but it can also be the difference between two means, for example, the difference between average weight of yellow candies and average weight of red candies. In the latter case, the difference is divided by a combined (*pooled*) standard deviation for yellow and red candy weight.

The direction of an effect is not relevant to effect size. For example, we do not care whether the yellow candies or the red candies are on average heavier. For this reason, Cohen's d is always positive. If you obtain a negative result, just drop the minus sign.

Using an inventory of published results of tests on one or two means, Cohen (1969) proposed rules of thumb for standardized effect sizes:

- 0.2: weak effect,
- 0.5: moderate effect,
- 0.8: strong effect.

Note that Cohen's d can take values above one. These are to be considered strong effects.

5.2.4 How to calculate Cohen's d from SPSS output

5.2.4.1 Instructions

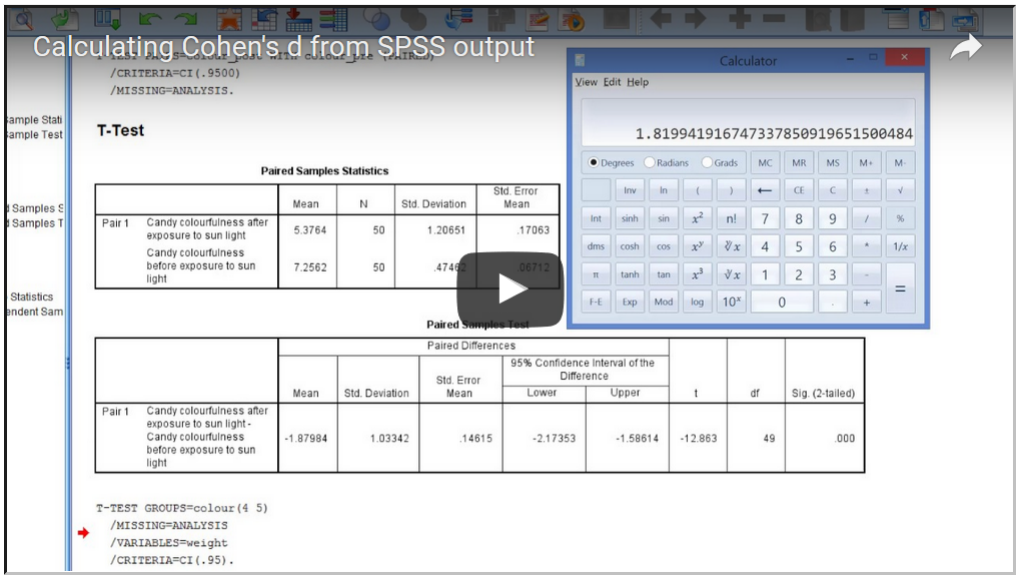


Figure 5.3: Calculating Cohen's d from SPSS output.

5.2.4.2 Exercises

1. Open data set voters.sav that contains information about the age and attitude towards immigration among a random sample of voters. What are the unstandardized and standardized effect sizes if the hypothesized average attitude towards immigrants in the population is 6.0?
2. What are the effect sizes if the null hypothesis states that the average attitude towards immigrants in the population is at least 6.0? And what if it states that average attitude is at most 6.0?
3. What are the unstandardized and standardized effect sizes of a test in which we compare the attitude towards immigrants of young voters to the attitude of old voters? Again, use data set voters.sav.

5.2.5 Association as effect size

Measures of association such as Pearson's product-moment correlation coefficient or Spearman's rank correlation coefficient express effect size if the null hypothesis expects no

correlation in the population. If zero correlation is expected, a correlation coefficient calculated for the sample expresses the difference between what is observed (sample correlation) and what is expected (zero correlation in the population).

Effect size is also zero according to the stadard null hypotheses used for tests on the regression coefficient (b), R^2 for the regression model, and eta^2 for analysis of variance. As a result, we can use the standardized regression coefficient (Beta in SPSS and b^* according to APA6), R^2, and eta^2 as standardized effect sizes.

Because they are standardized, we can interpret their effect sizes using rules of thumb, e.g., an association between 0 and .10 is interpreted as no or a very weak association, between .10 and .30 is weak, between .30 and .50 is moderate, .50 to .80 is strong, and .80 to 1.00 is very strong, while exactly 1.00 is a perfect association (if 1.00 is the maximum value). Note that we ignore the sign (plus or minus) of the effect if we interpret its size.

5.2.6 Effect size and sample size

We can use standardized effect size to express the effects that we are interested in without caring about the precise size of differences. We merely have to choose whether small, moderate, or large effects are of practical interest to us. Preferably, we know from previous research whether small, moderate, or large effects are common in our type of research. If moderate or large effects are rare, we should use a sample size that allows detecting small effects. In contrast, when large effects occur frequently, we can do with a smaller sample that may miss small effects.

If we know the effect size in the sample for which we want statistically significant results, we can figure out the minimum sample size for which the test statistic is statistically significant.

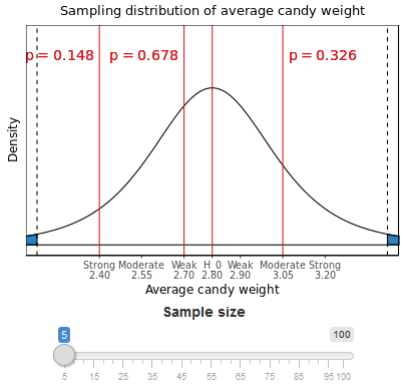


Figure 5.4: What is the minimum sample size required for a significant test result if the sample mean has a particular effect size?

1. Use the slider in Figure 5.4 to find the minimum sample size that we need for a statistically significant test result.

2. What is the meaning of the p values and why do they decrease if we increase sample size?

3. Compare the p values to the blue tails. Is there something wrong in this app?

Effect size as well as test statistics reflect the difference between what we expect according to the null hypothesis and what we observe in our sample. As a consequence, effect size indicators and test statistics are related. In some cases, such as Cohen's d, the relation between effect size and test statistic is very simple.

The test statistic t for a t test on one mean is equal to Cohen's d times the square root of sample size. Here, the only difference between the two is sample size! Sample size influences the test statistic—the larger the sample, the larger the test statistic—but it does not affect effect size. This is one reason why effect size is more interesting than test statistics and their p values.

5.3 Hypothetical World Versus Imaginary True World

In the preceding paragraphs, we determined sample size using the effect size that we expect to find in our sample. We should realize, however, that we are interested in the effect size in the population. The 'true' effect size, so to speak.

The effect of a new medicine or a media campaign in our sample is not important but the effect in the population is. This complicates the calculation of our sample size. Instead of using the effect size in our (future!) sample, we must use the effect size in the population.

5.3.1 Imagining a population with a small effect

Our null hypothesis states that average candy weight in the population is 2.8 grams. Let us decide that a small effect size is practically significant. We can think now of a population that could be the true population if the effect size is small. For example, a population in which average candy weight is 2.9 grams (and the standard deviation is 0.5).

We do not know whether average candy weight is 2.9 grams in the true population. So we may regard this as another hypothesis. Let us call this the alternative hypothesis H_1. Note that this is not an ordinary alternative hypothesis because it does not include all outcomes not covered by the null hypothesis (H_0). Instead, it represents only one value, which is an important value to us because it represents a population with a small but interesting effect size.

Our habit of formulating a null hypothesis and an alternative hypothesis for all situations not covered by the null hypothesis is generally attributed to the statistician R.A. Fisher. This, however, is not entirely correct (see, e.g., Halpin & Stam, 2006). Fisher introduced the concept of a null hypothesis (Ronald Aylmer Fisher, 1935: 18) but not the concept of an alternative hypothesis. The statisticians Jerzy Neyman and Egon Pearson introduced

the idea of working with two or more hypotheses. But the two hypotheses do not cover all possible population values and they were usually not called a null and alternative hypothesis. They specify two or more different population values. A statistical test is used to determine which of the hypotheses fits the sample best. (J. Neyman & Pearson, 1933)

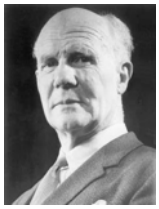
[htbp] 

Figure 5.5: Egon Pearson.

Figure 5.6 illustrates this situation. The top graph represents the sampling distribution according to our null hypothesis. This sampling distribution is derived from our hypothetical population in which there is no effect. Our null hypothesis is true for this population. In our current example, average candy weight is 2.8 grams in this hypothetical population.

The bottom graph represents the sampling distribution for an imaginary population with a small effect size. Here, the alternative hypothesis is true, for instance, average candy weight is 2.9 grams, which is a bit higher than in the hypothetical population.

By the way, average population candy weights are not depicted in the graphs but you should know by now that the average in a normal or t distribution is situated at the top of the bell shape and that the average of a sample mean sampling distribution is equal to the population average because a sample mean is an unbiased estimator.

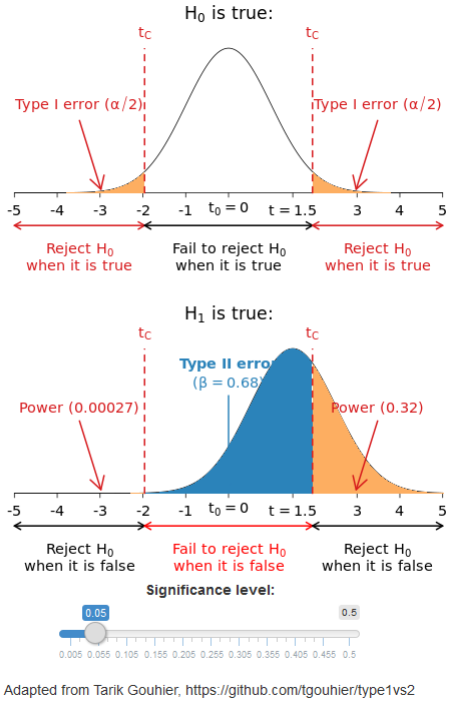


Figure 5.6: Simulation of Type I and Type II error.

Before reading on, try to make sense of the two graphs in Figure 5.6 and how they relate to each other:

1. What is the relation between significance level and Type I error? Formulate your answer very precisely: Details matter now! Check your answer by changing the significance level.
2. What exactly is Type II error?
3. How does the probability of a Type II error relate to the probability of a Type I error? Try to explain the relation in your own words.

5.3.2 Type I error

We have two populations, a hypothetical population and an imaginary true population. Once we have drawn our sample, we only deal with the hypothetical population, for instance, the top graph in Figure 5.6, as we have done in all preceding chapters.

Acting as if the null hypothesis is true, we determine how (un)likely the sample is that we have drawn. If it is very unlikely, we have a p value below the significance level and we

reject the null hypothesis. We say: If the null hypothesis was true, our sample would be too unlikely, so we reject the null hypothesis.

We may be wrong. Perhaps the null hypothesis is actually true and we were just very unfortunate to draw a sample that is very different from the population. If so, we make a Type I error (see Section 4.5.4). The probability that we will make this error is equal to the significance level, which is usually set to .05.

5.3.3 The world of the researcher

This is what we are doing once we have the sample. Let us call this the world of the researcher. At present, we have not yet stepped into the world of the researcher because we are still thinking about the size of the sample that we are going to draw.

We can experiment a bit and that is what we do if we ask ourselves: What is going to happen to our statistical test if the true population from which we draw our sample has average candy weight that is a bit higher (small effect) than candy weight according to our null hypothesis?

5.3.4 The alternative world of a small effect

If we actually sample from this imaginary true population, the bottom graph in Figure 5.6 represents our true sampling distribution. It shows us the true probabilities (areas under the curve) of drawing a sample with a particular minimum or maximum value for the test statistic t. These are the probabilities of our sample if there is a small effect in the population.

Now that we know the true sampling distribution if there is a small effect in the population, we can foresee what is going to happen when we enter the world of the researcher. The researcher is going to use the test values of the top graph to decide on the null hypothesis. If the sample t value is between, say, plus and minus two (the critical values, t_c in Figure 5.6), the researcher is not going to reject the null hypothesis.

5.3.5 Type II error

If there is a (small) effect in the population, the null hypothesis is not true. For example, average candy weight is not 2.8 gram, it is 2.9 gram. If our sample mean is close to 2.8 gram, we may not reject the null hypothesis even if it is not true. This is a *Type II error*: not rejecting a false null hypothesis.

The probability that we make a Type II error if there is a small effect is expressed by the blue section in the bottom graph. It is usually denoted by the Greek letter beta (β). The blue section represents the probability of drawing a sample from this population with a small effect size that has a t value that is NOT in the rejection region, so the null hypothesis is NOT rejected. See the top graph.

Table 5.2: Error types and their probabilities.

	Null is true	Null is false
Null is rejected	Type I error, Significance level (alpha)	No error, Power (1 - beta)
Null is not rejected	No error, (1 - alpha)	Type II error, (beta)

Table 5.2 summarizes the four possible situations that may arise if we test a null hypothesis. The null hyothesis may be true or false and we may or may not reject the null hypothesis.

5.3.6 Power of the test

The probability of NOT making a Type II error is called the *power of the test*. It is of course equal to one minus the probability of making a Type II error, that is, 1 - β. The power of the test is represented by the orange sections in the bottom graph. They represent the probability of getting a sample t value that makes the researcher reject the null hypothesis. So a false null hypothesis is rejected and we do not make an error.

Note that we can reject the null hypothesis in two ways: If our sample happens to have a test statistic that is much higher than expected under the null hypothesis or if it is much lower. In the example above, the imagined true population has a mean that is higher than the hypothesized population mean. The bulk of the power of the test therefore is in the right tail of the bottom graph.

However, a little bit of power is situated in the left tail. It is so small that we usually cannot see the orange section in the left tail of the bottom graph but the displayed probability shows that it is there. This is a bit strange because one could say that we reject the null hypothesis for the wrong reason: We think our null hypothesis is too high whereas it actually is too low.

The probability that this happens is very small and usually negligible. In the interactive content, you may encounter power values in the left tail that are so small that they have to be written in scientific notation, e.g., 1.0E-10, which means 1 at the tenth decimal place: 0.0000000001. Anyway, the important thing is that we reject a false null hypothesis even if it is for the 'wrong' reason. Rejecting a false null hypothesis, our conclusion is not erroneous.

5.3.7 Effect size, sample size, and power

Figure 5.7 illustrates the concept of test power. It draws 1,000 samples from a population in which the true population mean is equal or larger than the population mean according to the null hypothesis. *True effect size* reflects how much the true population mean is larger than the hypothesized mean. (Note that this is different from effect size based on the sample value that we discussed in Section 5.2.)

For each sample, the test statistic t is calculated and the right-sided p value. The 1,000 t values are shown in the blue histogram and the p values are collected in the red histogram.

If the test is significant, the null hypothesis is rejected. Test power and the proportion of samples for which the null hypothesis is rejected are shown above the blue histogram.

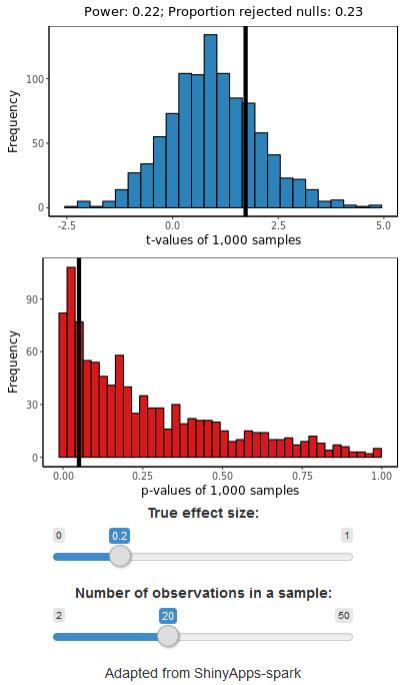


Figure 5.7: How does test power relate to true effect size and sample size in a right-sided test?

First, familiarize yourself with the histograms in Figure 5.7 by figuring out the answers to the following questions:

1. What does the vertical black line in the blue histogram represent?
2. Which blue bars in the histogram represent the samples with statistically significant test results, that is, samples for which the null hypothesis is rejected?
3. What does the vertical black line in the red histogram represent?
4. Which red bars in the histogram represent the samples with statistically significant test results, that is, samples for which the null hypothesis is rejected?
5. Next, formulate for yourself how test power will change if you increase true effect size or sample size. Check your expectations by adjusting the values in the interactive content.
6. Finally, think about this. There is one situation in which power is meaningless. Which value should you assign to true effect size or sample size to create that situation? In this situation, what does the proportion of rejected nulls indicate?

5.4 Sample Size and Power

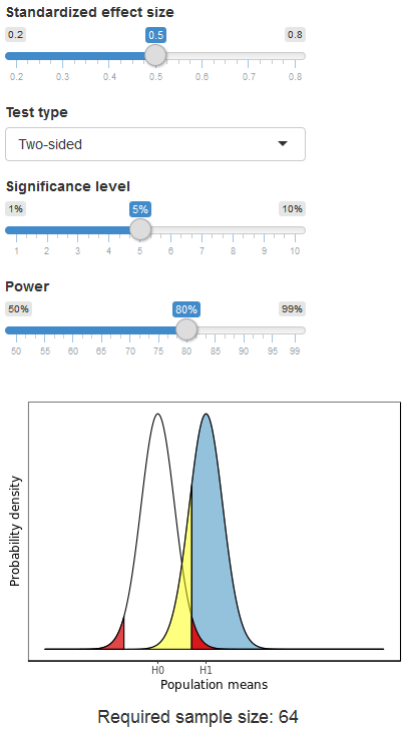


Figure 5.8: How does sample size depend on test power, significance, and effect size?

1. Figure 5.8 shows the sampling distributions of the sample mean under the null hypothesis (H_0, left-hand curve) and under the assumed true value of the population mean (H_1, right-hand curve). Explain the meaning of the red, yellow, and blue surfaces in the graph.
2. What happens to the red, yellow, and blue surfaces if you set power to 50%? And what happens to the minimum sample size? Adjust the power slider to check your answers.
3. Do we need a smaller or a larger sample to achieve the specified test power for a larger effect size? Move the effect size slider to check your answer.
4. Do we need a smaller or a larger sample to achieve the specified test power for a one-sided test instead of a two-sided test? Change the test type to check your answer.
5. Do we need a smaller or a larger sample to achieve the specified test power for a higher significance level? Move the significance level slider to check your answer.
6. Why do the sampling distributions become wider if we increase effect size or significance

level, or if we decrease test power?

Sample size, statistical significance, effect size, and test power are related. To determine the size of your sample, you have three buttons that you should adjust simultaneously. Statistical significance is the easiest button to decide on; we usually leave the significance level at .05. We do not select a smaller value because it will reduce the power of the test (with the same sample and effect size) as you may have noticed in one of the figures in the preceding section.

For effect size, we have to choose among a small, moderate, or large effect. Previous results of research similar to our research project can help us decide whether we have to reckon with small effect sizes (need a larger sample) or not. If we have a concrete number for the (standardized) minimum effect size that is of practical significance, we can use that number.

For power, the conventional rule of thumb is that we like to have at least 80% probability of rejecting a false null hypothesis. You may note that the probability of NOT rejecting a true null hypothesis is higher: .95. After all, it is one minus the probability of rejecting a true null hypothesis (Type I error), which is the significance level.

Power is set to a lower level because the null hypothesis is usually assumed to reflect our best knowledge about the world. From this perspective, we are keener on avoiding the error of falsely rejecting the null hypothesis (our current best knowledge) than falsely accepting it. This approach, however, is not without criticisms as we will discuss in Chapter 6. Anyway, if you want to raise the power to the same level of .95, you can do so; it will require a larger sample.

Unfortunately, test power receives little attention in several software packages for statistical analysis. Using power and effect size to calculate the required sample size is usually not provided in the package. To calculate sample size, we need dedicated software, for example GPower.

5.4.1 So how do we determine sample size?

All in all, using effect size and test power to determine the size of the sample requires several decisions on the part of the researcher. It can be difficult to specify the effect size that we should expect or that is practically relevant. If there is little prior research comparable to our new project, we cannot reasonably specify an effect size and calculate sample size.

Of course, it is important to ensure that our sample meets the requirements of the tests that we want to specify (Section 5.1). In practice, researchers often go well beyond this minimum. They try to collect as large a sample as is feasible just to be on the safe side.

Does this mean that all we have learned about effect size and test power is useless? Certainly not. First of all, we should have learned that effect size is more important than statistical significance because effect size relates to practical significance.

Second, test power and Type II errors are important in situations in which we do not reject the null hypothesis. Then, we should calculate test power to get an impression of

our confidence in the result (see the next section). Is our test of sufficient power to yield significant results if there is an effect in the population?

5.5 Research Hypothesis as Null Hypothesis

As noted before (Section 4.3), the research hypothesis usually is the alternative hypothesis. We expect something to change, to be(come) different rather than be or stay the same. We expect an association to be present rather than absent.

In this situation, rejection of the null hypothesis supports our alternative hypothesis, hence our research hypothesis, so we are glad if we reject the null hypothesis. Of course, we know that we can be wrong. Our null hypothesis may still be true even if the probability of drawing a sample like the one we have drawn is so small that we have to reject the null hypothesis. This is the Type I error.

Fortunately, we know the probability of making this error because it is the significance level that we have chosen, five per cent usually. We can live with this probability of making an error if we reject the null hypothesis. So we are doubly glad: We found support for our research hypothesis *and* we know how confident we are about this support.

What if our research hypothesis is our null hypothesis? For example, we have a specific idea of average candy weight in the population from previous research or from specifications by the candy factory. If we want to test whether the candies have the hypothesized average weight, our research hypothesis would specify this average weight. Specifying a particular value, the research hypothesis must be the null hypothesis.

If the research hypothesis is the null hypothesis because it contains a single value for the population parameter, we find support for our research hypothesis if we do *not* reject the null hypothesis. We can be wrong in not rejecting the null hypothesis. If we do not reject a null hypothesis that is actually false, we make a Type II error.

The significance level is irrelevant now because the significance level is the probability of making a Type I error. But now, we do not reject the null hypothesis, so we can never reject a true null hypothesis (Type I error). Instead, the probability of making a Type II error is important, or rather, the probability of not making this error. This is the power of the test.

So if our research hypothesis represents the null hypothesis and our research hypothesis is supported (not rejected), we need the test power to know how confident we can be about the support that we have found. Here, test power is key, not statistical significance.

5.6 Take-Home Points

- Effect size is related to practical significance. Effect sizes are expressed by (standardized) mean differences, regression coefficients, and measures of association such as the correlation coefficient, R^2, and eta^2.

- Statistical significance of a test depends on effect size and sample size.
- Not rejecting a false null hypothesis is a Type II error. A researcher can make this error only if the null hypothesis is not rejected.
- The probability of making a Type II error is commonly denoted with the Greek letter beta (β).
- The probability of *not* making a Type II error is the power of the test.
- The power of a test tells us the probability that we reject the null hypothesis if there is an effect of a particular size in the population. The larger this probability, the more confident we are that we do not overlook this effect when we do not reject the null hypothesis.

Chapter 6

Critical Discussion of Null Hypothesis Significance Testing

Key concepts: problems with null hypothesis significance testing, meta-analysis, replication, frequentist versus Bayesian inference.

Summary

Null hypothesis significance testing is widely used in the social and behavioral sciences. There are, however, problems with null hypothesis significance tests that are increasingly being recognized.

Statistical significance of a null hypothesis test depends strongly on the size of the sample, so non-significance may merely mean that the sample is too small. In contrast, irrelevant tiny effects can be statistically significant in a very large sample. Finally, we normally test a null hypothesis that there is no effect whereas we have good reasons to believe that there is an effect in the population. So what does a significant test result really tell us?

Among the alternatives to null hypothesis significance testing, using a confidence interval to estimate effects in the population is easiest to apply. It is closely related to null hypothesis testing, as we have seen in Section 4.8 but it offers us information with which we can draw a more nuanced conclusion about our results.

Test your intuition and understanding

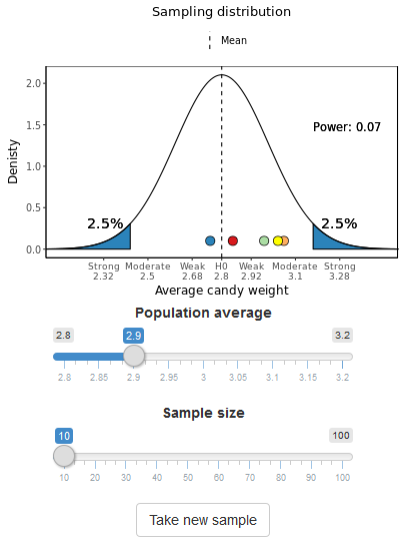


Figure 6.1: How do statistical significance, effect size, sample size, and power relate?

Figure 6.1 displays the sampling distribution for candy weight under the null hypothesis that average candy weight is 2.8 in the population. The horizontal axis shows average candy weight and the standardized effect size (Cohen's d) in a sample: weak, moderate, or strong . Five samples are drawn from a population with the average candy weight specified by the top slider. The samples' average candy weights are represented by coloured dots on the horizontal axis.

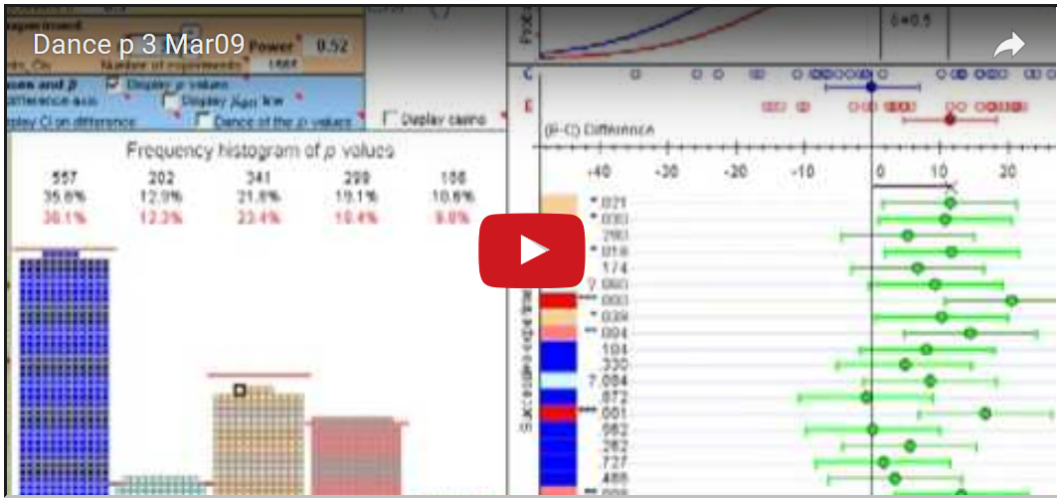
1. Which sample means are statistically significant (5% two-sided) and which are not?

2. Is the null hypothesis true for samples with non-significant mean scores?

3. What happens to the statistical significance of the sample means and to test power if you change sample size?

6.1 Criticisms of Null Hypothesis Significance Testing

In null hypothesis significance testing, we totally rely on the test's p value. If this value is below .05 or another significance level, we reject the null hypothesis and we accept it otherwise. Is this a wise thing to do? Watch the video.



6.1.1 Statistical significance depends primarily on sample size

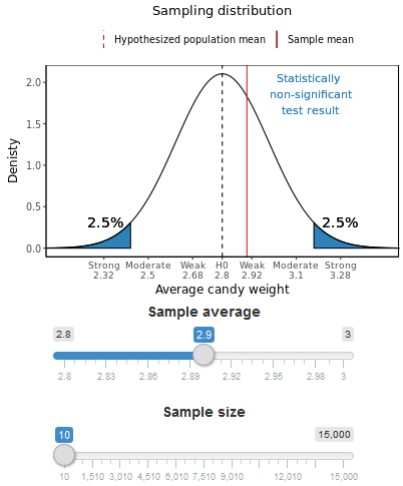


Figure 6.2: Any effect can be statistically significant.

1. In Figure 6.2, what should you do to obtain a statistically significant result for a sample average of 2.9 gram if the null hypothesis states that average candy weight is 2.8?

2. Can you get a statistically significant result for the smallest effect size, that is, for the smallest non-zero difference between the observed sample average and the hypothesized population average?

3. There is one sample mean for which we can never reject the null hypothesis, no matter how large we make the sample. Which sample mean would that be?

Perhaps, Chapter 4 on null hypothesis testing should have been titled *Am I Lucky or Unlucky?* instead of *Am I Right or Am I Wrong?* When our sample is small, the power to reject a null hypothesis is rather small, so it occurs often that we retain the null hypothesis even if it is wrong. There is a lot of uncertainty about the population if our sample is small. So we must be lucky to draw a sample that is sufficiently at odds with the null hypothesis to reject it.

If our sample is large or very large, small differences between what we expect according to our null hypothesis can be statistically significant even if the differences are too small to be of any practical value. A statistically significant result need not be practically relevant.

It is, however, a common mistake to think that statistical significance is a measure of the strength or practical significance of an effect. In the video, this mistaken interpretation is expressed by the type of sound associated with a p value: the lower the significance level of the test result, the more joyous the sound.

It is wrong to use statistical significance as a measure of strength or importance. In a large sample, even irrelevant results can be highly significant and in small samples, as demonstrated in the video, results can sometimes by highly significant and sometimes be insignificant. Never forget:

> A statistically significant result ONLY means that the null hypothesis must be rejected.

6.1.2 Statistical significance depends on sample size because of test power

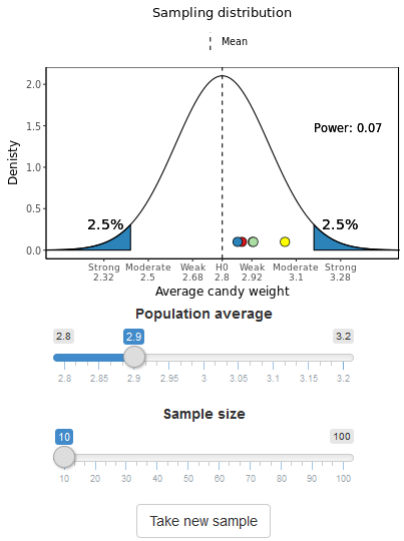


Figure 6.3: The relations between significance, effect size, sample size, and power.

Figure 6.3 displays the sampling distribution for average candy weight that you have already seen at the start of this chapter.

1. What is the null hypothesis in Figure 6.3?
2. What is the relation between test power as displayed in Figure 6.3 and the statistical significance of the sample means in this figure? It may help to draw new samples a couple of times.
3. How can we use sample size to increase the probability of statistically significant results if the null hypothesis is not true?
4. When is a statistically significant result more surprising: with high or low test power?

If we want to say something about the magnitude of an effect in the population, we should use effect size. All we have is the effect size measured in our sample and a statistical test usually telling us whether or not we should reject the null hypothesis that there is no effect size in the population.

If the statistical test is significant, we conclude that an effect probably exists in the population. We may use the effect size in the sample as a point estimate of the population effect. This effect size should be at the core of our interpretation. Is it large (strong), small (weak), or perhaps tiny and practically irrelevant?

If the statistical test is not significant, it is tempting to conclude that the null hypothesis is true, namely, that there is no effect in the population and we need not interpret the effect

that we find in our sample. But this is not right. Finding insufficient proof for rejecting the null hypothesis does not prove that the null hypothesis is true.

In a two-sided significance test, the null hypothesis specifies one particular value for the sample outcome. If the outcome is continuous, for instance, a mean or regression coefficient, the null hypothesis can hardly ever be true. The true population value is very likely not exactly the same as the hypothesized value. It may be only slightly different but it is different.

Instead of focusing on true versus false, we had better take into account the probability that we reject the null hypothesis, which is test power. If test power is low, as it often is in social scientific research without very large samples, we should realize that there can be a substantive difference between true and hypothesized population values even if the test is not statistically significance.

With low power, we have high probability of not rejecting a false null hypothesis even if the true population value is quite different from the hypothesized value. The statistical test result should not make us conclude that there is no interesting effect.

In contrast, if our test has very high power, we should expect effects to be statistically significant. Even tiny effects that are totally irrelevant from a substantive point of view. For example, an effect of exposure on attitude of 0.001 on a 10-point scale, is likely to be statistically significant in a very large sample but it is substantively uninteresting.

As noted before (Section @ref()), standard statistical software usually does not report the power of a test. For this reason, it is not common practice to evaluate the statistical significance of results in combination with test power.

By now, however, you understand that test power is affected by sample size. You should realize that null hypotheses are easily rejected in large samples but they are more difficult to reject in small samples. Don't let your selection of interesting results be guided predominantly by statistical significance if your sample is not very large.

6.1.3 Knocking down straw men (over and over again)

There is another aspect in the practice of null hypothesis significance testing that is not very satisfactory. Remember that null hypothesis testing was presented as a means for the researcher to use previous knowledge as input to her research. The development of science requires us to expand existing knowledge. Does this really happen in the practice of null hypothesis significance testing?

Imagine that previous research has taught us that one additional unit of exposure to advertisements for a brand increases a person's brand awareness on average by 0.1 unit if we use well-tested standard scales for exposure and brand awareness. If we want to use this knowledge in our own research, we would hypothesize that the regression coefficient of exposure is 0.1 in a regression model predicting brand awareness.

Well, try to test this null hypothesis in your favourite statistics software. Can you actually tell the software that the null hypothesis for the regression coefficient is 0.1? Most likely

you can't because the software automatically tests the null hypothesis that the regression coefficient is zero in the population.

This approach is so prevalent that null hypotheses equating the population value of interest to zero have received a special name: the *nil hypothesis* or *the nil* for short (see Section 4.3.3). So you simply cannot include previous knowledge in your test if the software always tests the nil.

The null hypothesis that there is no association between the predictor variable and the outcome variable in the population may be interesting to reject if you really have no clue about the association. But in the example above, previous knowledge makes us expect a positive association of a particular size. Here, it is not interesting to reject the null hypothesis of no association. The null hypothesis of no association is a *straw man* in this example. It is unlikely to stand the test and nobody should applaud if we knock it down.

Rejecting the nil time and again should make us wonder about scientific progress and our contribution to it. Are we knocking down straw men hypotheses over and over again? Is there no way to accumulate our efforts?

6.2 Alternatives for Null Hypothesis Significance Testing

In the social and behavioral sciences, null hypothesis testing is still the dominant type of statistical inference. For this reason, an introductory text like the current one must discuss null hypothesis significance testing. But it should discuss it thoroughly, so the problems and errors that occur with null hypothesis testing become clear and can be avoided.

The problems with null hypothesis significance testing are increasingly being recognized. Alternatives to null hypothesis significance testing have been developed and are becoming more accepted within the field. In this section, some alternatives are briefly sketched.

6.2.1 Estimation instead of hypothesis testing

Following up on a report commissioned by the American Psychological Association APA (Wilkinson, 1999), the 6$^{\text{th}}$ edition of the *Publication Manual of the American Psychological Association* recommends reporting and interpreting confidence intervals rather than relying solely on null hypothesis tests.

Estimation is becoming more important: Assessing the precision of our statements about the population rather than deciding pro or con our hypothesis about the population. This is an important step forward and it is easy to accomplish if your statistical software reports confidence intervals.

[htbp]

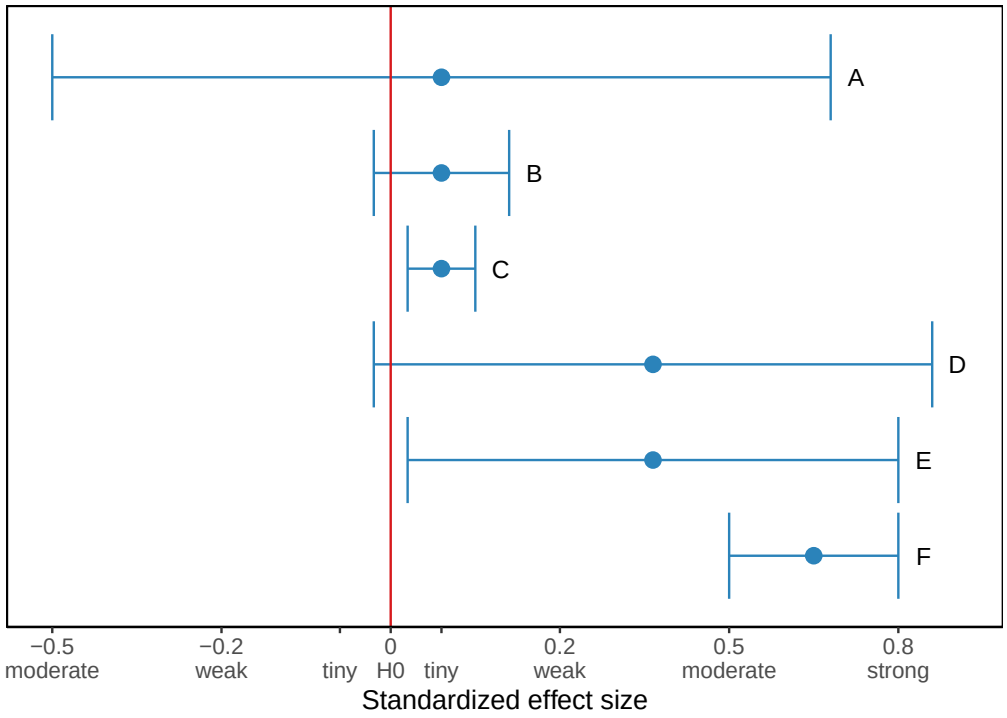


Figure 6.4: What is the most sensible interpretation of the result represented by the confidence interval ?

Figure 6.4 shows six confidence intervals for a population value, for instance, the effect of exposure to advertisements on brand awareness, and the sample result as point estimate (dot). The horizontal axis is labeled by the size of the effect: the difference between the effect in the sample and the absence of an effect according to the null hypothesis.

1. Would you advise the company to use the advertisement based on a null hypothesis significance test?
2. Would you advise the company to use the advertisement based on the confidence interval in Figure 6.4?

A confidence interval shows us whether or not our null hypothesis must be rejected (see 4.8). The rule is simple: If the value of the null hypothesis is within the confidence interval, the null hypothesis must not be rejected. By the way, note that a confidence interval allows us to test a null hypothesis other than the nil. If we hypothesize that the effect of exposure on brand awareness is 0.1, we reject the hypothesis if the confidence interval of the regression coefficient does not include 0.1.

At the same time, however, confidence intervals allow us to draw a more nuanced conclusion. A confidence interval displays our uncertainty about the result. If the confidence interval is

wide, we are quite uncertain about the true population value. If a wide confidence interval includes the null hypothesis near one of its boundaries, we reject the null hypothesis but it still is plausible that the population value is substantially larger (or substantially smaller) than the hypothesized value.

We should report that the population value seems to be larger (smaller) than specified in the null hypothesis but that we have inconclusive evidence because the test is not statistically significant. This is better than reporting that there is no difference because the statistical test is not significant.

The fashion of speaking of a null hypothesis as "accepted when false", whenever a test of significance gives us no strong reason for rejecting it, and when in fact it is in some way imperfect, shows real ignorance of the research workers' attitude, by suggesting that in such a case he has come to an irreversible decision.

The worker's real attitude in such a case might be, according to the circumstances:

(a) "The possible deviation from truth of my working hypothesis, to examine which the test is appropriate, seems not to be of sufficient magnitude to warrant any immediate modification."

Or it might be:

(b) "The deviation is in the direction expected for certain influences which seemed to me not improbable, and to this extent my suspicion has been confirmed; but the body of data available so far is not by itself sufficient to demonstrate their reality." (Ronald Aylmer Fisher, 1955: 73)

[htbp] 

Figure 6.5: Sir Ronald Ayler Fisher.

In a similar way, a very narrow confidence interval including the null hypothesis and a very narrow confidence interval near the null hypothesis but excluding it should not yield opposite conclusions because the statistical test is significant in the first but not in the second situation. After all, even for the non-significant situation, we know with high confidence (narrow confidence interval) that the population value is close to the hypothesized value.

Using confidence intervals in this way, we avoid the problem that statistically non-significant effects are not published. Not publishing non-significant results, either because of self-

selection by the researcher or selection by journal editors and reviewers, offers a misleading view of research results.

If results are not published, they cannot be used to design new research projects. For example, effect sizes that are not statistically significant are just as helpful to determine sample size as statistically significant effect sizes. A predictor variable without statistically significant effect may have a significant effect in a new research project and should not be discarded if the potential effect size is so substantial that it is practically significant. Moreover, combining results from several research projects helps making more precise estimates of population values, which brings us to meta-analysis.

6.2.2 Meta-analysis

Meta-analysis is a method that capitalizes on previous knowledge. In this method, we collect previous research on the same topic that use the same or highly similar variables. Combining the results of these studies, we can make statements with higher precision about the population. Basically, we combine the separate samples used for each single study into a large sample, which reduces the uncertainty and allows more precise inferences about the population.

Meta-analysis is a good example of combining research efforts to increase our understanding. It favours estimation over hypothesis testing because the goal is to obtain more precise estimates of population values or effects. It may also refine our theories if we can identify features of the research project that systematically affect analysis results.

Consider, for instance, the effect of advertisement exposure on brand awareness. Usually, a research project focuses on one brand and consumers in one country. If we have a collection of previous research projects, we may compare effects among brands and countries. Thus, we can discover whether the effect depends on the type of brand or country.

Meta-analysis is strongly recommended as a research strategy by Geoff Cumming, who coined the concept *New Statistics*. See Cumming's book (2012), website, or YouTube channel if you are curious to learn more. The video at the start of this chapter is made by Geoff Cumming.

6.2.3 Replication

Another approach that builds upon previous results is *replication*. If we collect new data including the variables that are central in prior research and we execute the same analyses, we *replicate* previous research.

Replication is the surest tool to check results of previous research. Checks do not necessarily serve to expose fraud and mistakes. They tell us whether prior research results still hold at a later time and perhaps in another context. Thus, we can decrease the chance that our previous results derive from an atypical sample. But replication also helps us to develop more general theories and discard theories that apply only to special situations.

6.2.4 Bayesian inference

A more radical way of including previous knowledge in statistical inference is *Bayesian inference*. Bayesian inference regards the sample that we draw as a means to update the knowledge that we already have or think we have on the population. Our previous knowledge is our starting point and we are not going to discard our previous knowledge if a new sample points in a different direction, as we do when we reject a null hypothesis.

Think of Bayesian inference as a process similar to when we predict the weather. If I try to predict tomorrow's weather, I am using all my weather experience to make a prediction. If my prediction turns out to be more or less correct, I don't change the way I predict the weather. But if my prediction is patently wrong, I try to reconsider the way I predict the weather, for example, paying attention to new indicators of weather change.

Bayesian inference uses a concept of probability that is fundamentally different from the type of inference presented in previous chapters, which is usually called *frequentist inference*. Bayesian inference does not assume that there is a true population value. Instead, it regards the population value as a random variable, that is, as something with a probability.

Again, think of predicting the weather. I am not saying to myself: "Let us assume that tomorrow will be a rainy day. If this is correct, what is the probability that the weather today looks like it does?" Instead, I think of the probability that it will rain tomorrow. Bayesian probabilities are much more in line with our everyday concept of probability than the dice-based probabilities of frequentist inference.

Due to this more intuitive notion of probability, the *credible interval*, which is the Bayesian equivalent of the confidence interval, means what we would like the confidence interval to mean, namely the interval within which the population value is located with the selected probability.

Bayesian inference is intuitively appealing but it has not yet spread widely in the social and behavioral sciences. Therefore, I merely mention this strand of statistical inference and I refrain from giving details. Its popularity, however, is increasing, so you may come in contact with Bayesian inference sooner or later.

6.3 What If I Do Not Have a Random Sample?

In our approach to statistical inference, we have assumed all the time that we could have drawn a very large number of random samples from the same population. The large number of samples constitutes the sampling distribution that tells us about the probability of drawing the one random sample that we have actually drawn.

What if I do not have a random sample? Can I still estimate confidence intervals or test null hypotheses? If you carefully read reports of scientific research, you will encounter examples of statistical inference on non-random samples or data that are not samples at all but rather represent an entire population, for instance, all people visiting a particular web site. Statistical inference is clearly being applied to data that are not sampled at random

from an observable population. The fact that it happens, however, is not a guarantee that it is right.

We should note that statistical inference based on a random sample is the most convincing type of inference because we exactly know the nature of the uncertainty in the data, namely the chance introduced by our random sampling. Think of exact methods for creating a sampling distribution. If we know the distribution of candy colours in the population of all candies, we can calculate the exact probability of drawing a sample bag with, for example, 25 per cent of all candies being yellow if we carefully draw the sample at random.

We can calculate the probability because we understand the process of random sampling. For example each candy has the same probability to be included in the sample. The uncertainty or probabilities arise from the way we designed our data collection, namely as a random sample from a much larger population.

In summary, we know the population and how chance affects our sample if we draw a random sample. We know neither the population nor the workings of chance if we want to apply statistical inference to data that were not collected as a random sample. We have to substantiate the claim that our data set can be regarded as a random sample.

6.3.1 Theoretical population

Sometimes, we have data for a population instead of a sample. For example, we have data on all visitors of our website because our website logs visits. If we investigate all people visiting a particular website, what is the wider population?

We may argue that this set of people is representative of a wider set of people visiting similar web sites or of the people visiting this website at different time points. This is called a *theoretical population* because we imagine such a population instead of actually sampling from an observable population.

We have to motivate why we think that our data set (our website visitors) can be regarded as a random sample from the theoretical population. This can be difficult. Is it really just chance that some people visit our website whereas other people visit another (similar) website? Is it really just chance that some visit our website this week but not next week and the other way around? And how about people visiting our website both weeks?

If it is plausible that our data set can be regarded as a random sample from a theoretical population, we may apply inferential statistics to our data set to generalize our results to the theoretical population. Of course, a theoretical population, which is imaginary, is less concrete than an observable population. The added value of statistical inference is more limited.

6.3.2 Data generating process

An alternative approach discards with generalization to a population. Instead, it regards our observed data set as the result of a theoretical *data generating process* (for instance, see

Frick, 1998; and Hayes, 2013: 50-51). In an experiment, for example, exposure to a celebrity endorsing a fund-raising campaign triggers a process within the participants that results in a particular willingness to donate. Under similar circumstances and personal characteristics, this process yields the same outcomes, that is, generates the same data set.

There is a complication. The circumstances and personal characteristics are very unlikely to be the same every time the process is at work (generates data). A person may pay more or less attention to the stimulus material, she may be more or less susceptible to this type of message, or in a better or worse mood for caring about other people, and so on.

As a consequence, we have variation in the outcome scores for participants who are exposed to the same celebrity and that have the same scores on personal characteristics that we measured. This variation is supposed to be random, that is, the result of chance. In this approach, then, random variation is not caused by random sampling but by fluctuations in the data generating process.

Compare this to a machine producing yellow candies. Fluctuations in the temperature and humidity within the factory, vibrations due to heavy trucks passing by, and irregularities in the base materials may affect the weight of individual candies. The weights are the data that we are going to analyze and the operation of the machine is the data generating process.

We can use the inferential techniques developed for random samples on data with random variation stemming from the data generation process if the probability distributions for sampling distributions apply to random variation in the data generating process. This is the tricky thing about the data generating process approach.

It has been shown that means of random samples have a normal or t distributed sampling distribution (under particular conditions). The normal or t distribution is a correct choice for the sampling distribution here. In contrast, we have no correct criteria for choosing a probability distribution representing chance in the process of generating data that are not a random sample. We have to make up a story about how chance works and to what probability distribution this leads. This is a more contestable choice.

What arguments can a researcher use to justify the choice of a theoretical probability distribution for the sampling distribution? A bell-shaped probability model such as the normal or t distribution is a plausible candidate for capturing the effects of many independent causes on a numeric outcome (see Lyon, 2014 for a critical discussion). If we have many unrelated causes that affect the outcome, for instance, a person's willingness to donate to a charity, particular combinations of causes will push some people to be more willing than the average and other people to be less willing.

So we should give examples of unobserved independent causes that are likely to affect willingness to donate to justify a normal or t distribution. For example, mood differences between participants, fatigue, emotions, prior experiences with the charity, and so on.

This is an example of an argument that can be made to justify the application of t tests in tests on means, correlations, or regression coefficients to data that is not collected as a random sample. The argument can be more or less convincing. The chosen probability distribution can be right or wrong and we will probably never know which of the two it is.

[htbp] 

Figure 6.6: Carl Friedrich Gauss.

The normal distribution is usually attributed to Carl Friedrich Gauss (1809). Pierre-Simon Laplace (1812), among others, proved the central limit theorem, which states that under certain conditions the mean of a large number of independent random variables are approximately normally distributed. Based on this theorem, we expect that the overall (average) effect of a large number of independent causes (random variables) produces a variation that is normally distributed.

[htbp] 

Figure 6.7: Pierre-Simon Laplace.

6.4 Take-Home Points

- Null hypothesis significance test results should be interpreted in relation to sample size and, if possible, test power.
- Statistically significant results need not be relevant or important. A small, negligible difference between the sample outcome and the hypothesized population value can be statistically significant in a very large sample with high test power.
- A relevant and important difference between the sample outcome and the hypothesized population value need not be statistically significant in a small sample or with a test with low power.
- Give priority to effect size over statistical significance in your interpretation of results.
- A confidence interval shows us how close to and distant from the hypothesized value the true population value is likely to be. It helps us to draw a more nuanced conclusion about the result than a null hypothesis significance test.

- Applying statistical inference to data other than random samples requires justification of either a theoretical population or a data generating process with a particular probability distribution.

Chapter 7

Moderation with Analysis of Variance (ANOVA)

Key concepts: eta-squared, between groups variance, within groups variance, F test on analysis of variance model, pairwise comparisons, post-hoc tests, one-way analysis of variance, two-way analysis of variance, factorial design, balanced design, main effects, moderation, interaction effect, higher-order interactions.

Summary

If we want to compare the level of outcome scores among more than two groups, we may use analysis of variance. Analysis of variance does not produce confidence intervals; it is purely a statistical test.

The null hypothesis tested in analysis of variance states that all groups have the same average outcome score in the population. This null hypothesis is similar to the one we test in an independent-samples t test for two groups. With three or more groups, we must use the variance of the group means (between-groups variance) to test the null hypothesis. If the between-groups variance is zero, all group means are equal.

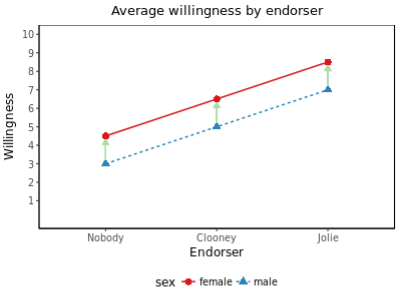
In addition to between-groups variance, we have to take into account the variance of outcome scores within groups (within-groups variance). within-groups variance is related to random group mean differences that we may expect in random samples. The ratio of between-groups variance over within-groups variance gives us the F test statistic, which has an F distribution.

Differences in average outcome scores for groups on one predictor variable (factor) are called a main effect. A main effect represents an overall or average effect of a factor. If we have only one factor in our model, we apply a one-way analysis of variance. With two factors, we have a two-way analysis of variance, and so on.

With two or more factors, we can have interaction effects in addition to main effects. An

interaction effect is the joint effect of two or more factors on the outcome variable. An interaction effect is best understood as different effects of one factor across different groups on another factor. This is called moderation and we usually think of one factor as the predictor and the other factor as the moderator. The moderator changes the effect of the predictor on the outcome.

Test your intuition and understanding



Endorser effect: F(2, 54) = 28.96, p < .001, eta^2 = 0.47
Sex effect: F(1, 54) = 12.22, p < .001, eta^2 = 0.10
Interaction effect: F(2, 54) = 0.00, p = 1.000, eta^2 = 0.00

	Nobody	Clooney	Jolie	Total:
Women				6.5
Men				5
Total:	3.75	5.75	7.75	5.75

Figure 7.1: How do we recognize main effects and interaction effects in a means plot and in a table of means?

1. what is or are the main effects in Figure 7.1? Explain how you can recognize main effects both in the means plot and in the reported numbers.

2. Change some group means to create substantial and statistically significant moderation of the effect of endorser (Nobody, Clooney, or Jolie) on willingness.

3. What is the null hypothesis of the F tests reported in Figure 7.1?

4. How should we interpret the eta^2 values in Figure 7.1?

7.1 Different Score Levels for Three or More Groups

Celebrity endorsement theory states that celebrities who publicly state that they favour a product, candidate, or cause, help to persuade consumers to adopt or support the product, candidate, or cause (for a review, see Erdogan, 1999; for an alternative approach, see McCracken, 1989).

Imagine that we want to test if the celebrity who endorses a fund raiser in a fund-raising campaign makes a difference to people's willingness to donate. We will be using the celebrities George Clooney and Angelina Jolie, and we will compare campaigns with one of them to a campaign without celebrity endorsement.

Figure 7.2: George Clooney and Angelina Jolie.

Let us design an experiment to investigate the effects of celebrity endorsement. We sample a number of people (participants), whom we assign randomly to one of three groups. We show a campaign video with George Clooney to one group, a video with Angelina Jolie to another group, and the third group—the control group—sees a campaign video without celebrity endorsement. So we have three experimental conditions (Clooney, Jolie, no endorser) as our predictor variable.

Our outcome is a numeric scale assessing the participant's willingness to donate to the fund raiser on a scale from 1 ("absolutely certain that I will not donate") to 10 ("absolutely certain that I will donate"). We will compare the average outcome scores among groups. If groups with Clooney or Jolie as endorser have systematically higher average willingness to donate than the group without celebrity endorsement, we conclude that celebrity endorsement has a positive effect.

In statistical terminology, we have a categorical predictor and a numerical outcome. In experiments, we usually have a very limited set of treatment levels, so our predictor is categorical. For nuanced results, we usually want to have a numeric outcome. Analysis of variance was developed for this kind of data (R. A. Fisher, 1919), so it is widely used in the context of experiments. Note, however, that it can also be used in non-experimental situations as long as the predictor is categorical and the outcome numeric.

7.1.1 Mean differences as effects

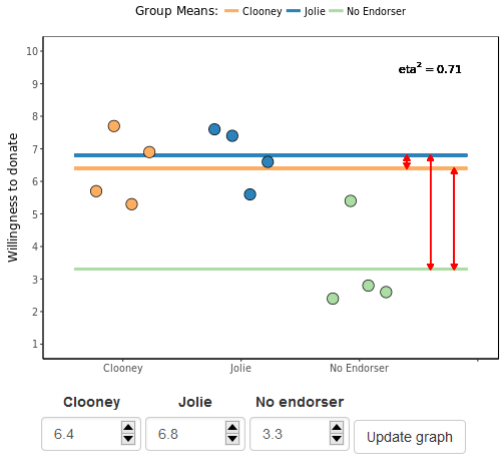


Figure 7.3: How do group means relate to effect size?

1. In the sample of (12) participants displayed in Figure 7.3, what do the double-sided vertical arrows represent?
2. How do the double-sided vertical arrows relate to effect size (eta^2)? Explain the relation in your own words and change group means to verify your expectations.

Average outcome score for a group represents a group's score level. The exact score level for a group, for instance, the average willingness to donate for participants who have seen George Clooney endorse the fund raiser, depends on all kinds of causes. The level itself is not of much interest to us. Instead, we focus on the differences between the score levels of groups.

Random assignment of test participants to experimental groups creates groups that are in principle equal on all imaginable characteristics except the experimental treatment(s) administered by the researcher to the participants. If this was done successfully, differences between group score levels can only be caused by the experimental treatment. Mean differences are said to represent the effect of experimental treatment in analysis of variance.

Analysis of variance was developed for the analysis of randomized experiments, where effects can be interpreted as causal effects. Note, however, that analysis of variance can also be applied to non-experimental data. Although mean differences are still called effects in the latter type of analysis, these need not be causal effects.

In analysis of variance, then, we are simply interested in the differences between group means. The conclusion for a sample is easy: Which groups have higher average score on the outcome variable and for which are they lower? A simple means plot, such as Figure 7.4, aids interpretation and helps communicating results to the reader.

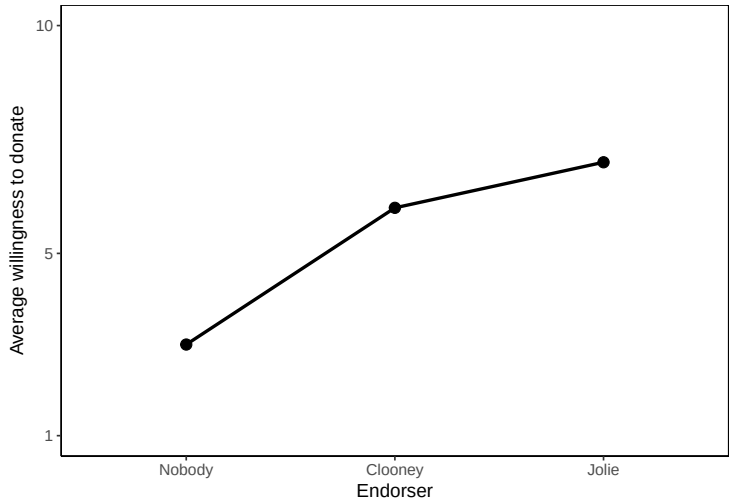


Figure 7.4: A means plot showing that average willingness to donate is higher with a celebrity endorser than without a celebrity endorser.

Effect size in an analysis of variance refers to the overall differences between group means. We use eta^2 as effect size, which gives the proportion of variance in the outcome (willingness to donate) explained or predicted by the group variable (experimental condition).

Rules of thumb for the interpretation of eta^2:

- 0,01 = small or weak effect; 1% variance explained matches a correlation r = 0,10 because R^2 in simple regression analysis equals r squared,
- 0,09 = medium-sized or moderate effect, matches r = 0,30,
- 0,25 = large or strong effect; matches r = 0,50.

7.1.2 Between-groups variance and within-groups variance

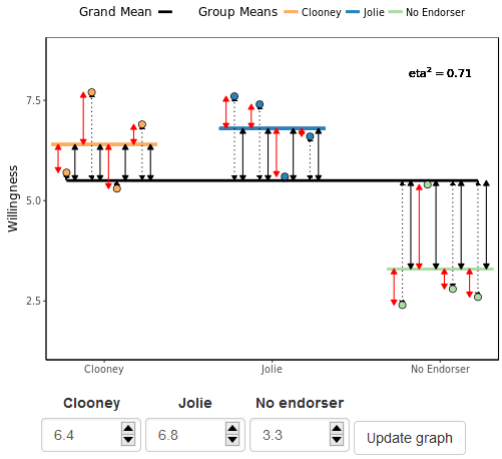


Figure 7.5: Which part of score differences tell us about the differences between groups?

1. In Figure 7.5, what do the solid red arrows represent?
2. What do the solid black arrows represent?
3. What do the dotted black arrows in Figure 7.5 represent?
4. Which arrows relate directly to effect size eta^2? Change group means (and press the *Update graph* button) to verify your expectation.

What does it mean if we say that a percentage of the variance is explained when we interpret eta^2? The variance that we want to explain consists of the differences between the scores of the participants on the outcome variable and the overall or grand mean of all outcome scores. The dotted black arrows Figure 7.5 express the distances between outcome scores and the grand average. Squaring and averaging these distances over all observations gives us the total variance in outcome scores.

Why do some participants have above average willingness to donate and other participants below average willingness? We want to explain the variation in willingness from the experimental treatment of the participants: Which endorser are the participants exposed to? If an endorser is more effective, the overall level of willingness should be higher. In other words, the average willingness should be higher for participants confronted with this endorser.

So group average willingness is what we can predict from the experimental treatment. If we know the group to which a participant belongs—which celebrity she saw endorsing the fundraising campaign—we can use the average outcome score for the group as the predicted

outcome for each group member—her willingness to donate. The predicted group scores are represented by the horizontal lines for group means in Figure 7.5.

Now what part of the variance in outcome scores (dotted black arrows in Figure 7.5) is explained by the predicted values, that is, group means? It is the variance of the predicted scores, which is the average (squared) distance between the group mean and the grand mean for all observations. This is called the *between-groups variance* and it is represented by the solid black arrows in Figure 7.5.

Playing with the group means in Figure 7.5, you may have noticed that eta^2 is high if there are large differences between group means. In this situation we have high between-groups variance—large black arrows in Figure 7.5—so we can predict a lot of the variation in outcome scores between participants.

In contrast, small differences between group averages allow us to predict only a small part of the variation in outcome scores. If all group means are equal, we can predict none of the variation in outcome scores because the between-groups variance is zero. As we will see in Section 7.1.3, zero between-groups variance is central to the null hypothesis in analysis of variance.

Within-groups variance in outcome scores is what we cannot predict with our grouping variable; it is prediction error. In some SPSS output, it is therefore labeled as "Error". After all, each member of the same group has the same predicted score, namely the group average. within-groups variance in a sample is represented by the dotted double-sided arrows in Figure 7.5.

7.1.3 F test on the model

Average group scores tell us whether the experimental treatment has effects within the sample(s) (Section 7.1.1). If the group who saw Angelina Jolie as endorser has higher average willingness to donate than the group who did not see an endorser, we conclude that Angelina Jolie makes a difference in the sample. But how about the population?

If we want to test whether the difference that we find in the sample also applies to the population, we use the substantive null hypothesis that all average outcome scores are equal in the populations from which the samples were drawn. In our example, the null hypothesis states that people who would see George Clooney as endorser are just as willing to donate as people who would see Angelina Jolie or who would not see a celebrity endorser at all.

We use the variation in group means as the number to express the size of differences between group means. If all groups have the same average outcome score, the between-groups variance is zero. The larger the differences, the larger the between-groups variance.

We cannot just use the between-groups variance as the test statistic because we have to take into account chance differences between sample means. If we draw samples from the same population, the sample means can still be different because we draw samples at random. These sample mean differences are due to chance, they do not reflect true differences between the populations.

We have to correct for chance differences and this is done by taking the ratio of between-groups variance over within-groups variance. This ratio gives us the relative size of observed differences between group means over group mean differences that we expect by chance.

Our test statistic, then, is the ratio of two variances: between-groups variance and within-groups variance. The F distribution approximates the sampling distribution of the ratio of two variances, so we can use this probability distribution to test the significance of the group mean differences we observe in our sample.

Remember that we used the F distribution before for testing a ratio of two variances, namely, in Levene's F test for the null hypothesis that two groups have the same population variance (Section 4.2.6). Now we use it to test if three or more means are equal in the population.

Long story short: We test the substantive null hypothesis that all groups have the same population means in an analysis of variance. But behind the scenes, we actually test between-groups variance against within-groups variance. That is why it is called analysis of variance.

7.1.4 Assumptions for the F test in analysis of variance

There are two important assumptions that we must make if we use the F distribution in analysis of variance: (1) Independent samples and (2) homogeneous population variances.

7.1.4.1 Independent samples

The first assumption is that the groups can be regarded as independent samples. As in an independent-samples t test, it must be possible *in principle* to draw a separate sample for each group in the analysis. Because this is a matter of principle instead of how we actually draw the sample, we have to argue that the assumption is reasonable. We cannot check the assumption against the data.

This is an example of an argument that we can make. In an experiment, we usually draw one sample of participants but we assign participants randomly to one of the experimental conditions. This could have easily been done separately for each experimental group. For example, we first draw a participant for the first condition: seeing George Clooney endorsing the fundraising campaign. Next, we draw a participant for the second condition, e.g., Angelina Jolie. The two draws are independent: whomever we have drawn for the Clooney condition is irrelevant to whom we draw for the Jolie condition. Therefore, draws can be independent and the samples can be regarded as independent.

Situations where samples cannot be regarded as independent are the same as in the case of t tests (see Section 2.5.6). For example, samples of first and second observations in a repeated measurement design should not be regarded as independent samples. Some analysis of variance models can handle repeated measurements but we do ot discuss them here.

7.1.4.2 Homogeneous population variances

The F test in analysis of variance assumes that the groups are drawn from the same population. This implies that they have the same average score on the outcome variable in the population as well as the same variance of outcome scores. The null hypothesis tests the equality of population means but we must assume that the groups have equal outcome variable variances in the population.

We can use a statistical test to decide whether or not the population variances are equal (homogeneous). This is the same Levene's F test that we have used in combination with independent samples t tests (Section 4.2.9). The test's null hypothesis is that the population variances of the groups are equal. If we do *not* reject the null hypothesis, we decide that the assumption of equal population variances is plausible.

The assumption of equal population variances is less important if group samples are more or less of equal size (a balanced design, see Section 7.3.2). We use a rule of thumb that groups are of equal size if the size of the largest group is less than 10% larger than the size of the smallest group. If this is the case, we do not care about the assumption of homogeneous population variances.

7.1.5 Which groups have different average scores?

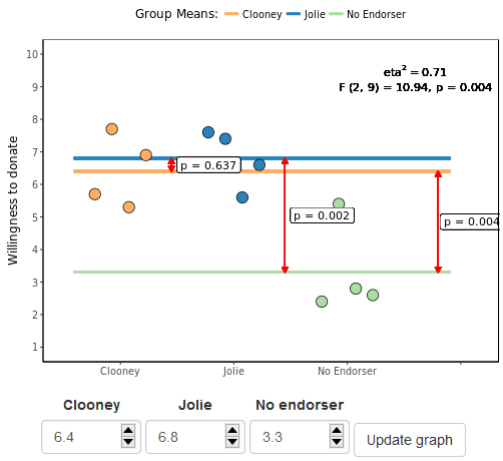


Figure 7.6: Which groups have different average outcome scores in the population?

1. Does the F test in analysis of variance tell us which groups have significantly different average population outcome scores? In other words, can we have the same F test result with different sets of group means? Adjust group means in Figure 7.6 to demonstrate your answer.

2. Is it possible that the F test is statistically significant but none of the t tests that compare groups one by one? Check your answer with Figure 7.6.
3. Is it okay that we apply both an F test and several t tests to the same group differences?

If the F test is statistically significant, we reject the null hypothesis that all groups have the same population mean on the outcome variable. In our current example, we reject the null hypothesis that average willingness to donate is equal for people who saw George Clooney, Angelina Jolie, or no endorser for the fund raiser. In other words, we *reject* the null hypothesis that the endorser does *not* matter to willingness to donate.

7.1.5.1 Pairwise comparisons as post-hoc tests

With a statistically significant F test, several questions remain to be answered. Does an endorser increase or decrease the willingness to donate? Are both endorsers equally effective? The F test does not provide answers to these questions. We have to compare groups one by one to see which condition (endorser) is associated with a higher level of willingness to donate.

In a pairwise comparison, we have two groups, for instance, participants confronted with George Clooney and participant who did not see a celebrity endorse the fund raiser, that we want to compare on a numeric outcome, namely their willingness to donate. An independent-samples t test is appropriate here.

With three groups, we can make three pairs: Clooney versus Jolie, Clooney versus nobody, and Jolie versus nobody. We have to execute three t tests on the same data. We already know that there are most likely differences in average scores, so the t tests are executed after the fact, in Latin *post hoc*. Hence the name *post hoc tests*.

Applying more than one test to the same data increases the probability of finding at least one statistically significant difference even if there are no differences at all in the population. Section 4.9 discussed this phenomenon as capitalization on chance and it offered a way to correct for this problem, namely Bonferroni correction. We ought to apply this correction to the pairwise t tests that we execute if the analysis of variance F test is statistically significant.

7.1.5.2 Two steps in analysis of variance

Analysis of variance, then, consists of two steps. In the first step, we test the general null hypothesis that all groups have equal average outcome scores in the population. If we cannot reject this null hypothesis, we have too little evidence to conclude that there are differences between the groups. Our analysis stops here although it is recommended to report the confidence intervals of the group means to inform the reader. Perhaps our sample was just too small to reject the null hypothesis.

If the F test is statistically significant, we proceed to the second step. Here, we apply independent-samples t tests with Bonferroni correction to each pair of groups to see which groups have significantly different means. In our example, we would compare the Clooney

and Jolie groups to the group without celebrity endorser to see if celebrity endorsement increases willingness to donate to the fund raiser. In addition, we would compare the Clooney and Jolie groups to see if one celebrity is more effective than the other.

7.1.5.3 Contradictory results

It may happen that the F test on the model is statistically significant but none of the post hoc tests is statistically significant. This usually happens when the p value of the F test is near .05. Perhaps the correction for capitalization is too strong; this is known to be the case with the Bonferroni correction. Alternatively, the sample is too small for the post hoc test. Note that we have fewer observations in a post hoc test than in the F test because we only look at two of the groups.

This situation illustrates the limitations of null hypothesis significance tests (Chapter 6). Remember that the 5% significance level remains an arbitrary boundary and statistical significance depends a lot on sample size. So do not panic if the F and t tests have contradictory results.

A statistically significant F test tells us that we may be quite confident that at least two group means are different in the population. If none of the post hoc t tests is statistically significant, we should note that it is difficult to pinpoint the differences. Nevertheless, we should report the sample means of the groups (and their standard deviations) as well as their confidence intervals. The two groups that have the most different sample means are most likely to have different population means.

7.2 One-Way Analysis of Variance in SPSS

7.2.1 Instructions

Applying one-way analysis of variance in SPSS and interpreting the results is explained in Section 4.2.9, see Video 4.10.

7.2.2 Exercises

1. How does celebrity endorsement affect the willingness to donate and is one celebrity more effective than the other? Use the data in donors.sav.

2. The data set smokers.sav contains (simulated) information on smoking behaviour and attitude towards smoking for a random sample of adults. Does the attitude towards smoking differ among smokers, former smokers, and non-smokers (variable: *status3*)?

7.3 Different Score Levels for Two Factors

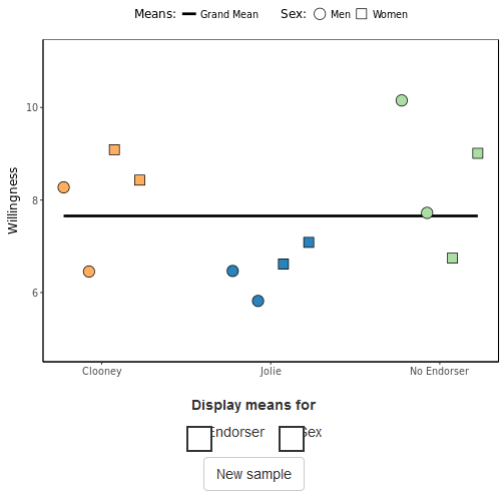


Figure 7.7: How do group means tell us about (main) effects in analysis of variance?

1. How does an analysis of variance test the effect of endorser on willingness to donate with the data displayed in Figure 7.7? Select the endorser factor to check your answer.

2. Which effect on willingness to donate is probably stronger: the effect of endorser or of sex? Motivate your answer, for example, using the grey arrows in the plot. Compare a plot with the endorser factor selected to a plot with the sex factor selected.

3. Where do you expect the group means to show up in the graph if you select both the Endorser and Sex check boxes?

In the preceding section, we have looked at the effect of a single factor on willingness to donate, namely, the endorser to whom participants are exposed. Thus, we take into account two variables: one predictor and one outcome variable. This is an example of a bivariate analysis.

Usually, however, we expect an outcome to depend on more than one variable. Willingness to donate does not depend only on the celebrity endorsing a fundraising campaign. It is easy to think of more factors, such as a person's available budget, her personal level of altruism, and so on.

It is straightforward to include more factors in an analysis of variance. These can be additional experimental treatments in the context of an experiment as well as participant characteristics that are not manipulated by the researcher. For example, we may hypothesize that females are generally more charitable than males.

Table 7.1: Number of observations per subgroup in a balanced 3x2 factorial design.

	Female	Male
Clooney	5	5
Jolie	5	5
No endorser	5	5

7.3.1 Two-way analysis of variance

If we use one factor, the analysis is called one-way analysis of variance. With two factors, it is called two-way analysis of variance, and with three factors... well, you probably already guessed that name.

A two-way analysis of variance using a factor with three levels, for instance, exposure to three different endorsers, and a second factor with two levels, for example, female versus male, is called a 3x2 (say: three by two) factorial design.

7.3.2 Balanced design

In analysis of variance with two or more factors, it is quite nice if the factors are statistically independent from one another. In other words, it is nice if the scores on one factor are not associated with scores on another factor. This is called a balanced design.

In an experiment, we can ensure that factors are independent if we have the same number of participants in each combination of levels on all factors. In other words, a factorial design is balanced if we have the same number of observations in each subgroup. A subgroup contains the participants that have the same level on both factors just like a cell in a contingency table.

Table 7.1 shows an example of a balanced 3x2 factorial design. Each subgroup (cell) contains five participants (cases). If you remember the principles of statistical association and independence in contingency tables (Section 4.2.10), you know that equal distributions of frequencies across columns or across rows indicate statistical independence. In the example, the distributions are the same across columns (and rows), so the factors are statistically independent.

A balanced design is nice but not necessary. Unbalanced designs can be analyzed but estimation is more complicated (a problem for the computer, not for us) and the assumption of equal population variances for all groups is more important (a problem for us, not for the computer). With a balanced design, you are on the safe side.

7.3.3 Main effects in two-way analysis of variance

A two-way analysis of variance tests the effects of both factors on the outcome variable in one go. It tests the null hypothesis that participants exposed to Clooney have the same

average willingness to donate in the population as participants exposed to Jolie or those who are not exposed to an endorser. At the same time it tests the null hypothesis that females and males have the same willingness to donate in the population.

The tested effects are *main effects*, that is, an overall or average difference between the mean scores of the groups on the outcome variable. The main effect of the endorser factor shows the mean differences for endorser groups if we do not distinguish between females and males. Likewise, the main effect for sex shows the average difference in willingness to donate between females and males without taking into account the endorser to whom they were exposed.

We could have used two separate one-way analyses of variance to test the same effects. Moreover, we could have tested the difference between females and males with an independent-samples t test. The results would have been the same (if the design is balanced.) But there is an important advantage to using a two-way analysis of variance, to which we turn in the next section.

7.4 Moderation: Score Level Differences that Depend on Context

In the preceding section, we have analyzed the effects both of endorser and sex on willingness to donate to a fund raiser. The two main effects isolate the influence of endorser on willingness from the effect of sex and the other way around. This assumes that endorser and sex have an effect on their own, a general effect.

We should, however, wonder whether endorser always has the same effect. Even if there is a general effect of endorser on willingness to donate, is this effect the same for females and males? Note that one endorser is a male celebrity who is reputed to be quite attractive to women. The other endorser is a female celebrity with a similar reputation among men. In this situation, shouldn't we expect that one endorser is more effective among female participants and the other among male participants?

If the effect of a factor is different for different groups on another factor, the first factor's effect is *moderated* by the second factor. The phenomenon that effects are moderated is called *moderation*.

With moderation, factors have a combined effect. The context (group score on one factor) affects the effect of the other factor on the outcome variable. The conceptual diagram for moderation expresses the effect of the moderator on the effect of the predictor as an arrow pointing at another arrow. Figure 7.8 shows the conceptual diagram for participant's sex moderating the effect of endorsing celebrity on willingness to donate.

[htbp]

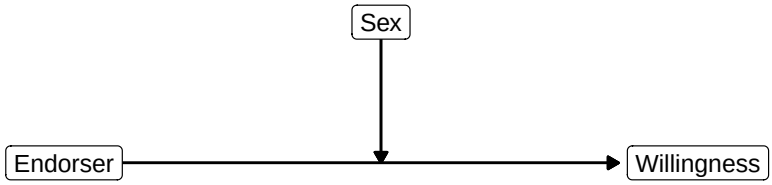


Figure 7.8: Conceptual diagram of moderation.

7.4.1 Types of moderation

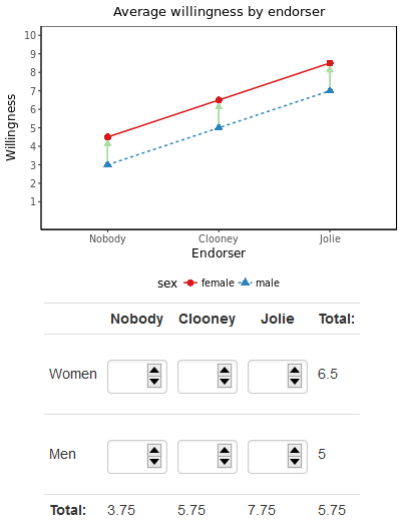


Figure 7.9: How can we recognize main effects and moderation in a means plot?

1. Does the plot in Figure 7.9 display a main effect of the factor sex? Motivate your answer.
2. Is there a main effect of endorser? Again, motivate your answer.
3. Does participant's sex moderate the effect of endorser? If so, interpret the difference between the effects. If not, explain why there is no moderation.
4. Adjust the means in such a way that the effect of endorser is stronger for males than females.

5. Adjust the means in such a way that the effects of Clooney and the effects of Jolie cancel out, so there is an interaction effect of endorser with sex but not a main effect of endorser.

Moderation happens a lot in communication science for the simple reason that the effects of messages are stronger for people who are more susceptible to the message. If you know more people who have adopted a new product or a healthy/risky lifestyle, you are more likely to be persuaded by media campaigns to also adopt that product or lifestyle. If you are more impressionable in general, media messages are more effective.

7.4.1.1 Effect strength moderation

Moderation refers to contexts that strengthen or diminish the effect of, for instance, a media campaign. Let us refer to this type of mediation as *effect strength moderation*. In our current example, we would hypothesize that the effect of George Clooney as an endorser is stronger for female participants than male participants.

In analysis of variance, effects are differences between average outcome scores. The effect of Clooney on willingness to donate, for instance, is the difference between the average willingness score of participants exposed to Clooney and the average score of participants who were not exposed to a celebrity endorser.

Different "Clooney effects" for female and male participants imply different differences! The difference in average willingness scores between females exposed to Clooney and females who are not exposed to an endorser is different from the difference in average scores for males. We have four subgroups with average willingness scores that we have to compare. We have six subgroups if we also include endorsement by Angelina Jolie.

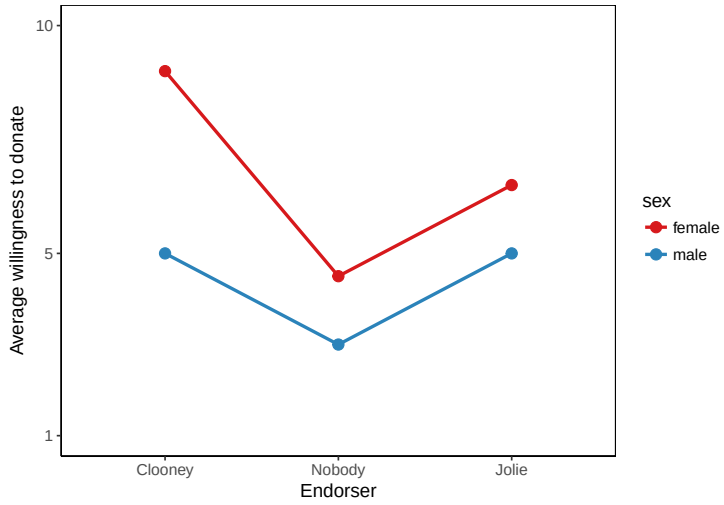


Figure 7.10: Moderation as a stronger effect within a particular context. The difference between the average score of males who saw Clooney and males who did not see a celebrity endorser is represented by the slope of the blue line segment at the left. The same effect for females is expressed by the red line segment at the left. The red line segment at the left is steeper than the blue line segment, so the Clooney effect is stronger among females than males. The red and blue line segments to the right are parallel, so the Jolie effect is the same for females and males.

A means plot is a very convenient tool to interpret different differences. Connect the means of the subgroups by lines that belong to the same group on the factor you use as moderator. Each line or trace in the plot represents the effect differences within one moderator group. If a line goes up or down, predictor groups have different means, so the predictor has an effect within that moderator group. A flat (horizontal) lines tells us that there is no effect at all within that moderator group

The distances between the lines show the difference of the differences. If the lines for females and males are parallel, the difference between endorsers is the same for females and males. Then, the effects are the same and there is *no* moderation. In contrast, if the lines are not parallel but diverge or converge, the differences are different for females and males and there is moderation.

A special case of effect strength moderation is the situation in which the effect is absent (zero) in one context and present in another context. A trivial example would be the effect of an anti-smoking campaign on smoking frequency. For smokers (one context), smoking frequency may go down with campaign exposure and the campaign may have an effect. For non-smokers (another context), smoking frequency cannot go down and the campaign cannot have this effect.

Except for trivial cases such as the effect of anti-smoking campaigns on non-smokers, it does not make sense to distinguish sharply between moderation in which the effect is strengthened

and moderation in which the effect is present versus absent. In non-trivial cases, it is very rare that an effect is precisely zero.

7.4.1.2 Effect direction moderation

In the other type of moderation the effect in one group is the opposite of the effect in another group. For example, Clooney is a more effective endorser among females than males whereas Jolie is more effective among males than females. Let us call this *effect direction moderation*. Females reverse the Jolie effect and males reverse the Clooney effect.

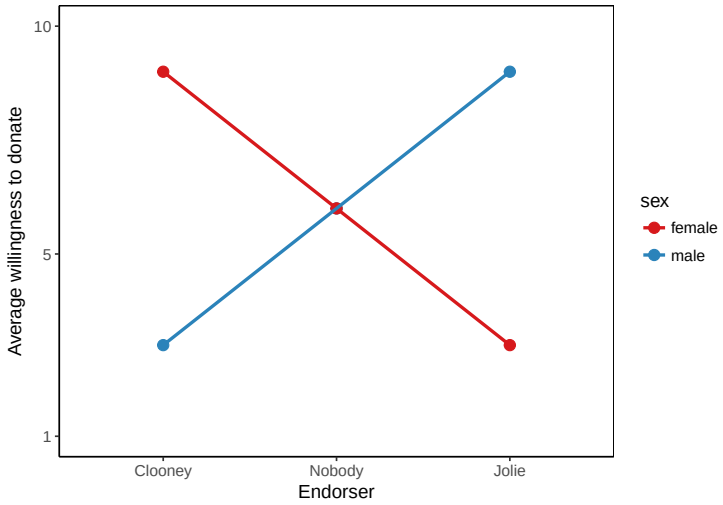


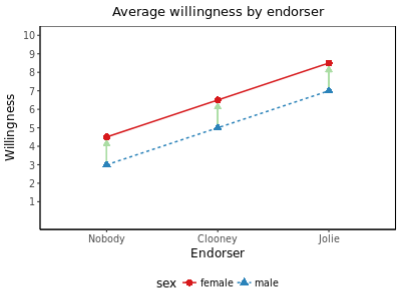
Figure 7.11: Moderation as opposite effects in different contexts. The Clooney effect is positive for female participants: The red line segment at the left shows that females exposed to Clooney are much more willing to donate than females who did not see a celebrity endorser. In contrast, Clooney as endorser reduces the willingness among males (blue line segment at the left). The Jolie effect is the opposite: positive for males, negative for females. In this special situation the effect for females and males cancel out, so there is no main effect of endorser.

The effect in one group can compensate for the effect in another group if it is about as strong but of the opposite direction. Imagine that George Clooney convinces females to donate but discourages males to donate because his charms backfires on men (pure jealousy, perhaps.) Similarly, Angelina Jolie may have opposite effects on females and males.

In this situation, the main effect of endorser on willingness to donate is (nearly) zero. If we average over females and males, there is no net difference between Clooney, Jolie, and the condition without an endorser. This does not mean that the endorser does not matter. On the contrary, the interaction effects tell us that the endorser is effective for one group but counterproductive for another group. The second part of the conclusion is just as important

as the first part. The campaign should avoid to decrease the willingness to donate among particular target groups.

7.4.2 Testing main and interaction effects



Endorser effect: F(2, 54) = 28.96, p < .001, eta^2 = 0.47
Sex effect: F(1, 54) = 12.22, p < .001, eta^2 = 0.10
Interaction effect: F(2, 54) = 0.00, p = 1.000, eta^2 = 0.00

	Nobody	Clooney	Jolie	Total:
Women				6.5
Men				5
Total:	3.75	5.75	7.75	5.75

Figure 7.12: How can we recognize main effects and moderation in a means plot?

1. Adjust the means in Figure 7.12 in such a way that the mean effect of endorser and the interaction effect of endorser and sex are statistically significant.
2. Adjust the means in such a way that the mean effect of endorser is *not* statistically significant but the interaction effect of endorser and sex is statistically significant.
3. Is it possible to have a statistically significant interaction effect but no statistically significant main effects? If so, adjust the scores in Figure 7.12 to prove your case.

For main effects we compare average scores among groups within one factor. A two-way analysis of variance includes two main effects, one for each factor (see Section 7.3.1). Females are on average more willing to donate than males in Figure 7.10.

For moderation, however, we compare average scores of subgroups, that is, groups that combine a level on one factor and a level on another factor. In Figure 7.10, for instance, we compare average willingness to donate for combinations of endorser and participant's sex. Interpretation of moderation requires some training because we must abstract from main effects. The fact that females score on average higher than males is irrelevant to moderation but it does affect all subgroup mean scores.

Moderation concerns the differences between subgroups that remain if we remove the overall differences between groups, that is, the differences that are captured by the main effects. The remaining differences between subgroup average scores provide us with a between-groups variance. In addition, the variation of outcome scores within subgroups yield a within-groups variance.

We can use the between-groups and within-groups variances to execute an F test just like the F test we use for main effects. The effect of differences among subgroups on the outcome variable is called an *interaction effect*. The null hypothesis of an F test on an interaction effect states that the subgroups have the same population averages if we correct for the main effects. In other words, the null hypothesis is that the effect of one factor is not moderated by the other factor.

Note that we must include the main effects in the model if we want to correct for them in our test of an interaction effect. If we would exclude main effects, we assume that there are no main effects. Why assume that if we can test for the presence or absence of main effects?

Moderation between three or more factors is possible. These are called *higher-order interactions*. It is wise to include both main effects and lower-order interactions if we test a higher-order interaction. As a result, our model becomes very complicated and hard to interpret. If a (first-order) interaction between two predictors must be interpreted as different differences, an interaction between three factors must be interpreted as different differences in differences. That's difficult to imagine, so let us avoid them for now.

7.4.3 Assumptions for two-way analysis of variance

The assumptions for a two-way analysis of variance are the same as for a one-way analysis of variance (Section 7.1.4). Just note that equal group sizes and equal population variances now apply to the subgroups formed by the combination of the two factors.

7.5 Reporting Two-Way Analysis of Variance

The main purpose of reporting a two-way analysis of variance, is to show the reader the differences between average outcome scores between groups on the same factor (main effects) and different differences for groups on a second factor (interaction effect). A means plot is very suitable for this purpose. Conventionally, we place the predictor groups on the horizontal axis and we draw different lines for the moderator groups. But you can switch them if it produces a more appealing graph.

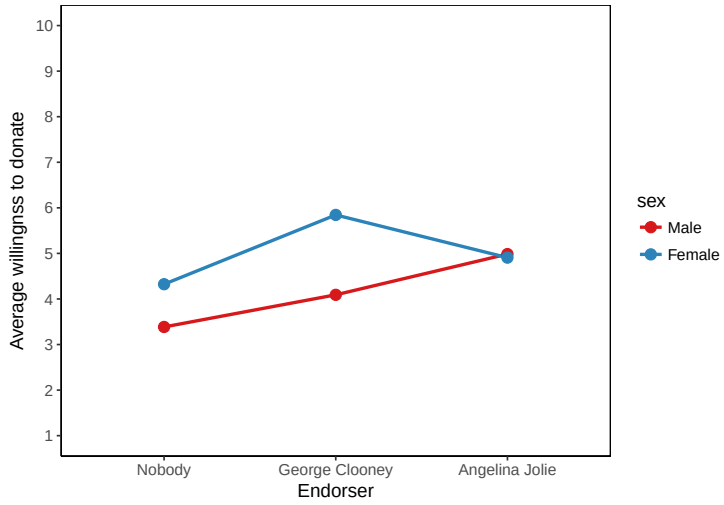


Figure 7.13: An example of a means plot.

For the statistically informed reader, you should include the following information somewhere in your report:

- That you used analysis of variance and the analysis of variance type (one-way or two-way).
- The test result for every effect, consisting of the test name (F), the degrees of freedom, and the significance (p value). APA6 prescribes the following format if you report the test result within your text: F (df1, df1) = F value, p = p value.
- For each effect worth interpretation, because it is sizable and/or statistically significant, report eta-squared (eta^2) and interpret it in terms of effect size. If you have to calculate eta-squared by hand, divide the between-groups sum of squares of an effect by the total sum of squares (SPSS: corrected total).
- For each effect worth interpretation, clarify which group or subgroup scores higher. Report the group means and their standard deviations or the mean difference (from the post-hoc tests) for comparisons between groups as well as their p values here.
- As always, don't forget to mention the units (cases) and the meaning of the variables (factors and outcome). They describe the topic of the analysis.
- Report it if the main assumption is violated, that is, if you have (sub)groups of unequal size and the test on homogeneous variances is statistically significant. In this situation, report the test result of the latter test just like you report the F test of a main effect (see above).

In a two-way analysis of analysis, the number of numeric results can be large. It is recommended to present them as a table (in the text or in an appendix). If you report the

Table 7.2: An example of a table summarizing results of a two-way analysis of variance.

	Sum of Squares	df	Mean Square	F	p
sex	26.37	1.00	26.37	11.86	0.001
endorser	38.05	2.00	19.03	8.56	< 0.001
endorser*sex	20.60	2.00	10.30	4.63	0.011
Error	304.54	137.00	2.22		
Total	142.00	57.92			

table, include the error, the sums of squares and mean squares in the same way that SPSS reports them. Table 7.2 presents an example.

7.6 Two-Way Analysis of Variance in SPSS

7.6.1 Instructions

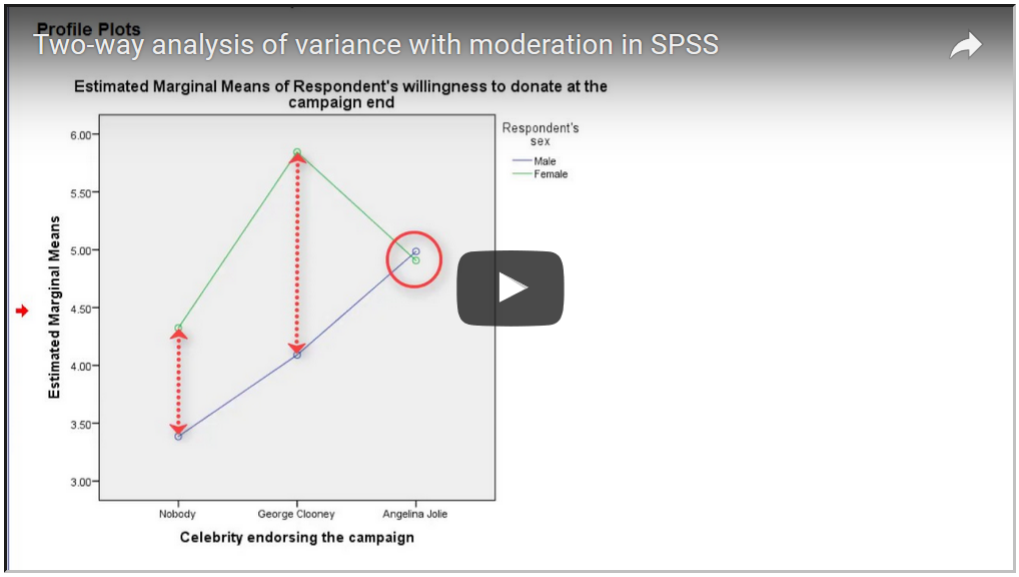


Figure 7.14: Two-way analysis of variance with moderation in SPSS.

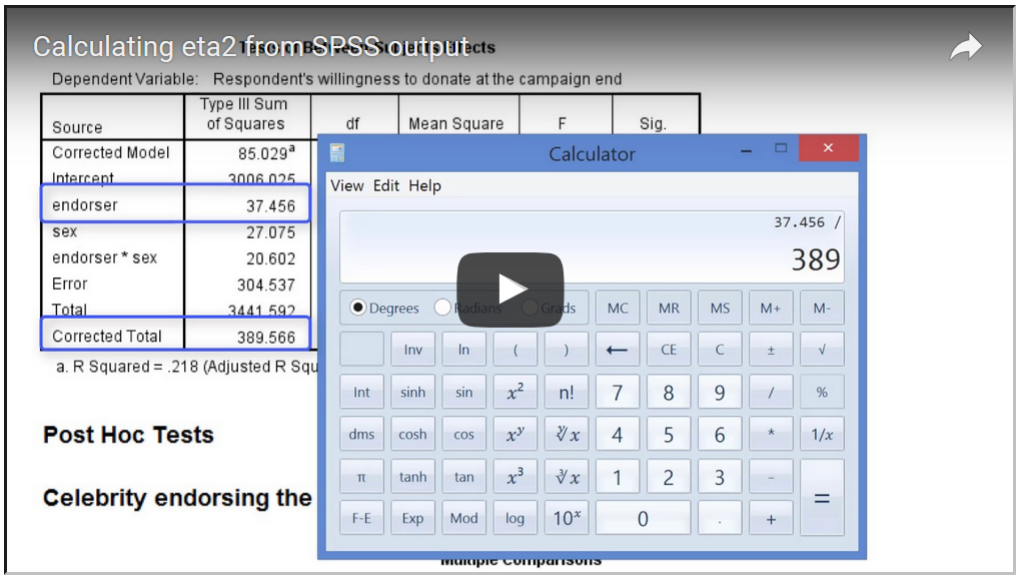


Figure 7.15: Calculating eta^2 from SPSS output.

7.6.2 Exercises

1. Use the data in donors.sav to test if the effect of celebrity endorsement on adults' willingness to donate differs for females and males. Check the assumptions and interpret the results. Create a plot to communicate your results.
2. Use the same data as in Exercise 1 to test if the effect of celebrity endorsement on willingness to donate depends on remembrance of the campaign. Check the assumptions and interpret the results. Again, create a plot to communicate your results.
3. Data set smokers.sav contains information about smoking on a random sample of adults. Does the attitude towards smoking depend on the adult's smoking behaviour (smoker, former smoker, or non-smoker) and on exposure to an anti-smoking campaign? Recode exposure scores into three groups: low exposure (scores 3 or less), medium exposure (scores 3 to 7), and high exposure (scores above 7).

7.7 Take-Home Points

- In an analysis of variance, we test the substantive null hypothesis that all groups have the same population means. Behind the scenes, we actually test the ratio of between-groups variance to within-groups variance.
- The overall differences in average outcome scores between groups on one factor (predictor) are a main effect in an analysis of variance.

- The differences in average outcome scores between subgroups, that is, groups that combine a level on one factor and a level on another factor, represent an interaction effect. Note that we are dealing with the differences between subgroup scores that remain after the main effects have been removed.
- Moderation is the phenomenon that an effect is different in different contexts. The effect can be stronger or it can have a different direction. In analysis of variance, interaction effects represent moderation.
- Eta-squared measures the size of a main or interaction effect in analysis of variance. It tells us the proportion of variance in the outcome variable that is accounted for by the effect.
- A means plot is very helpful for interpreting and communicating results of analysis of variance.
- The F tests in analysis of variance do not tell us which groups have different average outcome scores. To this end, we use independent-samples t tests as post hoc tests with a (Bonferroni) correction for capitalization on chance.
- To apply analysis of variance, we need a numeric outcome variable that has equal population variance in each group of a factor or each subgroup in case of an interaction effect. However, equality of population variances is not important if all groups on a factor or all subgroups in an interaction are more or less of equal size (the largest count is at most 10% larger than the smallest count.)

Chapter 8

Moderation with Regression Analysis

Key concepts: interaction variable, covariate, outcome, regression equation, dummy variables, normally distributed residuals, linearity, homoscedasticity, independent observations, statistical diagram, common support, simple slope, conditional effect, mean-centering.

Summary

The linear regression model is a powerful and very popular model for predicting a numeric outcome variable from one or more predictor variables. Predictor variables must be numeric or dichotomies. Regression coefficients show the predicted difference in the outcome for a one unit difference in the predictor.

But what if this predictive effect is not the same in all contexts? For example, exposure to an anti-smoking campaign may generally generate a more negative attitude towards smoking. The effect, however, is probably different for people who smoke than for people who do not smoke. The effect of campaign exposure on attitude towards smoking is moderated by the context: Whether or not the person exposed to the campaign is a smoker.

Different effect sizes for different contexts require different regression coefficients: regression lines with different slopes for different groups of people. We can use an interaction variable as a predictor in a regression model to accommodate for moderation as different slopes. An interaction variable is just the product of the predictor and moderator variables.

As a predictor in the model, an interaction variable has a confidence interval and a p value. The confidence interval tells us the plausible values for the size of the interaction effect in the population. The p value tests the null hypothesis that there is no interaction effect at all in the population.

To interpret the interaction effect, we must determine the size of the effect of the predictor on the outcome variable for several interesting values of the moderator. If the moderator is categorical, we want to know the effect (simple slope) within each category of the moderator. For example, the effect of campaign exposure on smoking attitude for smokers and the effect for non-smokers. If the moderator is a continuous variable, we may look at the effect for the mean value of the moderator (moderate score level) and one standard deviation below (low level) or above (high level) the mean.

Test your intuition and understanding

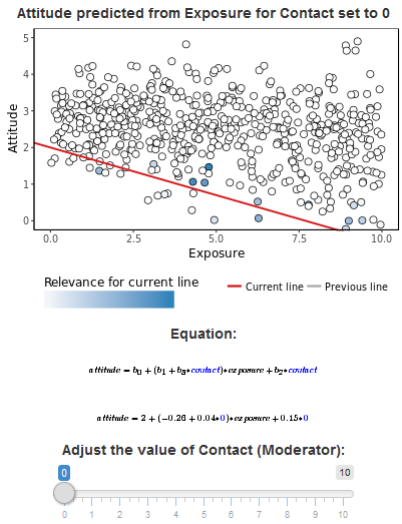


Figure 8.1: How does moderation work in a regression model?

1. What does the red line in Figure 8.1 mean?

2. What happens if you change the position on the slider? Explain you answer.

3. Why does *contact* (with smokers) appear in between brackets together with the regression coefficient for exposure in the regression equation?

4. Which of the regression coefficients represent(s) a partial effect and which a conditional effect? Explain your answer.

5. What is the null hypothesis of a significance test on the interaction effect (b_3)?

8.1 The Regression Equation

In the social sciences, we usually expect that a particular outcome has several causes. Investigating the effects of an anti-smoking campaign, for instance, we would not assume that a person's attitude towards smoking depends only on exposure to a particular anti-smoking campaign. It is easy to think of other and perhaps more influential causes such as personal smoking status, contact with people who do or do not smoke, susceptibility to addiction, and so on.

[htbp]

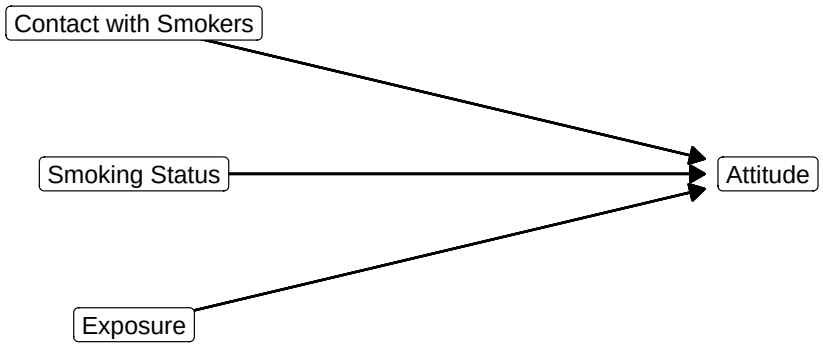


Figure 8.2: A conceptual model with some hypothesized causes of attitude towards smoking.

Figure 8.2 summarizes some hypothesized causes of the attitude towards smoking. A regression model translates this conceptual diagram into a statistical model. The statistical regression model is a mathematical function with the outcome variable (also known as the dependent variable, usually referred to with the letter y) as the sum of a constant (a), the effects (b) of predictors (x), which are *predictive effects*, and an error term (e), which is also called the *residuals*, see Equation (8.1).

$$y = a + b_1 * x_1 + b_2 * x_2 + b_3 * x_3 + e \tag{8.1}$$

8.1.1 Interpretion of a regression equation

[htbp]

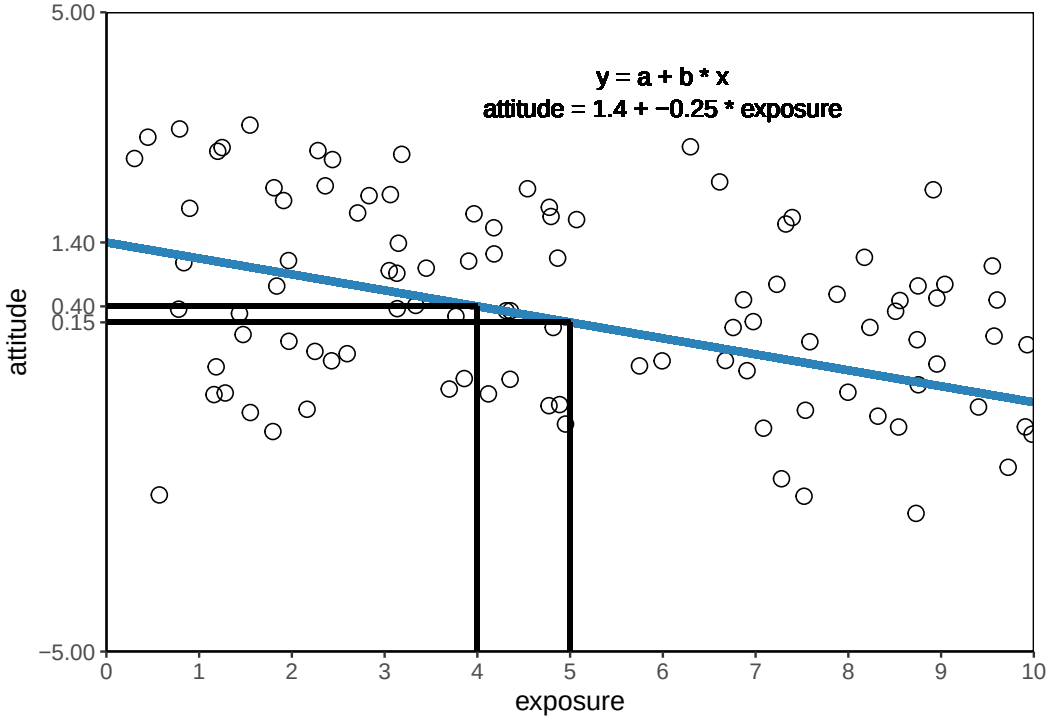


Figure 8.3: What is the meaning of the regression equation?

1. How does the plot visualize the constant of the regression equation?
2. Explain how the horizontal and vertical lines in the plot help to interpret the unstandardized regression coefficient b.

Good understanding of the regression equation is necessary for understanding moderation in regression models. So let us have a close look at an example equation (Eq. (8.2)). The outcome variable attitude towards smoking is predicted from a constant and three predictor variables.

$$attitude = constant + b_1 * exposure + b_2 * status + b_3 * contact + e \tag{8.2}$$

The constant adds a fixed quantity to the predicted attitude for all participants. It adjusts the overall level of the predicted attitude. As such, the constant is usually not interesting.

More precisely, the constant is the predicted attitude if a person scores zero on all predictor variables. To see this, plug in zero for all predictors in the equation (Eq. (8.3)) and remember

that zero times something is zero. This reduces the equation to the constant and the *error term e*. The error term is the error of our prediction, also known as the *residual*. It does not help to predict the outcome, so the constant is the only remaining predictor.

$$\begin{aligned} attitude &= constant + b_1 * 0 + b_2 * 0 + b_3 * 0 + e \\ attitude &= constant + 0 + 0 + 0 + e \\ attidude &= constant + e \end{aligned} \tag{8.3}$$

For all persons scoring zero on exposure, smoking status, and contact with smokers, the predicted attitude equals the value of the regression constant. This interpretation only makes sense if the predictors can be zero. If they include, for instance, scales ranging from one to seven, there are no persons with zero scores on all predictors and the constant has no meaning.

The regression coefficients b represent the predicted difference in the outcome for a difference of one unit in the predictor. For example, plug in the values 5 and 4 for the *status* predictor in the equation. If we take the difference of the two equations, we are left with b_1. All other terms in the two equations cancel out (except, perhaps, the error term e).

$$\begin{aligned} & attitude = constant + b_1 * 5 + b_2 * status + b_3 * contact + e \\ - \quad & attitude = constant + b_1 * 4 + b_2 * status + b_3 * contact + e \\ \hline & attitude\ difference = b_1 * 5 - b_1 * 4 = b_1 * (5 - 4) = b_1 \end{aligned} \tag{8.4}$$

We will be plugging in values for predictors in the regression equation a lot in this chapter. It is necessary for understanding and interpreting moderation.

8.1.2 Continuous predictors

In a linear regression, the outcome variable (y) must be numeric and in principle continuous. There are regression models for other types of outcomes, for instance, logistic regression for a dichotomous (0/1) outcome and Poisson regression for a count outcome, but we will not discuss them.

The predictor variables must be either numeric or dichotomous. If exposure is measured as a scale, for instance ranging from zero to ten, the interpretation of the effect of exposure (b_1) is the one that we have encountered in the preceding section: the predicted difference in the outcome for a one unit difference in exposure while all other predictor values do not change (are held constant).

Whether this predicted difference is small or large depends on the practical context: Is a small decrease in attitude towards smoking worth the effort of the campaign? If we want to apply a rule of thumb for the strength of the effect, we usually look at the standardized regression coefficient (b^* according to APA6, *Beta* in SPSS output). See Section 5.2.5 for some rules of thumb for effect size interpretation.

Note that the regression coefficient is calculated for the predictor values that occur within the data set. As a consequence, we do not know the relation between exposure and anti-smoking attitude for predictor values outside the range that actually occur in the sample. For example, if sample exposure scores are within the range three to seven, we should not pretend to know the effects of exposure levels below three or above seven. It is good practice to check the actual range of predictor values.

8.1.3 Dichotomous predictors

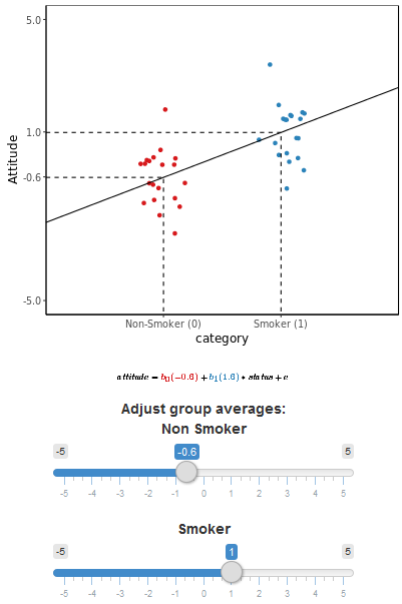


Figure 8.4: What is the difference in attitude between non-smokers and smokers?

1. What is the relation between the intercept of the regression line in Figure **??**fig:regression-dichotomy) and group averages? Motivate your answer by plugging values for smoking status into the regression equation.
2. Change the group means to detect the relation between group means and the unstandardized regression coefficient (b_1). How can we calculate the unstandardized regression coefficient (b_1) from the group averages? Again, show that your answer is correct by plugging values for smoking status into the regression equation.

Apart from numeric predictors, we can use dichotomous predictors, that is, predictors with only two values, which are preferably coded as 0 and 1 (*dummy coding*). The interpretation of the effect of a dichotomous predictor in a regression model is quite different from the interpretation of a numeric predictor.

For example, let us assume that smoking status is coded as smoker (1) versus non-smoker (0). Because this predictor can only take two values, we effectively have two versions of the regression equation. The first equation (8.5) represents all smokers, so their smoking status score is 1. This group has a fixed contribution to the predicted average attitude, namely b_2.

$$\begin{aligned} attitude &= constant + b_1 * exposure + b_2 * status + b_3 * contact + e \\ attitude &= constant + b_1 * exposure + b_2 * 1 + b_3 * contact + e \\ attitude &= constant + b_1 * exposure + b_2 + b_3 * contact + e \end{aligned} \tag{8.5}$$

Regression equation (8.6) represents all non-smokers. Their smoking status score is 0, so the smoking status effect drops from the model.

$$\begin{aligned} attitude &= constant + b_1 * exposure + b_2 * status + b_3 * contact + e \\ attitude &= constant + b_1 * exposure + b_2 * 0 + b_3 * contact + e \\ attitude &= constant + b_1 * exposure + b_3 * contact + e \end{aligned} \tag{8.6}$$

It makes no sense to interpret the regression coefficient of smoking status (b_2) as predicted difference in attitude for a difference of one in smoking status. After all, the 0 and 1 scores do not mean that there is a one unit difference. Instead, the coefficient indicates that we are dealing with different groups: smokers versus non-smokers. We have to interpret the effect as a difference between two groups. More specifically, as the difference between the group represented by the score 1 and the *reference group* represented by score 0.

If you compare the final equations for smokers (Eq. (8.5)) and non-smokers (Eq. (8.6)), the only difference is b_2, which is present for smokers but absent for non-smokers. It is the difference between the average outcome score (attitude) for smokers and non-smokers. In this example, it is the average attitude of smokers minus the average attitude of non-smokers. Just like an independent-samples t test!

Imagine that b_2 equals 1.6. This indicates that the average attitude towards smoking among smokers is 1.6 units above the average attitude among non-smokers. Is this a small or large effect? In the case of a dichotomous predictor, we should **not** use the standardized regression coefficient to evaluate effect size. The standardized coefficient depends on the distribution of 1s and 0s, that is, which part of the respondents are smokers. But this should be irrelevant to the size of the effect.

Therefore, it is recommended to interpret only the unstandardized regression coefficient for a dichotomous predictor. Interpret it as the difference in average outcome scores for two groups as we have done in the preceding paragraph.

Table 8.1: Dummy variables for a categorical predictor: One dummy variable is superfluous.

Original categorical variable:	neversmoked	smokesnomore	smoking
1 - Never smoked	1	0	0
2 - Former smoker	0	1	0
3 - Smoker	0	0	1

8.1.4 A categorical predictor and dummy variables

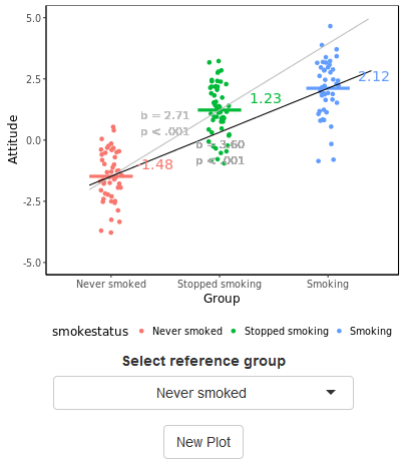


Figure 8.5: What are the predictive effects of smoking status?

1. Interpret the effects of smoking status in Figure 8.5.
2. In the initial state of Figure 8.5, can you tell whether the attitude of smokers is significantly different from the attitude of former smokers? Select a different reference group to motivate your answer.
3. Select some new plots. For each plot, determine which reference group you think is most convenient for summarizing the results.

What if smoking status was measured with three categories: (1) never smoked, (2) have smoked, (3) currently smoking? We can only include such a categorical predictor if we change it into a set of dichotomies.

A *categorical variable* contains three or more categories or groups. We can create a new dichotomous variable for each group, indicating whether (score 1) or not (score 0) the respondent is part of this group. In the example, we could create the variables *neversmoked*, *smokesnomore*, and *smoking*. Every respondent would score 1 on one of the three variables and 0 on the other two variables. These variables are called *dummy variables* or *indicator variables*.

If we want to include a categorical predictor in a regression model, we must use all dummy variables as predictors except one. In the example, we must include two out of the three dummy variables. We cannot include all three dummy variables because the score on the third dummy variable is determined by the score on the first two dummy variables.

If a respondent scores 1 on one of the first two dummy variables, her score must be 0 on the third dummy variable. Someone who is not a member of the Never Smoked or Smokes No More Groups, must be a member of the Smoking Group. A person scoring 0 on the first two dummy variables, then, must score 1 on the third.

We cannot include a predictor that is perfectly predictable from other predictors in the regression model. It is like including the same predictor twice: How can the estimation process decide which predictor is responsible for the effect? It can't decide, so the estimation process fails and no regression coefficients are estimated. If this happens, the predictors are said to be perfectly *multicollinear*.

The category or group that is left out of the regression model is the reference group. Remember that non-smokers were the reference group in the preceding section because the regression equation did not include a dichotomous predictor on which the non-smokers scored 1. The two groups were represented by only one dichotomy.

The interpretation of the effects (regression coefficients) for the included dummies is the same as for a single dichotomous predictor such as smoker versus non-smoker. It is the difference between average outcome score of the group scoring 1 on the dummy variable and the average outcome score of the reference group.

If we exclude the dummy variable for the respondents who never smoked, the regression weight of the dummy variable for the Smokes No More Group gives the average difference between former smokers and non-smokers. If the regression weight is positive, for instance -0.8, former smokers have a more negative attitude towards smoking than non-smokers. If the difference is positive, former smokers have a more positive attitude towards smoking.

Which group should we use as reference category, that is, which dummy should not be used in the regression model? This is hard to say in general. If one group is of greatest interest to us, we could use this as the reference group, so all dummy variable effects express differences with this group. Alternatively, if we expect a particular ranking in average outcome scores, we may pick the group at the highest, lowest or middle rank as the reference group. If you can't decide, run the regression model several times with a different reference group.

8.1.5 Sampling distributions and assumptions

If we are working with a random sample or we have other reasons to believe that our data could have been different due to chance (Section 6.3), we should not just interpret the outcomes for the data set that we collected. We should apply statistical inference—confidence intervals and significance tests—to our results. The confidence interval gives us bounds for the population value of the unstandardized regression coefficient. The p value is used to test the null hypothesis that the unstandardized regression coefficient is zero in the population.

Each regression coefficient as well as the constant may vary from sample to sample drawn from the same population, so we should devise a sampling distribution for each of them. Because the constant in a regression model is usually uninteresting, we will only discuss sampling distributions for regression coefficients. Their sampling distributions happen to have a t distribution under particular assumptions.

Chapters 3 and 4 have extensively discussed how confidence intervals and p values are constructed and how they must be interpreted. So we may as well focus now on the assumptions under which the t distribution is a good approximation of the sampling distribution of a regression coefficient.

8.1.5.1 Independent observations

The two most important assumptions require that the observations are *independent and identically distributed*. These requirements arise from probability theory. If they are violated, the statistical results should not be trusted.

Each observation, for instance, a measurement on a respondent, must be independent of all other observations. This respondent's outcome variable score may not depend on outcome scores of other respondents.

It is hardly possible to check that our observations are independent. We usually have to assume that this is the case. But there are situations in which we should not make this assumption. In time series data, for example, the daily amount of political news, we usually have trends, cyclic movements, or issues that affect the amount of news over a period of time. As a consequence, the amount and contents of political news in one day may depend on the amount and contents of political news in the preceding days.

Clustered data should also not be considered as independent observations. Think, for instance, of student evaluations of statistics tutorials. Students in the same tutorial group are likely to give similar evaluations because they had the same tutor and because of group processes: both enthusiasm and dissatisfaction can be contagious.

8.1.5.2 Identically distributed observations

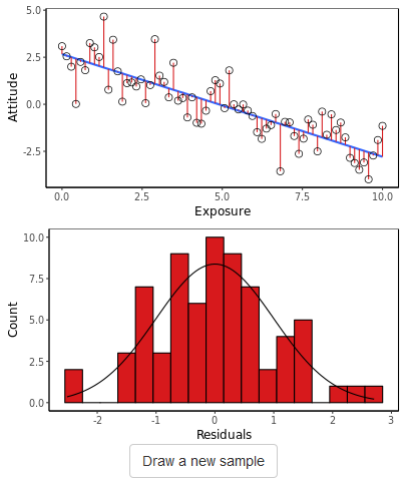


Figure 8.6: What are the residuals and how are they distributed?

1. What do the lines between dots and regression line represent in the scatterplot of Figure 8.6?
2. What is the relation between the scatterplot and the histogram? Can you point out the dot in the scatterplot that belongs to the leftmost bar in the histogram?
3. Draw some new samples. Are the residuals always normally distributed?

If we sample from a population where attitude towards smoking depends on exposure, smoking status, and contact with smokers, we will be able to predict attitude from the predictors in our sample. Our predictions will not be perfect, sometimes too high and sometimes to low. These are the residuals.

If our sample is truly a random sample with independent and identically distributed observations, our predictions should be equally bad or equally well for each value of the outcome variable, that is, attitude in our example. More specifically, the sizes of our errors (residuals) should be normally distributed for each attitude level (according to the central limit theorem).

So for all possible values of the outcome variable, we must collect the residuals for the observations that have this score on the outcome variable. For example, we should select all respondents who score 4.5 on the attitude towards smoking scale. Then, we select the residuals for these respondents and see whether they are approximately normally distributed.

Usually, we do not have more than a few observations for each single outcome score, so we cannot practically apply this check. Instead, we use a simple and coarse approach: Are all residuals normally distributed?

A histogram with an added normal curve helps us to evaluate the distribution of the residuals. If the curve more or less follows the histogram, we conclude that the assumption of identically distributed observations is plausible. If not, we conclude that the assumption is not plausible and we warn the reader that the results can be biased.

8.1.5.3 Linearity and prediction errors

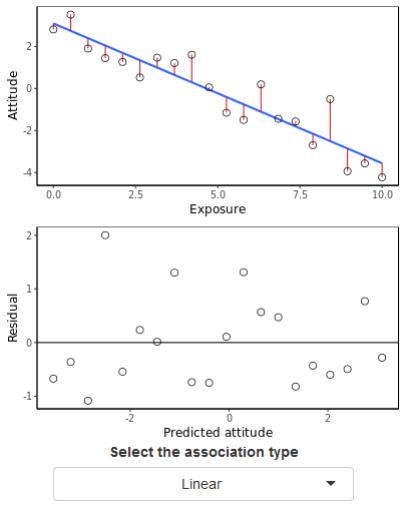


Figure 8.7: How do residuals tell us whether the relation is linear?

1. Think up which dot in the plot of residuals (Figure 8.7 bottom) corresponds with the left-most observation (dot) in the scatterplot of attitude by exposure (Figure 8.7 top). Drag your mouse around the left-most dot while pressing the left mouse button to check your choice. Repeat for more dots until you understand the relation between the two plots.
2. Select a U-shaped curve in Figure 8.7. Explain how the plot of residuals tells you that the association is not linear. Do the same for a curved association.

The other two assumptions that we use tell us about problems in our model rather than problems in our statistical inferences. Our linear regression model assumes a linear effect of the predictors on the outcome variable (*linearity*) and it assumes that we can predict the outcome equally well or equally badly for all levels of the outcome variable (*homoscedasticity*).

We can check the assumption of a linear model in a graph showing the (standardized) residuals (vertical axis) against the (standardized) predicted values of the outcome variable (on the horizontal axis). Note that the residuals represent prediction errors. If our regression predictions are systematically too low at some levels of the outcome variable and too high at other levels, the residuals are not nicely distributed around zero for all predicted levels of the outcome variable. This is what you see if the association is curved or U-shaped.

This indicates that our linear model does not fit the data. If it would fit, the average prediction error is zero for all predicted outcome levels. Graphically speaking, our linear model matches the data if at every horizontal position, positive prediction errors (residuals) are balanced by negative prediction errors.

8.1.5.4 Homoscedasticity and prediction errors

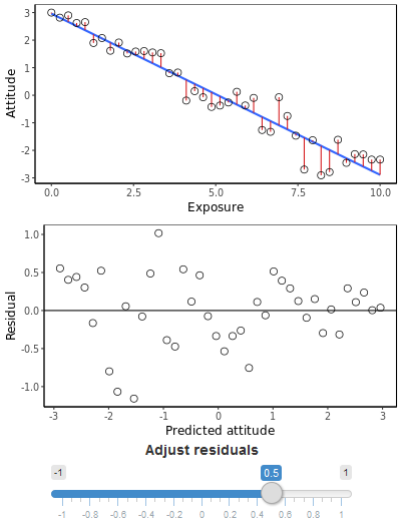


Figure 8.8: How do residuals tell us that we predict all values equally well?

1. What strikes you about the residuals in Figure 8.8?
2. What happens if you move the slider to the far left?
3. At which slider position are all attitude levels predicted equally well or equally badly?

The other assumption states that we can predict the outcome variable equally well at all outcome variable levels. In other words, the prediction errors (residuals) are more or less the same at all levels of the outcome variable. If we have large prediction errors at some levels of the outcome variable, we should also have large prediction errors at other levels. As a result, the vertical width of the residuals by predictions scatterplot should be more or less the same from left to right.

If the prediction errors are not more or less equal for all levels of the predicted outcome, our model is better at predicting some values than other values. For example, low values can be predicted better than high values of the outcome variable. This may signal, among other things, that we need to include moderation in the model.

8.1.6 Visualizing predictions

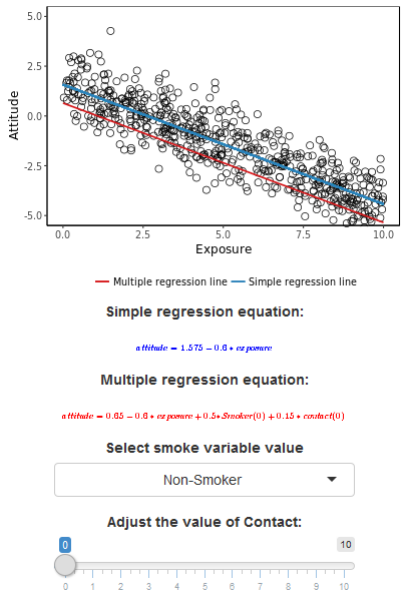


Figure 8.9: How do predictions based on exposure depend on values of smoking status and smoker contact?

1. What happens in Figure 8.9 if you change smoking status or smoking contact score? Can you explain the size of changes?

2. The line for a simple regression of attitude on exposure (without covariates) is displayed in blue in Figure 8.9. Can you make the multiple regression line equal to the simple regression line? If so, at what covariate values? If not, why not?

The regression equation without the error term e predicts the outcome variable scores from the predictor scores. Plug in values for the predictor variables and you can calculate the predicted outcome score. Figure 8.9, for instance, shows a regression equation for the effects of exposure and contact with smokers on attitude towards smoking. If you plug in a score of 4 for exposure, 0 for smoking status (non-smoker), and 6 for contact with smokers, the predicted attitude is 0.25 + -0.20 * 4 + 0.50 * 0 + 0.15 * 6 = 0.41.

If we focus on the relation between one predictor and the outcome variable, the predicted values can be represented by a straight line in a scatterplot. By convention, we display the predictor on the horizontal axis and the outcome variable on the vertical axis of the scatterplot.

In a simple regression, we only have one predictor, so we can only draw one regression line. In a multiple regression, however, we have several predictors. We can draw regression lines

for each predictor and, importantly, we can draw different regression lines for the same predictor.

If we want to draw the regression line for the predictive effect of one predictor, we regard the other predictors as covariates. Let us define a *covariate* as a variable that may predict the outcome but it is not our prime interest, so we mainly want to control for its effects. For example, if we focus on the predictive effect of exposure on attitude towards smoking, exposure is our predictor and smoking status and contact with smokers are covariates.

Note that the distinction between predictor and covariates is temporary. As soon as we focus on another variable, that variable becomes the predictor and the other predictors become covariates. The distinction between predictor and covariate is just terminology to show on which variable we focus.

To draw the regression line for the effect of exposure on attitude towards smoking, we must select a value for the covariates. If we would not do so, we have more than one variable that is allowed to vary but we can only display one predictor on the horizontal axis of our scatterplot.

$$\begin{aligned} attitude &= 0.25 + -0.20 * exposure + 0.5 * status + 0.15 * contact \\ attitude &= 0.25 + -0.20 * exposure + 0.5 * 0 + 0.15 * 3 \\ attitude &= 0.25 + -0.20 * exposure + 0 + 0.45 \\ attitude &= 0.70 + -0.20 * exposure \end{aligned} \tag{8.7}$$

Let us select non-smokers (*status* equals 0) who score 3 on *contact*. If we plug in these values in the regression equation, we obtain a simple regression—just one predictor, namely *exposure*—with a higher constant: 0.70 instead of 0.25. The constant is the intercept of the regression line, that is, the value of the vertical axis where the regression line crosses it.

The slope of the regression line, however, does not change no matter which values we select for the covariate. The regression coefficient of *exposure* remains -0.20. The regression line only moves up or down if we choose different values for the covariates. To visualize the exposure effect, it does not matter which values we chose for the covariates. A popular choice is using their average scores. When we add a moderator, however, the slope also changes as we will see in Section 8.3.

8.2 Regression Analysis in SPSS

8.2.1 Instructions

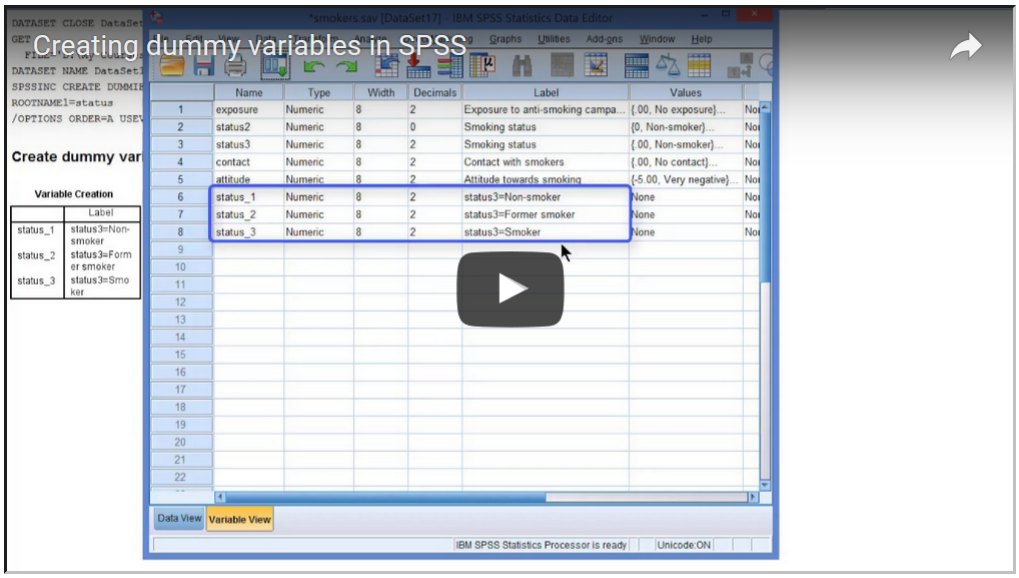


Figure 8.10: Creating dummy variables in SPSS.

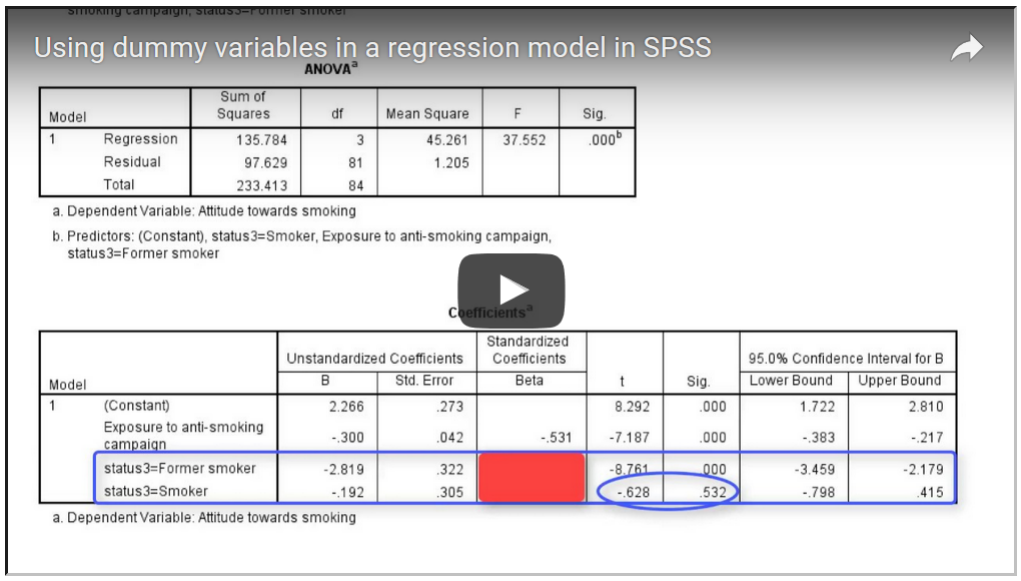


Figure 8.11: Using dummy variables in a regression model in SPSS.

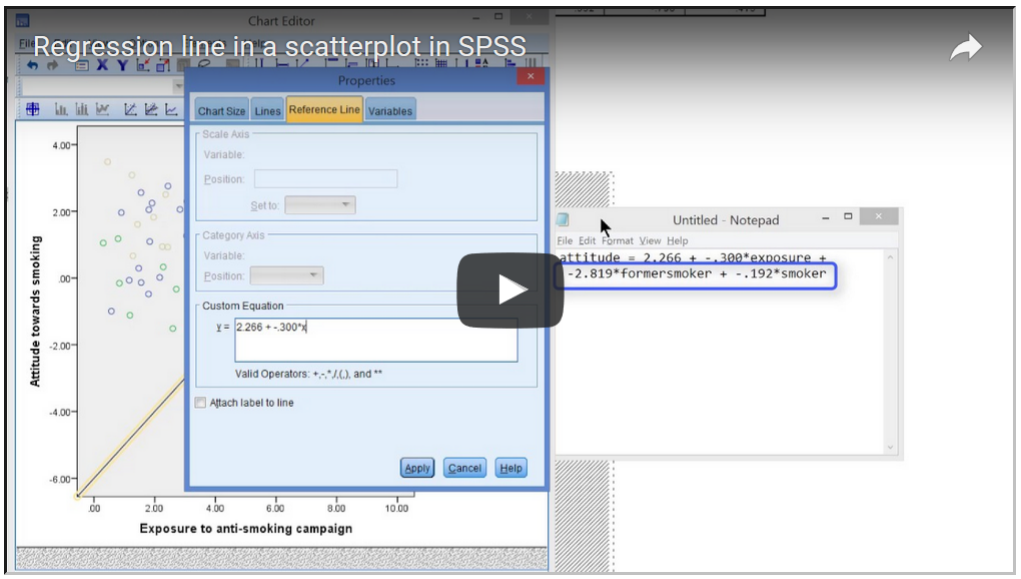


Figure 8.12: Adding a regression line to a scatterplot in SPSS.

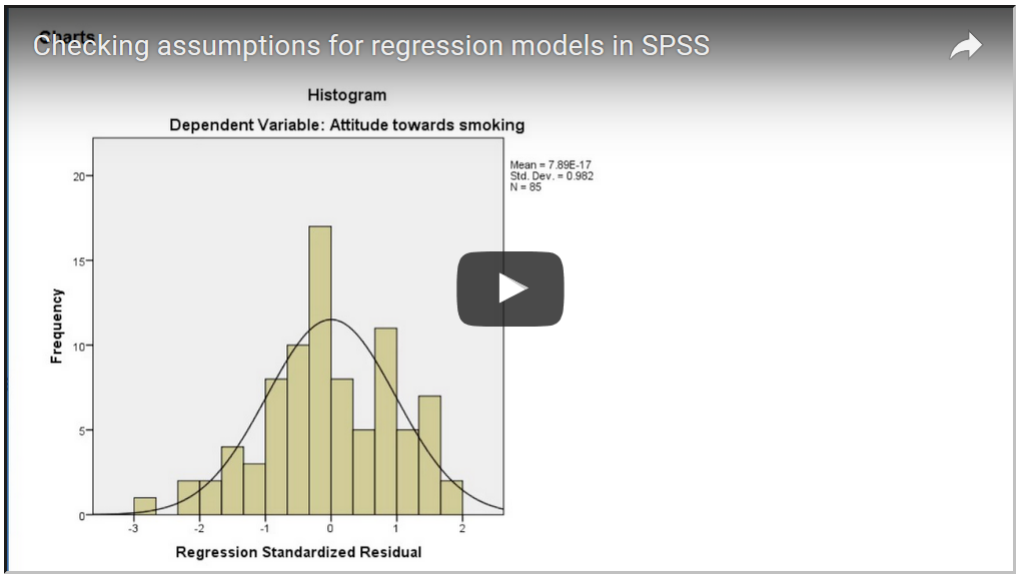


Figure 8.13: Checking assumptions for regression models in SPSS.

8.2.2 Exercises

1. Use the data in smokers.sav to predict the attitude towards smoking from exposure to an anti-smoking campaign. Check the assumptions and interpret the results.
2. Add smoking status (variable *status3*), and contact with smokers as predictors to the regression model of Exercise 1. Compare the effect of exposure between the two regression models. What is the difference and why is there a difference?
3. The data set children.sav contains information about the media literacy of children and parental supervision of their media use. Are the two related? Check the assumptions and interpret the results.

8.3 Different Lines for Different Groups

If we have a categorical independent variable, for instance, smoking status, and we want to determine its effect on a numerical variable, for example, attitude towards smoking, we compare group means. The difference between group means is the main effect of the categorical variable. For example, the average attitude towards smoking is 0.5 points more positive among smokers than among non-smokers.

In analysis of variance (Chapter 7), the main effect of smoking status is the average effect for all people regardless of their other characteristics or the contexts that they are in. In other words, a main effect is the overall difference in attitude between smokers and non-smokers.

What if the effect of smoking status on attitude may be different in different contexts, e.g., for people living among smokers versus those living among non-smokers? To model this, we added an interaction effect to the main effects in Chapter 7.

The interaction effect tells us whether the attitude difference between smokers and non-smokers differs between, on the one hand, people living among smokers and, on the other hand, people living among non-smokers. In a conceptual diagram, the interaction effect is represented by an arrow pointing to another arrow. The moderator (contact with smokers) changes the relation between the predictor (smoking status) and the outcome (attitude towards smoking).

[htbp]

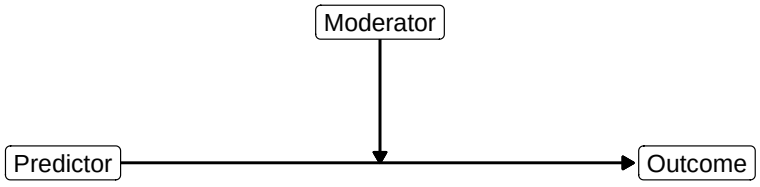


Figure 8.14: Conceptual diagram of moderation.

Analysis of variance (ANOVA), as discussed in Chapter 7, investigates the effects of categorical variables on a numeric outcome variable. It cannot handle numeric predictors or numeric covariates. Although there are ways to include numeric covariates in analysis of variance, for instance, in the analysis of covariance (ANCOVA), we use regression analysis if we have at least one numerical predictor or covariate and a numerical outcome.

In the current section, we discuss regression models with a numerical predictor and a categorical moderator. A later section (Section 8.5), presents regression models in which both the predictor and moderator are numeric.

8.3.1 A dichotomous moderator and continuous predictor

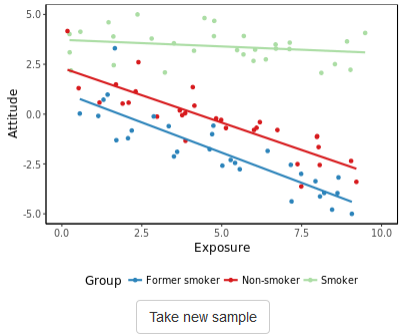


Figure 8.15: Is the effect of exposure on attitude moderated by smoking status?

1. Is the effect of exposure on attitude moderated by the smoking status of respondents (smokers versus non-smokers) in Figure 8.15? Motivate your answer. Press the *Take new sample* button to practice some more with recognizing moderation.

In Section 8.1, we have analyzed the predictive effects of exposure to an anti-smoking campaign and smoking status on a person's attitude towards smoking. We have found a negative effect for exposure and a positive effect for smoking. More exposure predicts a more negative attitude whereas smokers have a more positive attitude towards smoking.

Our current question is: Does exposure to the campaign have the same effect for smokers and non-smokers? We want to compare an effect (exposure on attitude) for different contexts (smokers versus non-smokers), so our current question involves moderation. Is the effect of exposure on attitude moderated by smoking status?

Our moderator (smoker vs. non-smoker) is a dichotomous variable but our predictor (exposure) is numeric, so we cannot use analysis of variance. Instead, we use regression analysis, which allows numeric predictors.

In the context of a regression model, moderation means **different slopes for different groups**. The slope of the regression line is the regression coefficient, which expresses the effect of the predictor on the outcome variable. If we have different effects in different contexts (moderation), we must have different regression coefficients for different groups.

8.3.2 Interaction variable

How do we obtain different regression coefficients and lines for smokers and non-smokers? The statistical trick is quite easy: Include a new predictor in the model that is the product of the predictor (exposure) and the moderator (smoking status). This new predictor is the *interaction variable*. It must be included together with the original predictor and moderator variables, see Equation (8.8). This is also visible in the statistical model (Figure 8.16) for moderation in a regression model.

$$\begin{aligned} attitude = {} & constant + b_1 * exposure + b_2 * smoker + b_3 * contact \\ & + b_4 * exposure * smoker + e \end{aligned} \tag{8.8}$$

[htbp]

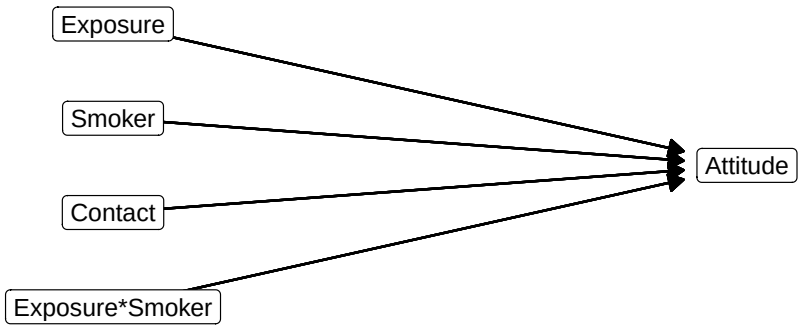


Figure 8.16: Statistical diagram of moderation.

The smoking status variable is coded 1 for smokers and 0 for non-smokers. For clarity, we name this variable smoker with score 1 for Yes and score 0 for No. Remember that we have two different regression equations, one for each group on the dichotomous predictor *status*. Just plug in the two possible values (1 and 0) for this variable. For non-smokers, the interaction variable drops from the model because multiplying with zero yields zero. For non-smokers, our reference group, b_1 represents the effect of exposure on attitude. It is called the *simple slope* of exposure for non-smokers.

$$\begin{aligned} attitude = {} & constant + b_1 * exposure + b_2 * smoker + b_3 * contact \\ & + b_4 * exposure * smoker + e \\ attitude = {} & constant + b_1 * exposure + b_2 * 0 + b_3 * contact \\ & + b_4 * exposure * 0 + e \\ attitude = {} & constant + b_1 * exposure + b_3 * contact + e \end{aligned} \tag{8.9}$$

In contrast, the interaction variable remains in the model for the smokers, who score 1 on smoking status. Note what happens with the coefficient of the exposure effect if we rearrange the terms a little: The exposure effect equals the effect for the reference group of non-smokers (b_1) plus the effect of the interaction variable (b_4). The simple slope for smokers, then, is $b_1 + b_4$.

$$\begin{aligned}
attitude &= constant + b_1 * exposure + b_2 * smoker + b_3 * contact \\
&\quad + b_4 * exposure * smoker + e \\
attitude &= constant + b_1 * exposure + b_2 * 1 + b_3 * contact \\
&\quad + b_4 * exposure * 1 + e \\
attitude &= constant + b_1 * exposure + b_4 * exposure + b_2 + b_3 * contact + e \\
attitude &= constant + (b_1 + b_4) * exposure + b_2 + b_3 * contact + e
\end{aligned} \tag{8.10}$$

The interaction effect (b_4) shows the difference between the simple slope of the exposure effect for smokers ($b_1 + b_4$) and the simple slope for non-smokers (b_1). This is the interpretation of the regression coefficient for a dichotomous interaction variable.

8.3.3 Conditional effects, not main effects

It is very important to note that the effects of exposure and smoking status in a model with exposure by smoking status interaction are **not** main effects as in analysis of variance. As we have seen in the preceding section (Equation (8.9)), the regression coefficient b_1 for exposure expresses the effect of exposure for the reference group of non-smokers. It is a *conditional effect*, namely the effect for non-smokers only. This is quite something different from a main effect, which is an average effect over all groups.

In a similar way, the regression coefficient b_2 for smoking status expresses the effect for persons who score zero on the exposure predictor. Simply plug in the value 0 for exposure in the regression equation (Equation (8.11)).

$$\begin{aligned}
attitude &= constant + b_1 * exposure + b_2 * smoker + b_3 * contact \\
&\quad + b_4 * exposure * smoker + e \\
attitude &= constant + b_1 * 0 + b_2 * smoker + b_3 * contact \\
&\quad + b_4 * 0 * smoker + e \\
attitude &= constant + b_2 * smoker + b_3 * contact + e
\end{aligned} \tag{8.11}$$

Smoking status is a dichotomy, so it tells us the average difference in attitude between smokers and non-smokers. Due to the inclusion of the interaction variable, it now tells us the difference in average attitude between smokers and non-smokers who have zero exposure to the anti-smoking campaign. AS you see again, this is a conditional effect, not a main effect.

8.3.4 Interpretation and statistical inference

In Table 8.2, non-smokers are the reference group because they are coded 0 on the *Status* variable. As a consequence, the regression coefficient for exposure gives us the effect of exposure on smoking attitude for non-smokers. It's value is -0.16, so an additional unit of exposure predicts a smoking attitude among non-smokers that is 0.16 points more negative.

Table 8.2: Predicting attitude towards smoking: regression analysis results.

	B	Std. Error	Beta	t	Sig.	Lower Bound	Upper Bound
(Constant)	0.900	0.357		2.521	0.014	0.190	1.610
Exposure	-0.162	0.061	-0.162	-2.651	0.010	-0.284	-0.040
Status (smoker)	1.980	0.738	1.980	2.683	0.009	0.512	3.448
Exposure*Status (smoker)	-0.327	0.142	-0.327	-2.311	0.023	-0.609	-0.045

More exposure to the campaign goes together with a more negative attitude towards smoking for non-smokers. The p value for this effect tests the null hypothesis that the effect is zero in the population. If we reject this null hypothesis, the exposure effect is statistically significant for non-smokers.

The effect of (smoking) status on attitude is conditional on exposure. The regression coefficient for status tells us the difference between smokers and non-smokers who have 0 exposure. So, without exposure to the campaign, smokers are on average 1.98 more positive towards smoking than non-smokers. The p value tests the null hypothesis that the difference is zero for people without exposure to the anti-smoking campaign.

Smokers are coded 1 on the (smoking) status variable, so the regression coefficient for the interaction tells us that the slope of the exposure effect is 0.33 lower for smokers than for non-smokers. In a preceding paragraph, we have seen that the estimated slope of the exposure effect is -0.16 for non-smokers. We can add the regression coefficient of the interaction variable to obtain the estimated slope for smokers, which is -0.49. Now we can compare the two regression lines for the two groups, which gives good insight in the nature of moderation in this example. A graph of the two regression lines is probably the best way to communicate your results.

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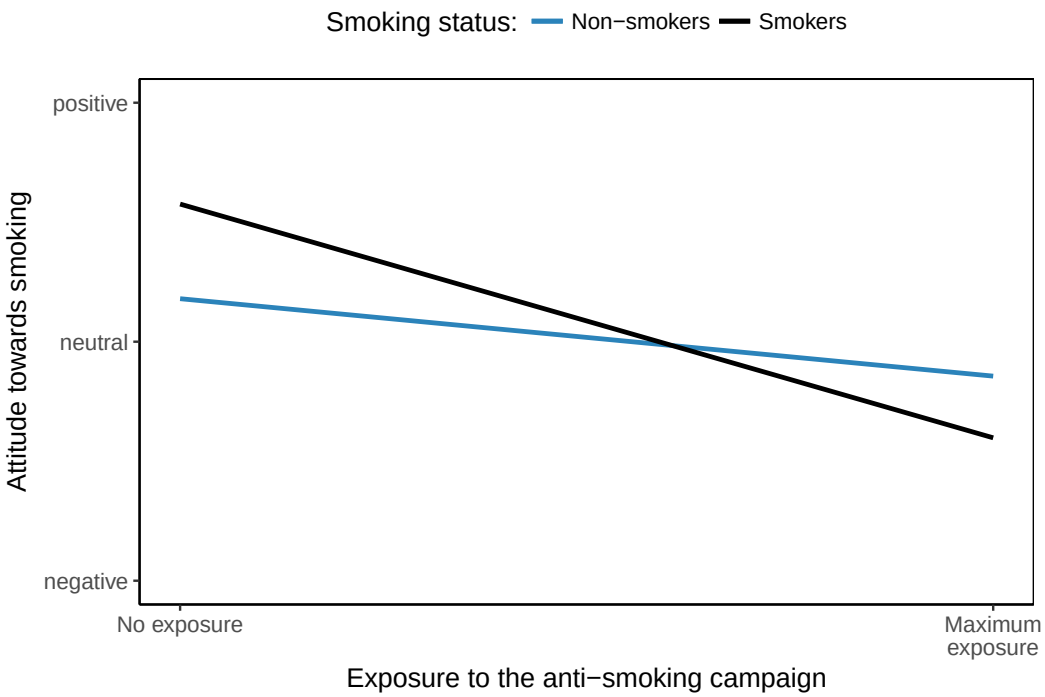

Figure 8.17: The effects of exposure to the anti-smoking campaign on attitude towards smoking among smokers and non-smokers.

The interaction variable is treated as an ordinary predictor in the estimation process, so it receives a confidence interval and a p value. The null hypothesis is that the interaction effect is zero in the population.

Remember that the regression coefficient for the interaction variable expresses the difference between the slope for the indicated group, e.g., smokers, and the slope for the reference group, e.g., non-smokers. If this difference is zero, as stated by the null hypothesis, the two groups have the same slope, so the effect is not moderated by the group variable.

So we know the confidence intervals and p values of the exposure effect for non-smokers and for the difference between their exposure effect and the exposure effect for smokers. We do not know, however, the confidence interval and statistical significance of the exposure effect for smokers. We cannot add confidence intervals or p values.

If you want to know the confidence interval or p value of the exposure effect for smokers, you have to rerun the regression analysis using a different indicator variable for the moderator. You should create a dichotomous variable that assigns the 1 score to non-smokers and an interaction variable created with this dichotomy.

Interaction variables are used just like ordinary predictors, so the general assumptions or

regression analysis apply. See Section 8.1.5 for a description of the assumptions and checks.

Let us conclude the interpretation with a warning. The standardized regression coefficients that SPSS reports must **not** be used. They are calculated in the wrong way if the regression model includes an interaction variable. As a result, they are meaningless.

8.3.5 Common support

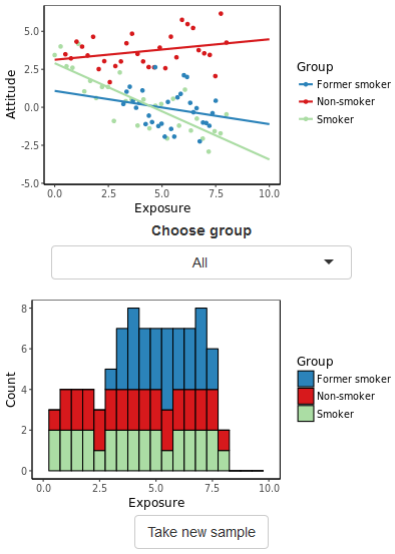

Figure 8.18: How well do the observations cover the predictor within each category of smoking status?

1. What does the histogram represent in Figure 8.18?
2. Are the exposure values nicely spread for each smoke status group? Inspect each smoke status group separately with the "Show groups" option.
3. What is the problem if exposure scores are not nicely spread over the same range for all smoke status groups?

In a regression model with moderation, we have to interpret the effect of a predictor involved in the interaction at a particular value of the moderator (Section 8.3.3). The estimated effect at a particular value of the moderator can only be trusted if there are quite some observations at or near this value of the moderator. In addition, these observations should cover the full range of values on the predictor. After all, the effect that we estimate must tell us whether higher values on the predictor go together with higher (or lower) values on the outcome.

For example, we need quite some observations for smokers to estimate the conditional effect of exposure on attitude for smokers. If there are hardly any smokers in our sample, we

cannot estimate the effect of exposure on attitude for them in a reliable way. Even if we have quite some observations for smokers but all smokers have low exposure, we cannot say much about the effect of exposure on attitude for them. If we cannot say much about the effect within this group, we cannot say much about the difference between this effect and effects for other groups. In short, the moderation model is problematic here.

The variation of predictor scores for a particular value of the moderator is called *common support* (Hainmueller, Mummolo, & Xu, 2016). If common support for predictors involved in moderation is bad, we should hesitate to draw conclusions from the estimated effects. Guidelines for good common support are hard to give. Common support is usually acceptable if there are observations over the entire range of the predictor.

It is recommended to check the number of observations per value of the moderator. For a categorical moderator, such as smoking status, a scatterplot of outcome (vertical axis) by predictor (horizontal axis) with dots coloured according to the moderator category may do the job. Check that there are observations for more or less all values of the predictor. In Figure 8.19, observations in each moderator category (dot colour) range from low to high predictor values.

[htbp]

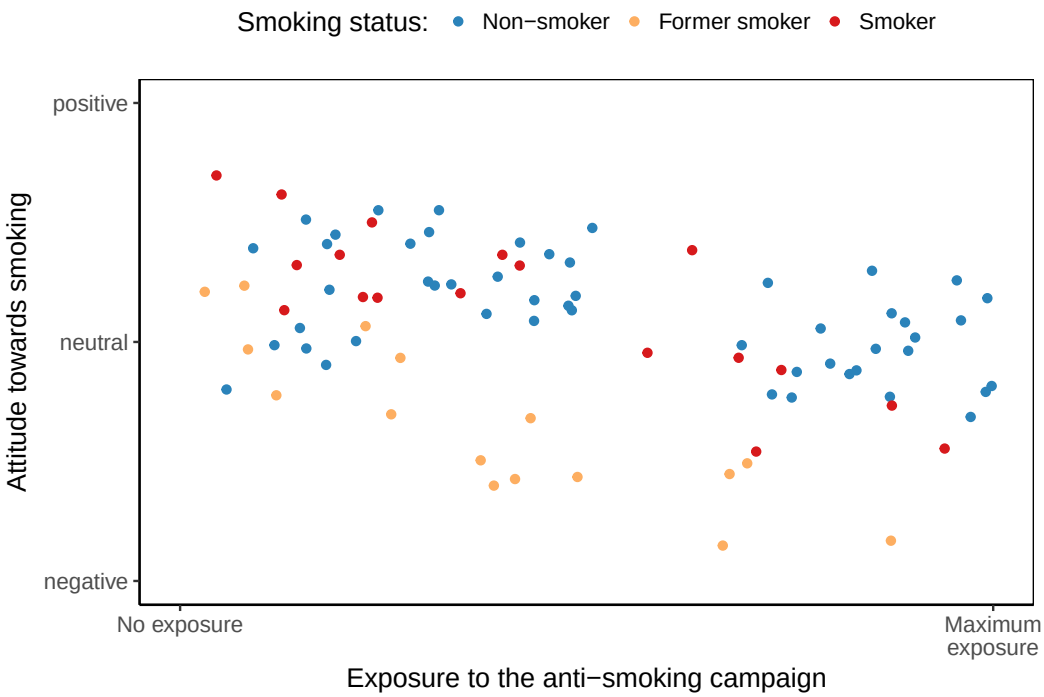

Figure 8.19: The effects of exposure to the anti-smoking campaign on attitude towards smoking among smokers and non-smokers.

8.3.6 A categorical moderator

What if we have three or more groups in our moderator? For example, smoking status measured with three categories: (1) never smoked, (2) have smoked, (3) currently smoking? Does the effect of exposure on attitude vary between people who never smoked, stopped smoking, and are still smoking?

In Section 8.1.4, we learned that we must create dummy variables for all but one groups of a categorical predictor in a regression model. This is what we have to do also for a categorical moderator because we must include the (conditional) effects of the categorical variable in the model. If the effect of another predictor, such as exposure, is moderated by the categorical variable, we have to create an interaction variable for each dummy variable in the equation. To create the interaction variables, we multiply the predictor with the dummy variable as we have done before.

[htbp]

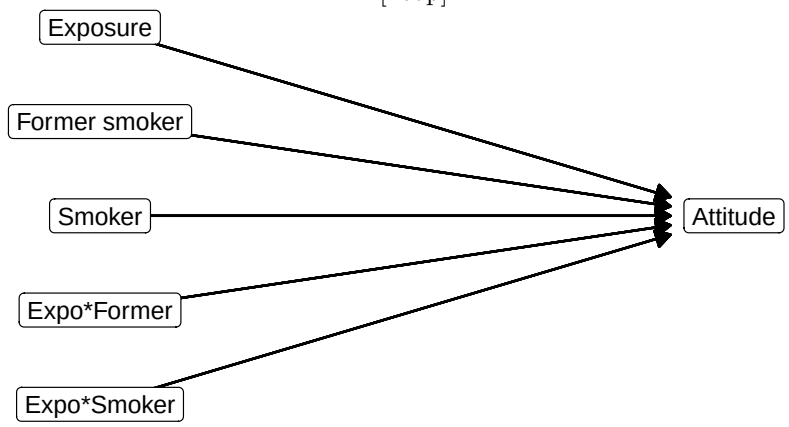

Figure 8.20: Statistical model with a moderator consisting of three groups. Non-smokers are the reference group

In the end, we have an interaction variable for all groups but one on the categorical moderator. Figure 8.20 shows the statistical model. Estimation of the model yields point estimates (regression coefficients), confidence intervals, and p values for all variables (Figure **??**).

Remember that the effects of predictors that are included in interactions are conditional effects: effects for the reference group or reference value. The p value for *Exposure* tests the hypothesis that the exposure effect for people who never smoked is zero in the population. For the two dummy variables *Former smoker* and *Smoker*, the null hypothesis is tested that they have the same average attitude in the population as the non-smokers (reference group) if they are not exposed to the anti-smoking campaign.

Interaction predictors show effect differences. In Table 8.3, the interaction predictors test the null hypothesis that the effect of exposure is equal for non-smokers and former smokers

Table 8.3: Predicting attitude towards smoking for three smoking status groups: regression analysis results.

	B	Std. Error	t	Sig.	Lower Bound	Upper Bound
(Constant)	1.644	0.288	5.717	0.000	1.072	2.216
Exposure	-0.185	0.046	-3.987	0.000	-0.277	-0.093
Former smoker	-1.095	0.544	-2.013	0.048	-2.178	-0.012
Smoker	1.235	0.521	2.372	0.020	0.199	2.272
Exposure*Former smoker	-0.405	0.112	-3.604	0.001	-0.629	-0.181
Exposure*Smoker	-0.304	0.098	-3.116	0.003	-0.498	-0.110

(*Exposure*Former smoker*) or for non-smokers and smokers (*Exposure*Smoker*) in the population.

If we would like to know whether the exposure effect for former smokers is significantly different from zero, we have to rerun the regression model using the people who stopped smoking as reference group. This new model would also tell us whether the exposure effect for people who stopped smoking is significantly different from the exposure effect for people who are still smoking.

8.4 A Dichotomous or Categorical Moderator in SPSS

8.4.1 Instructions

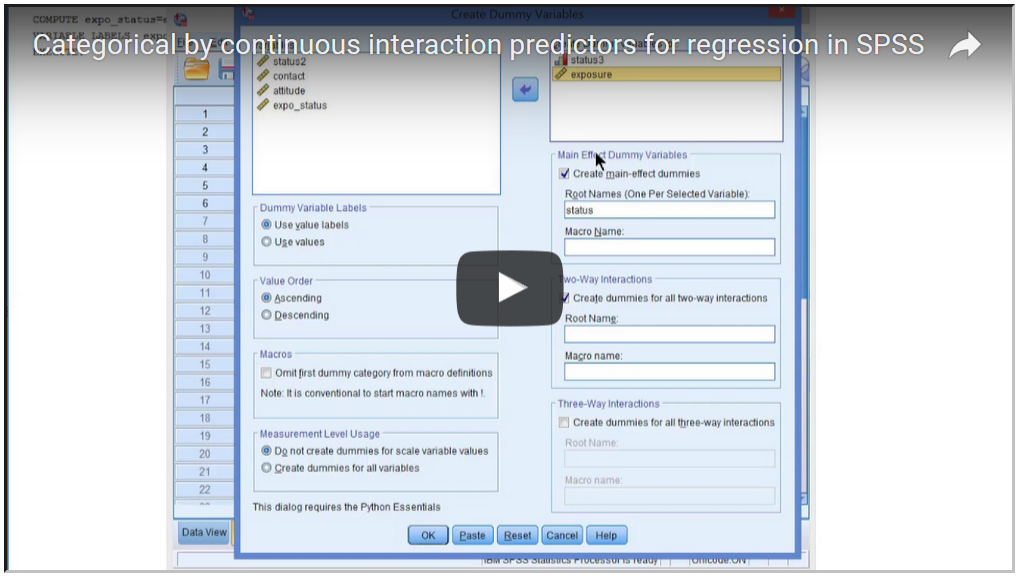

Figure 8.21: Creating categorical by continuous interaction predictors for regression in SPSS.

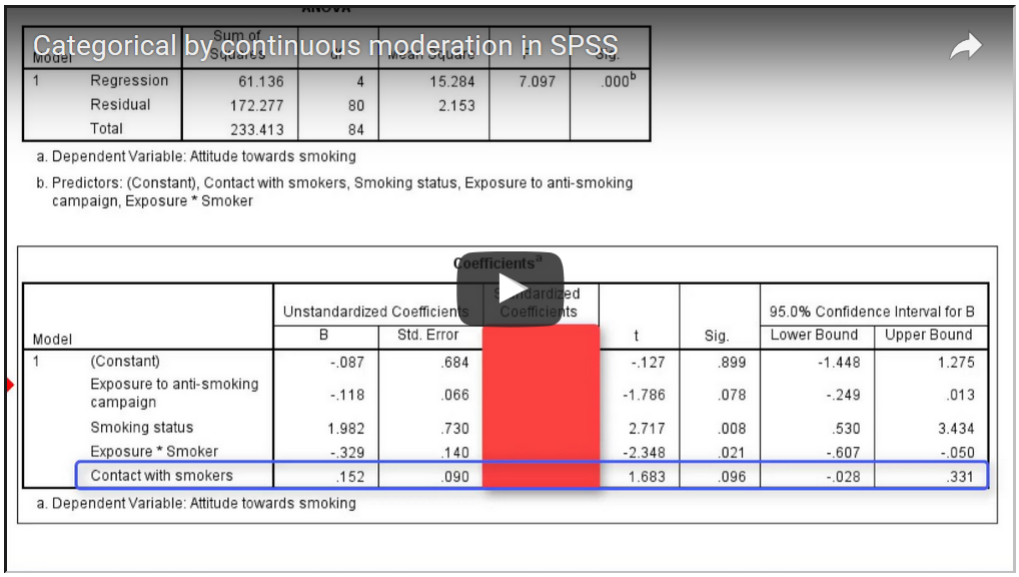

Figure 8.22: Estimating categorical by continuous moderation with regression in SPSS.

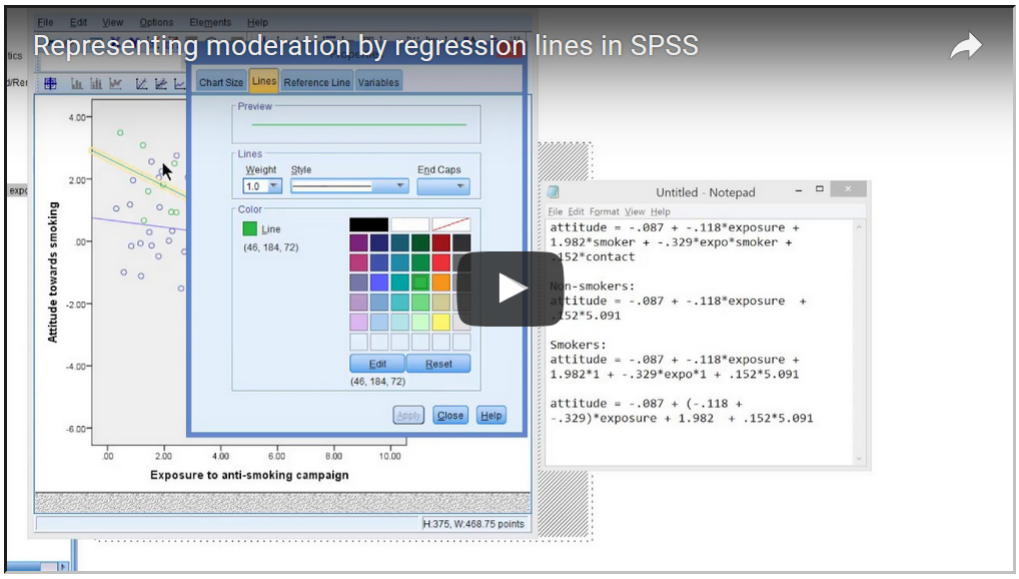

Figure 8.23: Representing moderation by regression lines in a scatterplot in SPSS.

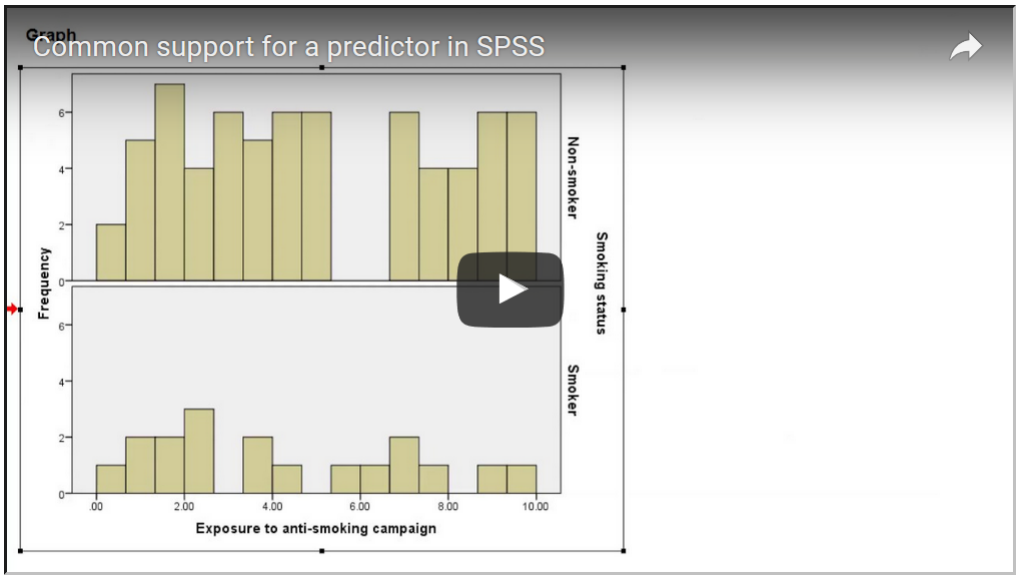

Figure 8.24: Checking common support for a predictor at different moderator values in SPSS.

8.4.2 Exercises

1. Use the data in smokers.sav to predict the attitude towards smoking from exposure moderated by smoking status (variable *status2*). Use contact with smokers as a covariate. Check the assumptions for regression analysis and interpret the results.

2. Visualize the moderated effects of exposure on attitude (Exercise 1). Create a scatterplot with two regression lines. Colour the regression lines and the dots (respondents) according to their smoking status category. Interpret the moderation of the exposure effect by smoking status.

3. Check the common support of the predictor (exposure) in all groups of the moderator (smoking status). Could you also check common support with the scatterplot you made for Exercise 2?

4. Repeat the analyses of Exercises 1 through 3 but use smoking status with three categories (*status3*).

8.5 A Continuous Moderator

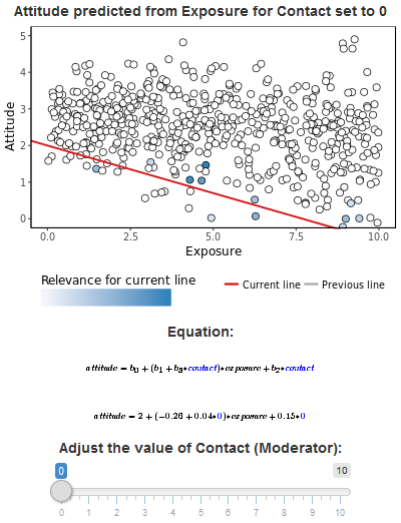

Figure 8.25: How do contact values affect the conditional effect of exposure on attitude?

1. The regression line depicted in Figure 8.25 represents the conditional effect of exposure on attitude for the value of contact with smokers selected with the slider. How many different conditional effects are there?
2. Is the effect of campaign exposure on attitude towards smoking always negative? Or does more exposure lead to a more positive attitude (higher score) in some cases? If so, in which cases?
3. How much does the slope increase if the moderator value is changed from 0 to 1? And how much if it changes from 6 to 7?

People hanging around a lot with smokers are likely to have a more positive attitude towards smokers than people who have little contact with smokers. After all, people who really hate smoking will avoid meeting smokers. This is a main effect of contact with smokers on attitude towards smoking.

In addition, the anti-smoking campaign may be less effective for people who spend a lot of time with smokers. Negative perceptions of smoking instilled by the campaign can be compensated by positive experiences of seeing people enjoy smoking. Contact with smokers would decrease the effect of campaign exposure on attitude. The effect of exposure is moderated by contact with smokers.

Our moderator, contact with smokers, is continuous. As a consequence, we can have an endless number of contact levels as groups for which the slope may change. This is the only difference with a categorical moderator. Other than that, we will analyze a continuous moderator in the same way as we analyzed a categorical moderator.

8.5.1 Interaction variable

We need one interaction variable to include a continuous moderator in a regression model. As before, the interaction variable is the product of the predictor and the moderator.

Although we have an endless number of different moderator values or groups, we only need one interaction variable. It represents the gradual (linear) change of the effect of the predictor for higher values of the moderator.

To see this, it is helpful to inspect the regression equation with rearranged terms (Equation (8.12)). Every little bit of extra contact with smokers adds to the slope ($b_1 + b_3 * contact$) of the exposure effect. The addition is gradual—a little bit of additional contact with smokers changes the exposure effect a little bit—and it is linear: A unit increase in contact adds the same amount to the effect whether the effect is at a low or a high level.

$$\begin{aligned} attitude &= constant + b_1 * exposure + b_2 * contact + b_3 * exposure * contact + e \\ attitude &= constant + (b_1 + b_3 * contact) * exposure + b_2 * contact + e \end{aligned} \tag{8.12}$$

We can interpret the regression coefficient of the interaction effect (b_3) here as the predicted difference of the exposure effect (slope) for a one unit difference in contact (the moderator). A positive coefficient indicates that the exposure effect is more positive for higher levels of contact with smokers. A negative coefficient indicates that the effect is more negative for people with more contacts with smokers.

Note that positive and negative are used here in there mathematical meaning, not in an appreciative way. A positive effect of exposure implies a more positive attitude towards smoking. Anti-smoking campaigners probably evaluate this as a negative result.

8.5.2 Conditional effect

The regression coefficients for exposure and contact represent conditional effects (see Section 8.3.3). These are the effects for cases that score zero on the other variable. Plug in zero for the moderator and you see that all terms with a moderator drop from the equation and only b_1 is left as the effect of exposure.

$$\begin{aligned} attitude &= constant + (b_1 + b_3 * contact) * exposure + b_2 * contact + e \\ attitude &= constant + (b_1 + b_3 * 0) * exposure + b_2 * 0 + e \\ attitude &= constant + b_1 * exposure + e \end{aligned} \tag{8.13}$$

The zero score on the moderator is the *reference value* for the conditional effect of the predictor. Cases that score zero on the moderator are the *reference group* just like cases scoring zero on the dummy variables are the reference group in a model with a categorical moderator (Section 8.1.3).

8.5.3 Mean-centering

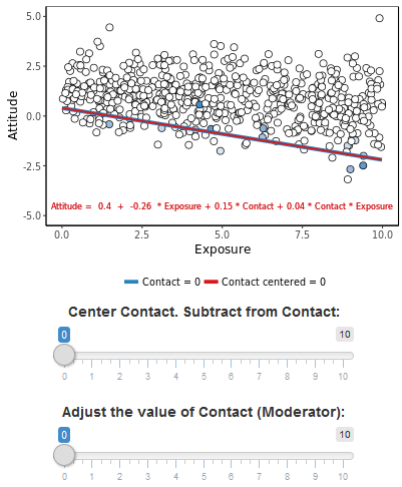

Figure 8.26: What happens if you mean-center the moderator variable?

1. What is the correct interpretation of the estimated regression coefficient of exposure in Figure 8.26?
2. What happens to the (thin) regression line and the regression equation if you subtract the mean (M) from the respondents' contact with smokers scores? Thus, you mean-center the moderator Contact. Use the slider **Center Contact. Subtract from Contract:** in Figure 8.26 to check your answer.
3. If Contact is mean-centered, the regression coefficient of exposure represents the effect of exposure on attitude for respondents with a particular score on the original Contact variable. What is this original Contact score (reference value of the moderator)? Use the slider **Adjust the value of Contact (Moderator):** to check your answer.

What if there are no people with zero contact? Then, the interpretation of the regression coefficient b_1 for exposure does not make sense. In this situation, it is better to mean-center the moderator (contact) before you add it to the regression equation and before you calculate the interaction variable.

To *mean-center* a variable, you subtract the variable's mean from all scores on the variable. As a result, a mean score on the original variable becomes a zero score on the mean-centered variable.

$$contactcentered = contact - mean(contact)$$

With mean-centered numerical moderators, a conditional effect in the presence of interaction always makes sense. It is the effect of the predictor for average score on the moderator. An

average score always falls within the range of scores that actually occur. If we mean-center the contact with smokers moderator, the regression coefficient b_1 for exposure expresses the effect of exposure on attitude for people with average contacts with smokers. This makes sense.

Remember that the interaction variable is the product of the predictor and moderator (Section 8.3.2). If any or both of these are mean-centered, you should multiply the mean-centered variable(s) to create the interaction variable, see Sections 8.3.3 and 8.5.2.

8.5.4 Symmetry of predictor and moderator

If we want to interpret the conditional effect of contact on attitude (b_2), we must realize that this is the effect for people who score zero on the exposure variable. This is clear if we rearrange the regression equation as in Equation (8.14).

$$\begin{aligned} attitude &= constant + b_1 * exposure + b_2 * contact + b_3 * exposure * contact + e \\ attitude &= constant + b_1 * exposure + (b_2 + b_3 * exposure) * contact + e \\ attitude &= constant + b_1 * 0 + (b_2 + b_3 * 0) * contact + e \\ attitude &= constant + b_2 * contact + e \end{aligned} \tag{8.14}$$

But wait a minute, this is what we would do if contact was the predictor and exposure the moderator. That is a completely different situation, is it not? No, technically it does not make a difference which variable is the predictor and which is the moderator. The predictor and moderator are symmetric. The difference is only in our theoretical expectations and in our interpretation.

The conditional effect of the moderator, as stated above, is the effect of the moderator if the predictor is zero. This interpretation makes sense only if there are cases with zero scores on the predictor. In the current example, the scores on exposure range from 0 to 10, so zero exposure is meaningful. But it represents an eccentric score with perhaps a very atypical effect of contact on attitude or few observations. For these reasons, it is recommended to *mean-center both the predictor and moderator if they are numeric.*

Mean centering does not change the interpretation of regression coefficients. An unstandardized regression coefficient still tells us the predicted difference in the outcome variable for a one unit difference in the predictor. Mean centering only changes the reference value, that is, the value of the other variable in the interaction to which the regression coefficient applies.

8.5.5 Visualization of the interaction effect

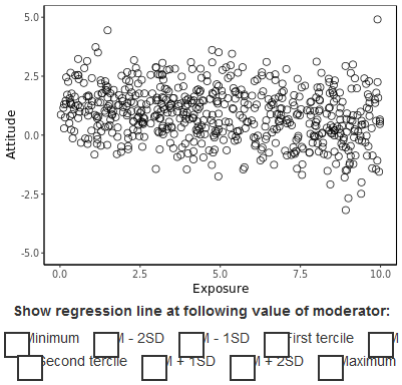

Figure 8.27: Which moderator values are helpful for visualizing moderation?

1. Select one or more options in Figure 8.27 to represent regression lines predicting attitude from exposure at different values of the moderator (contact with smokers). Respondents with moderator values close to the selected value are coloured. Which moderator values would you pick to communicate the results of moderation? Motivate your answer.

As we have seen in Section 8.5.1, the regression coefficient of an interaction effect with a continuous moderator can be directly interpreted. It represents the predicted difference in the unstandardized effect size for a one unit increase in the moderator. For example, one more contact with a smoker increases the exposure effect by 0.04.

The size of the interaction effect tells us the moderation trend, for instance, people who are more around smokers tend to be less opposed to smoking if they are exposed to the anti-smoking campaign. But we do not know how much an anti-smoking attitude is fostered by exposure to a campaign and whether exposure to the campaign increases anti-smoking attitude for everyone. Perhaps, people hanging out with smokers a lot may even get a more positive attitude towards smoking from campaign exposure.

We can be more specific about exposure effects at different levels of contact with smokers if we pick some interesting values of the moderator and calculate the conditional effects at these levels.

The minimum or maximum values of the moderator are usually not very interesting. We tend to have few observations for these values, so our confidence in the estimated effect at that level is low. Instead, the values one standard deviation below and above the mean of the moderator are popular values to be picked. One standard deviation below the mean (M - SD) indicates a low value, the mean (M) indicates a central value, and one standard deviation above the mean (M + SD) indicates a high value.

Having picked these values, we can visualize moderation as different regression lines in a plot. We use exactly the same approach as in visualizing moderation by a categorical variable. AS

Table 8.4: Predicting attitude towards smoking: regression analysis results with exposure and contact mean-centered.

	B	Std. Error	Beta	t	Sig.	Lower Bound	Upper Bou
(Constant)	0.169	0.204		0.825	0.412	-0.238	0.5
Exposure (mean-centered)	-0.174	0.063	-0.174	-2.740	0.008	-0.300	-0.0
Contact (mean-centered)	0.159	0.094	0.159	1.685	0.096	-0.029	0.3
Status (smoker)	0.533	0.405	0.533	1.318	0.191	-0.272	1.3
Exposure*Contact (mean-centered)	0.018	0.034	0.018	0.533	0.595	-0.049	0.0

a first step, we construct equations for conditional effects of the predictor at different levels of the moderator. Plug the selected value of the moderator into the regression equation. If there are covariates, we must also plug in a meaningful value for the covariates, usually the average for numeric covariates and zero or one for dichotomous covariates. As a second step, we use the equations to add regression lines to a scatterplot.

If contact (the moderator) is mean-centered, as in the current example, we simply plug in zero for the moderator to obtain the equation for the regression line at the mean of the moderator (contact with smokers). We plug in the value of the standard deviation of contact with smokers to get the regression equation for people who scored one standard deviation above the mean on the moderator. The standard deviation of contact is 2.0 in this example, so Equation (8.15) replaces contact by 2.0 everywhere. Finally, we plug in minus the value of one standard deviation if we want the regression line for the moderator at the mean minus one standard deviation.

We also have to plug in a value for each covariate. This example contains one covariate, namely (smoking) status. We plug in the score for non-smokers (0). In the end, our predictor (exposure) should be the only variable in the right hand side of the regression equation (the last line in Equation (8.15)). Note that we do not include the error term (e) in the equation if we predict values; the error term captures prediction errors.

$$\begin{aligned} attitude &= 3.6 + -0.1 * exposure + 0.1 * status + 0.1 * contact \\ &\quad + 0.03 * contact * exposure \\ attitude &= 3.6 + -0.1 * exposure + 0.1 * (0) + 0.1 * (2.0) + 0.03 * (2.0) * exposure \\ attitude &= 3.4 + -0.04 * exposure \end{aligned} \tag{8.15}$$

If the moderator is not mean-centered, we have to plug in the value of the mean of the moderator and the value of the mean plus or minus the standard deviation of the moderator. In this example, the mean score of contact with smokers is 5.1, so the moderator mean minus one standard deviation (2.0) equals 3.1 and the mean plus one standard deviation is 7.1.

8.5.6 Statistical inference on conditional effects

The regression model yields a p value and confidence interval for the predictor at the reference value of the moderator. In the model estimated in Table 8.4, for instance, we obtain a p

value of 0.008 and a 95% confidence interval of [-0.30, -0.05] for the effect of exposure on attitude. This is the conditional effect of exposure on attitude for cases that score zero on the moderator variable (contact with smokers) as we can verify in Equation (8.16).

$$\begin{aligned} attitude &= constant + b_1 * exposure + b_2 * contact + b_3 * status + \\ &\quad + b_4 * exposure * contact + e \\ attitude &= constant + (b_1 + b_3 * contact) * exposure + b_2 * contact + e \\ attitude &= constant + (b_1 + b_4 * 0) * exposure + b_2 * 0 + b_3 * status + e \\ attitude &= constant + b_1 * exposure + b_3 * status + e \end{aligned} \tag{8.16}$$

If the variable contact is mean-centered, the p value tests the null hypothesis that the effect of exposure is zero for people who have average contact with smokers. The confidence interval tells us that the effect of exposure on attitude for people with average contacts with smokers ranges between -0.30 and -0.05 with 95% confidence. If the moderator is not mean-centered, the results apply to people who have no contact with smokers.

Note that mean-centering of the moderator changes, so to speak, the regression line that we test from the effect of exposure for people with no smoker contact to the effect for people with average contact with smokers. If we would like to get the p value or confidence interval for the regression line at one standard deviation above or below the mean, we have to center the moderator at those values before we estimate the regression model.

8.5.7 Common support

In Section 8.3.5, we checked the support of the predictor in the data for different groups of the moderator. The basic idea is that we can only sensibly estimate and interpret a conditional effect at a moderator level if we have observations over the entire range of the predictor. For each moderator group, we checked the distribution of the predictor.

With a continuous moderator we can also do this if we group moderator scores. Hainmueller et all. (2016) recommend creating three groups, each containing one third of all observations. These low, medium, and high groups correspond more or less with the minus one standard deviation/mean/plus one standard deviation values that we used for visualizing and testing conditional effects. Create a histogram for the predictor in each of these groups to check common support of moderation in the data.

8.5.8 Assumptions

The general assumptions for regression analysis (Section 8.1.5) also apply to the interaction effect with a continuous moderator. The checks are the same: See if the residuals are more or less normally distributed and check the residuals by predicted values plot.

Note that the linearity assumption also applies to the interaction effect. If the interaction effect is positive, the exposure (predictor) effect must be higher for higher values of contact

with smokers (moderator). More precisely, a unit difference on the moderator should result in a fixed increase (or decrease) of the effect of the predictor. You may have noticed this linear change in the effect size in Figure 8.25 at the beginning of this section on continuous moderators.

If we would estimate a separate regression model for each selected moderator group, the linearity assumption says that the regression coefficients for the predictor should only go up (or down) if we progress from lower moderator scores to higher moderator scores. For example, the exposure effect for the 33% of all people with least contacts with smokers should be below the exposure effect for the 33% of all people with medium contact scores, which should be below the effect for people with most contact scores.

In principle, we can execute a separate regression analysis for each moderator group if we have a large sample, for instance, over 200 cases. There are some complications, however, so let us not pursue this here.

8.5.9 Higher-order interaction effects

An interaction effect with one moderator, albeit continuous or categorical, is called a *first-order interaction*. It is possible to have a moderated effect that is moderated itself by a second moderator. For example, the change in the exposure effect due to a person's contact with smokers may be different for smokers than for non-smokers. This is called a *second-order interaction* or *higher order interaction*. We can include more moderators, yielding even higher higher-order interactions, such as three or four moderators.

An interaction variable that is the product of the predictor and two moderators can be used to include a second-order interaction in a regression model. If you include a second-order interaction, you must also include the effects of the variables involved in the interaction as well as all first-order interactions among these variables in the regression model. All in all, these models become very complicated to interpret, so we do not pay further attention to them.

8.6 Reporting Regression Results with Moderation

Note. $N = 150$. CI = confidence interval.

* $p < .05$. ** $p < .01$. *** $p < .001$.

If we report a regression model, we first present the significance test and predictive power of the entire regression model. We may report that the regression model is statistically significant, F (7, 142) = 28.64, p < 0.001, so the regression model very likely helps to predict attitude towards smoking in the population. Retrieve the test information from SPSS; the APA6-style table (Table 8.5) only reports the F value and its significance level.

How well does the regression model predict attitude towards smoking? The effect size of a regression model or its predictive power is summarized by R^2 (*R Square*), which is the proportion of the variation in the outcome variable scores (attitude towards smoking) that can be predicted with the regression model. In this example, R^2 is 0.59, so the regression model predicts 59% of the variance

Table 8.5: Predicting attitude towards smoking. Results in APA6 style. Exposure and contact are mean-centered.

	B	95% CI
Constant	-1.08***	[-1.32, -0.85]
Exposure	-0.18***	[-0.26, -0.10]
Contact	0.21***	[0.12, 0.30]
Former smoker	-1.38***	[-1.74, -1.01]
Smoker	0.10	[-0.41, 0.60]
Exposure * Contact	0.06***	[0.02, 0.09]
Exposure * Former smoker	-0.20**	[-0.33, -0.07]
Exposure * Smoker	-0.02	[-0.17, 0.13]
R^2	0.59	
F	28.64***	

in attitude towards smoking among the respondents. In communication research, R^2 is usually smaller.

R^2 tells us how well the regression model predicts the outcome variable in the sample. Every predictor that we add to the regression model helps to predict results in the sample even if the predictor does not help to predict the outcome in the population. For a better idea of the predictive power of the regression model in the population, we may use *Adjusted R Square*. Adjusted R Square is usually slightly lower than R Square. In the example, Adjusted R Square is 0.56 (not reported in Table 8.5)

As a next step, we discuss the size, statistical significance, and confidence intervals of the regression coefficients. If a predictor is involved in one or more interaction effects, we must be very clear about the reference value and reference group to which the effect applies.

Exposure, in our example, has a negative predictive effect on attitude towards smoking for non-smokers with average contacts with smokers, t = -4.37, p < .001, 95%CI[-0.26, -0.10]. Note that SPSS does not report the degrees of freedom for the t test on regression coefficient, so we cannot report them.

Instead of presenting the numerical results in the text, we may summarize them in an APA6 style table, such as Table 8.5. Note that t and p values are not reported in this table, the focus is on the confidence intervals. The significance level is indicated by stars.

A sizable and statistically significant interaction effect signals that an effect is moderated. In the example reported in Table 8.5, the effect of exposure on attitude seems to be moderated by contact with smokers (b = 0.06, p < .001) and by smoking status (b = -0.20, p = 0.003).

The regression coefficients for interaction effects must be interpreted as effect differences. For a categorical moderator, the coefficient describes the effect size difference between the category represented by the dummy variable and the reference group. Among former smokers, the negative effect of exposure is stronger for former smokers than for the reference group non-smokers. The average difference is -0.20.

For a continuous moderator, we can interpret the general pattern reflected by the interaction effect. A positive interaction effect, such as 0.06 for the interaction between exposure and smoker contact,

signals that the effect of exposure is more strongly positive or less negative at higher levels of contact with smokers.

This interpretation in terms of effect differences remains a difficult to understand. It is recommended to select some interesting values for the moderator and report the size of the effect for each value. For a categorical moderator, each category is of interest. For a continuous moderator, the mean and one standard deviation below and above the mean are usually interesting values. The regression coefficients show whether the effect is positive, negative, or nearly zero at different values of the moderator.

Visualize the regression lines for different values of the moderator rather than presenting the numerical results. If the regression model contains covariates, mention the values that you have used for the covariates. Select one of the categories for a categorical covariate. For numeric covariates, the mean is a good choice. If you are working with mean-centered predictors, be sure to use the mean-centered predictor for the horizontal axis (as in Figure 8.28), not the original predictor.

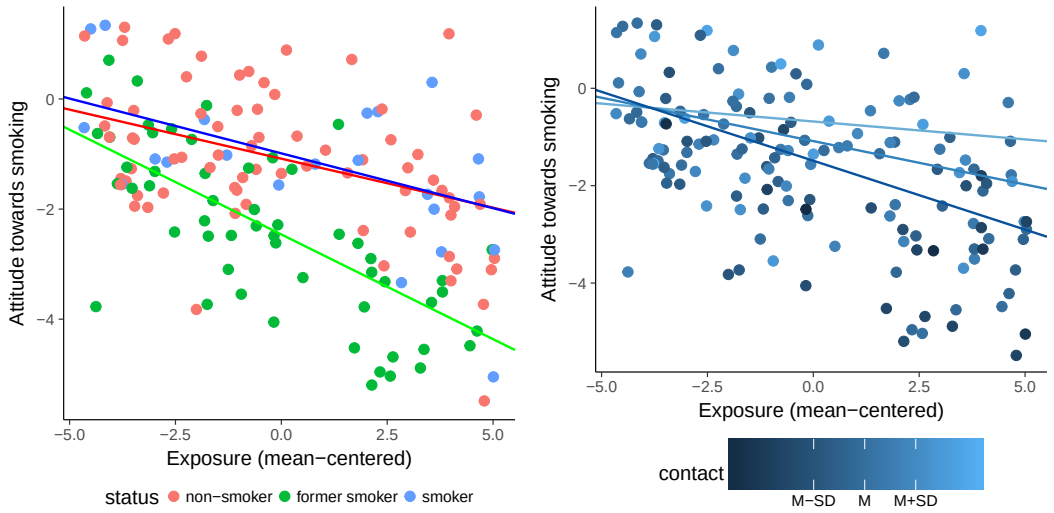

Figure 8.28: The effect of exposure on attitude towards smoking. Left: Effects for groups with different smoking status (at average contact with smokers). Right: Effects at different levels of contact with smokers (effects for non-smokers).

The left panel in Figure 8.28 clearly shows that the effect of exposure on attitude is more or less the same for non-smokers and smokers. The effect is different for former smokers, for whom the exposure effect is more strongly negative. It is more complicated to draw this conclusion from the table with regression coefficients.

Check that the predictor has good support at the selected values of the moderator. In the left-hand plot of Figure 8.28, the groups (colours) vary nicely over the entire range of the predictor *exposure*, so that is okay. It is more difficult to see good variation in the right-hand plot.

Do not report that common support is good. If it is bad, try to find other reference groups or values with adequate support. If they cannot be found, warn the reader that we cannot fully trust the

estimated moderation because we do not have a nice range of predictor values within each level of the moderator.

Finally, inspect the residual plots but do not include them in the report. Warn the reader if the assumptions of the linear regression model are not met. Do not mention the assumptions if they are met.

8.7 A Continuous Moderator in SPSS

8.7.1 Instructions

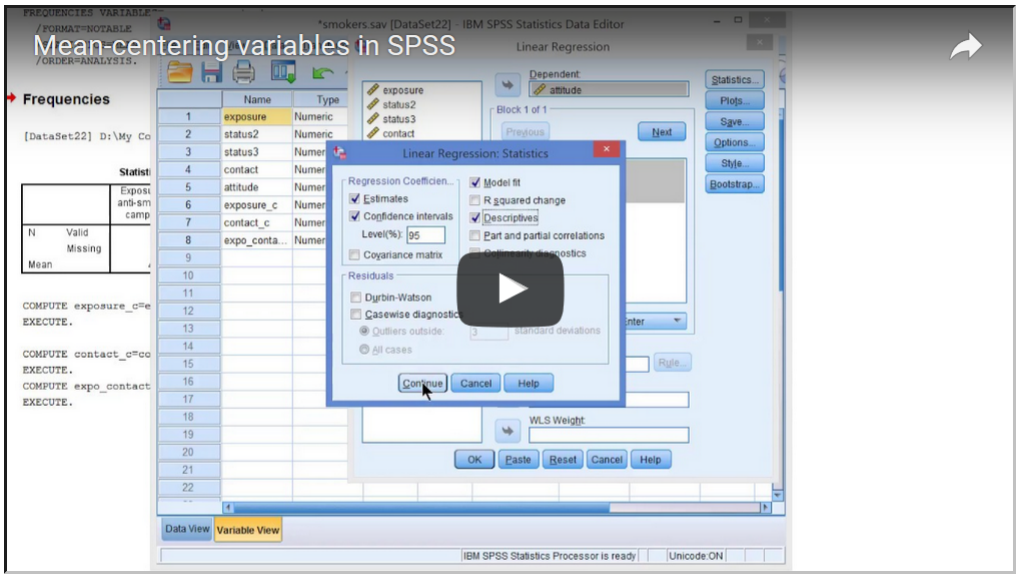

Figure 8.29: Mean-centering variables for regression analysis in SPSS.

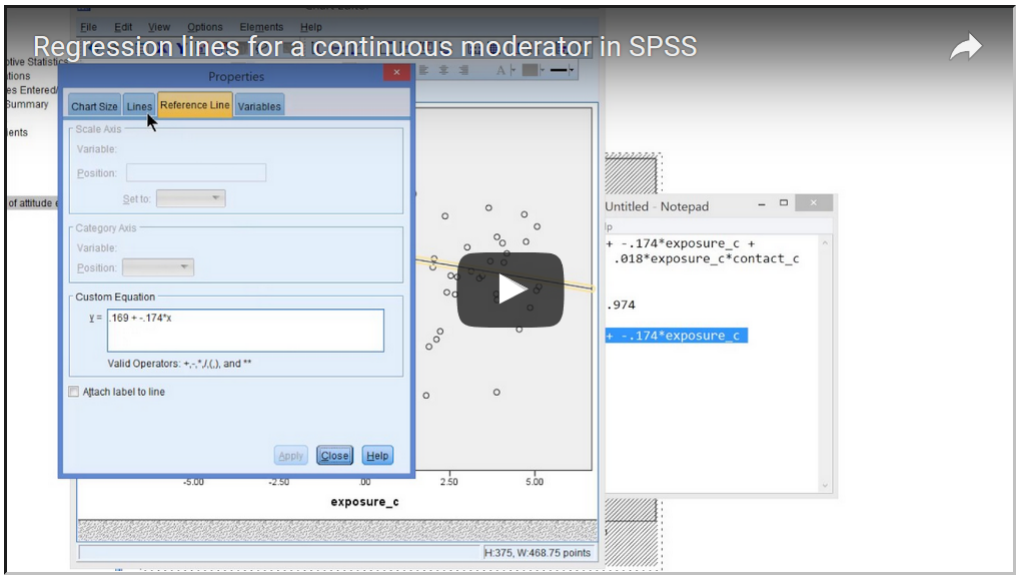

Figure 8.30: Regression lines for a continuous moderator in a scatterplot in SPSS.

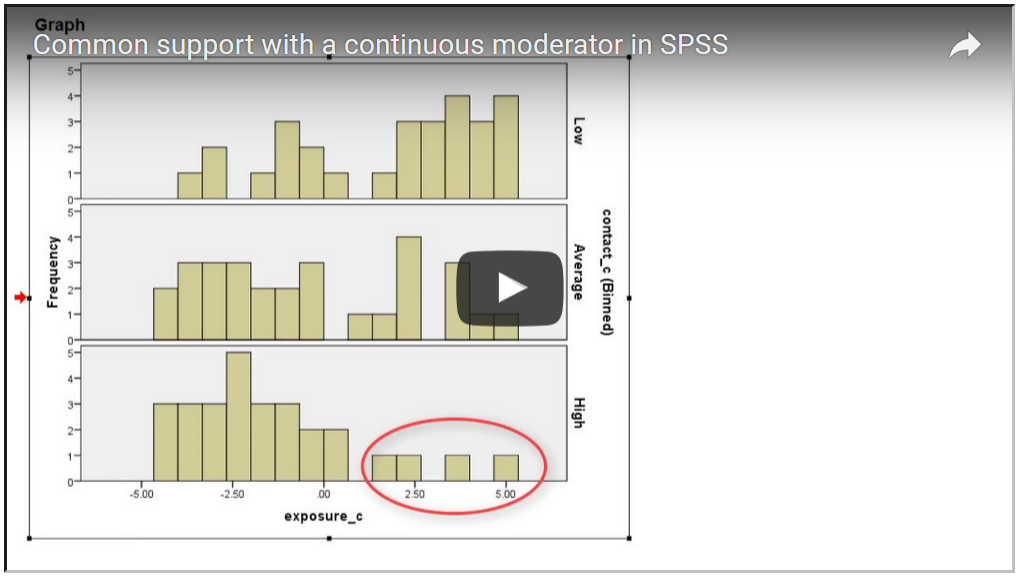

Figure 8.31: Checking common support with a continuous moderator in SPSS.

8.7.2 Exercises

1. With the data in smokers.sav, check if the effect of campaign exposure on attitude towards smoking depends on the contacts that people have with smokers. For now, do not mean-center the variables. Control for the respondent's smoking status (*status2*). Interpret the regression coefficients and check the assumptions of the regression model.
2. Visualize the moderating effect of contact with smokers on the exposure effect in a scatterplot with three regression lines. Explain the information conveyed by the plot to your reader
3. Mean-center the predictor and moderator and repeat the regression analysis of Exercise 1. Explain the differences in the results.
4. Check common support of the predictor for the moderator. Divide the moderator into three groups.
5. Let us hypothesize that children's media literacy depends on sex, age, and parental supervision. Is the effect of parental supervision moderated by the child's age? Use children.sav to answer this research question and apply mean-centering. Report the results as required in this course (APA6), include a moderation plot, and discuss coverage.
6. Is the effect of parental supervision moderated by sex? Use the data of Exercise 5 to answer this question. You may omit the age predictor from the model. Again, illustrate your answer with a moderation plot.

8.8 Take-Home Points

- In a regression model, moderation means that there are different slopes (of the predictor) for different groups or contexts (moderator).
- Interaction variables represent moderation in a regression model.
- An interaction variable is the product of the predictor and moderator. If the moderator is categorical, it is represented by one or more dummy variables. There is an interaction variable for each of the moderator's dummy variables.
- Statistical inference for an interaction variable is exactly the same as for "ordinary" regression predictors.
- The effect of the predictor in a model with an interaction variable does *not* represent a main or average effect. It is a conditional effect: The effect for cases that score zero on the moderator. The same applies to the effect of the moderator, which is the conditional effect for cases scoring zero on the predictor.
- To interpret moderation, describe the effects (slopes, unstandardized regression coefficients) and preferably visualize the regression lines for different groups or contexts. For a numerical variable, select some interesting levels of the moderator, such as the mean and one standard deviation below or above the mean.
- Interpret regression lines for groups or moderator levels only if the predictor scores are nicely distributed for this group or level (common support).
- Don't use the standardized regression coefficients (Beta) for interaction variables in SPSS.

Chapter 9

Mediation with Regression Analysis

Key concepts: partial effect, statistical controlling for effects of other predictors, indirect correlation, confounders, suppression and suppressor, spuriousness and reinforcer, causality, causal and time order, common cause, antecedent variable, direct, indirect, and total effects, causal model, path diagram and path model, parallel and serial mediation, partial mediation, covariate, controlling mediator values.

Summary

If we analyze the effects of two or more predictors on an outcome variable in a regression model, the effect of a predictor is adjusted for the effects of other predictors. Each predictor only predicts the part of the outcome scores that cannot be predicted by the other predictors.

Because of adjustment for other predictors, adding new predictors to a regression model may change the effects of all predictors. The effects can become stronger (the new variable was a suppressor), weaker, or change direction (the effect was partly spurious). For this reason, we cannot be sure that the regression estimates represent the true effects of the predictors.

Indirect correlations play a central role here. The (spurious) correlation of a predictor with the outcome due to the fact that the predictor is correlated with another predictor that is correlated with the outcome. The size of the indirect correlation is simply the product of the correlation between the two predictors and the standardized regression effect of the other predictor on the outcome variable.

If we add a causal order among the predictors of our regression model, we obtain a causal model or path model. Instead of a correlation between two predictors, that is, an undirected association, we now have a directed association, usually called an indirect effect: The first predictor affects the scores on the second predictor, which affects the outcome scores. In this path model, the second predictor mediates the effect of the first predictor on the outcome variable. The second predictor is a mediator.

We can estimate a path model as a series of regression models. With additional software, we can also estimate the confidence interval and p value of an indirect effect. The causal order underlying the path model, however, is an assumption that we make. A regression model shows the predictive effects, which need not be causal. We cannot prove that the predictive effects are causal. We can only think of arguments that make a causal effect plausible.

Test your intuition and understanding

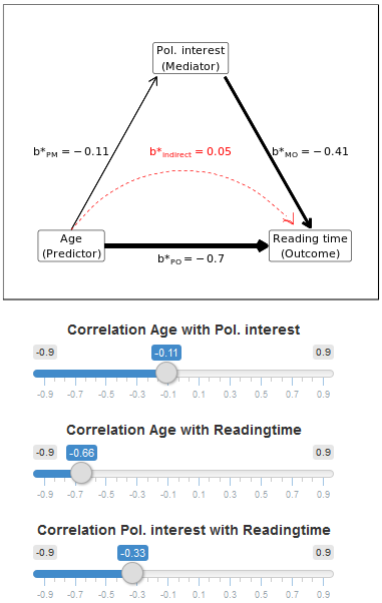

Figure 9.1: How does mediation work and how can we analyze mediation with regression models? The values to the arrows in the diagram are standardized regression coefficients.

1. In Figure 9.1, what does the curved arrow represent? How is its value calculated?
2. How do the numbers tell you that the regression effect of political interest on newspaper reading time is controlled for age?
3. If age is excluded from the model as presented in Figure 9.1, would it suppress or reinforce the effect of political interest on newspaper reading time? When would age suppress, reinforce, or not confound the effect of political interest on newspaper reading time? Use the sliders to check your answer.
4. When is the correlation between political interest and reading time completely spurious in this model? Use the sliders to check your answer.
5. Can the standardized effect of political interest on reading time be larger than 1.0 or smaller than -1.0? If so, in which situation? If not, why not? Use the sliders to check your answer.
6. How many path models do we need to estimate the model of Figure 9.1?

9.1 Controlling for Effects of Other Predictors

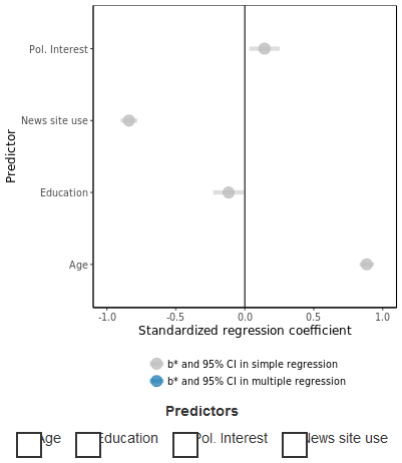

Figure 9.2: How do regression coefficients change if new predictors for reading time are added to the model? The grey dots and lines represent the simple regression coefficients and their 95 per cent confidence intervals in a model predicting newspaper reading time. Blue dots and lines represent results in a regression model including all selected predictors.

1. Select Age and Education in Figure 9.2. Compare the regression coefficients and their confidence intervals for the multiple regression model including the selected predictors (blue dots and lines) to the results for the simple regression models including only one predictor (gray dots and lines).
2. Try other combinations of Age and a second predictor. When does the regression coefficient of Age change markedly? Can you explain why it changes as it does?
3. Interpret the meaning of the simple regression models and explain why they do not change if predictors are added. In which situation are the light and dark results equal?

In a regression model, we use the variation in scores on predictor variables to predict the variation of scores in the outcome variable: Does a person with a higher score on a predictor also have a higher score or, on the contrary, a lower score on the outcome variable? A simple regression model contains only one predictor but a multiple regression model includes more than one.

For example, European citizens who are older spend more time on reading newspapers and so do citizens who are more interested in politics. We have two predictors (age and interest in politics) to predict the outcome variable (newspaper reading time). The two predictors can be correlated: Older citizens tend to be more interested in politics. How does the regression model decide which predictor is responsible for which part of the variation in outcome scores?

9.1.1 Partial effect

Conceptually, the regression model first removes the variation in the outcome that is predicted by all other predictors. Then it determines how well the variable predicts the variation that is left

(residual variation). This is the variation in outcome scores than can be predicted by this particular variable but not by any of the other predictors in the model.

In this sense, a regression coefficient in a multiple regression model expresses the unique contribution of a variable to the prediction of the outcome. It is the contribution to the prediction of the outcome variable over and above the predictions that we can make with all other predictors in the model. This is called a *partial effect*.

This is what we mean if we say that we are *controlling for all other predictors* in our interpretation of a regression model. We are not controlling as in an experiment where we ensure that participants get a particular value on a predictor (treatment) variable. It is controlling in a statistical sense, using the data that we have collected.

9.1.2 Confounding variables

It is important to note that the effect is only unique in comparison to the other predictors that are included in the model. It may well be that we did not include variables in the model that are actually responsible for part of the unique (partial) effects estimated for the predictors in the model. Such left-out variables are called *confounding variables* or, for short, *confounders*.

If we include a confounder as a new predictor in the model, the partial effects of old predictors change. In Figure 9.2, for instance, this happens if you add news site use to a model containing age as a predictor for newspaper reading time. The effects of old predictors are adjusted to a new situation, namely a situation with an added new predictor. The new predictor helps to predict variation in the outcome variable, so the variation left to be explained by old predictors changes. In Section 9.3), we will learn that regression coefficients can go up and down if confounders are included in the model.

With non-experimental data, we must include all confounders to ensure that the estimated regression coefficients represent the effects of the predictors and not effects of confounders. In practical applications, we can only include a limited number of variables in our research and we do not always know what are the confounders. We should strive to include the most important confounders in our research project but we should always keep in mind that the predictive effects that we find may be due to variables not included in our regression model.

9.2 Indirect Correlation

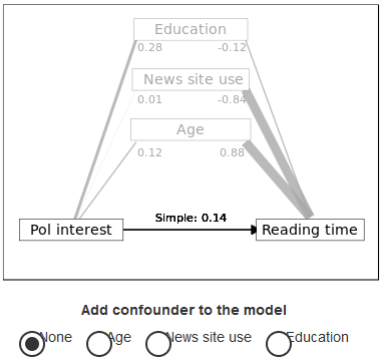

Figure 9.3: What happens to the regression coefficient if we add a confounder to the model? Numbers represent correlations (lines) or regression coefficients (arrow).

1. Which variable confounds the effect of political interest on newspaper reading time most? And why is that so? After formulating your answer, add confounders to the model in Figure 9.3 to check if you are right.

When is a variable a confounder and when is it a stronger confounder, changing the effect of another predictor a lot? The answer to the first part of this question is easy: A *confounder* is a variable that is correlated with both the predictor and outcome but it is not (yet) included itself in the regression model. Because of the correlations, a confounder establishes an *indirect correlation* between the predictor and outcome variable.

The size of the indirect correlation is equal to the product of the correlation between confounder and predictor and the correlation between confounder and outcome variable. In Figure 9.3, the correlation between age and interest in politics is .12 and the correlation between age and newspaper reading time is .88, the indirect correlation between interest in politics and reading time established by age is .12 * .88 = .11.

9.2.1 Multiplication of correlations

Multiplication makes intuitively sense. If two predictors are perfectly correlated ($r = 1$), the first predictor can exactly predict the second predictor. As a consequence it can predict the outcome via the second predictor (indirect correlation) just as well as the second predictor can predict it itself. For example, if age is perfectly correlated with interest in politics ($r = 1$) and the correlation between age and newspaper reading time is .88, the latter correlation is exactly the same as the indirect correlation that we get through multiplication (1.00 * .88 = .88).

If the correlation between the two predictors is below one (disregarding the sign of the correlation), the first predictor can only predict a proportion of the second predictor. As a consequence, the first predictor can also predict only a proportion of the outcome via the second predictor. This is a proportion of what the second predictor can predict by itself. A correlation below one (and above minus one) is a proportion, so multiplying the second predictor's correlation by the correlation between the two predictors does the job.

9.2.2 Indirect correlation and size of confounding

As long as the confounder is not included in the regression model, the model believes that the predictions due to the indirect correlation are due to the predictor that is correlated with the confounder. It includes the predictions erroneously in the partial effect of the predictor, that is, in the predictor's regression coefficient. In this situation, the regression coefficient expresses both the effect of the predictor itself and the effect of the confounder.

Once we add the confounder as a new predictor to the regression model, the predictions due to the indirect correlation are removed from the effect of the old predictor. The predictions are now correctly assigned to the effect of the new predictor. As a result, the value of the old predictor's regression coefficient changes if we add the confounder as a new predictor.

The size of the change usually is closely related to the size of the indirect correlation, so the larger the indirect correlation, the more the old predictor's regression coefficient changes if the confounder is included as a new predictor. This answers the second part of the question with which we started Section 9.2: When is a variable a stronger confounder?

If you love the details: The size of the change is not exactly the same as the size of the indirect correlation. It is equal to the correlation between the confounder and the predictor times the partial effect of the confounder on the outcome variable. This quantity is subtracted from the partial effect of the predictor if we add a new predictor to the regression model. Formally, a confounder does not need to be correlated to the outcome but it must have a partial effect.

9.2.3 Confounders are not included in the regression model

Finally, it is important to note again that a confounder is a variable that is not included in our regression model. As long as it is not included, the indirect correlation between predictor and outcome via the confounder is not controlled for when the effect of the predictor is estimated. The estimated effect is not correct, it is confounded (confused) with the effect of the confounding variable.

Once the confounder is added to the regression model, however, the estimated effects are controlling for the variable formerly known as a confounder. The effects no longer partly represent the effect of the former confounder. In other words, they are no longer confounded by the effect of that variable. The former confounding variable now is a predictor or, if we are not interested in its effects, a control variable in the regression model.

9.3 Two Types of Confounders

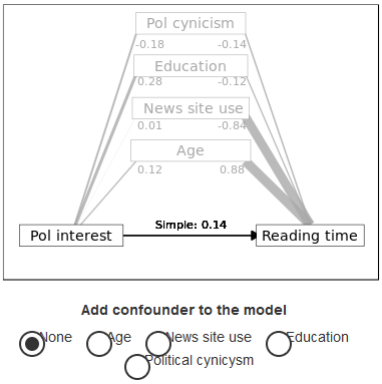

Figure 9.4: When is a regression effect too large and when is it too small due to a confounder?

1. When is a partial regression effect weaker than the simple regression effect and when is it stronger? Formulate a general rule and check it in Figure 9.4.

2. According to your general rule, what happens to the partial regression effect if we would add interest in sports as a predictor, which is negatively correlated with interest in politics but positively correlated with newspaper reading time?

In the preceding section, we learned that a partial effect expressed by a regression coefficient may change if a new predictor is added to the regression model. The partial effect of a predictor changes if the added variable is a confounder: It is correlated both with the predictor and outcome variable. In other words, there is an indirect correlation between the predictor and outcome via the confounding variable.

The partial effect of a predictor can become stronger, weaker, or even change direction if we add a confounder to the regression model. The current section describes the two types of confounders that are responsible for these changes: suppressors and reinforcers.

9.3.1 Suppression

A predictor's partial effect becomes stronger if we include a confounding variable that is responsible for an indirect correlation that points in the opposite direction of the effect of the predictor. Here, the indirect correlation contradicts the true effect of the predictor and as a result, the effect of the predictor is underestimated.

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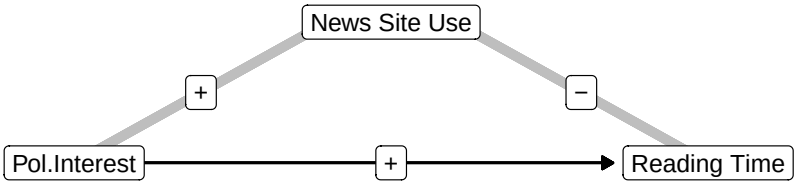

Figure 9.5: News site use as a confounder of the effect of interest in politics on newspaper reading time.

Let us assume that political interest has a positive effect on reading newspapers. People who are more interested in politics tend to spend more time on reading newspapers than people who are less interested in politics. The use of news media confounds this effect if it is correlated with both political interest and newspaper reading time. What happens if people interested in politics use news sites more often (positive correlation) but using news sites decreases newspaper reading time (negative correlation)?

In this situation, the indirect correlation between political interest and newspaper reading time via news site use is negative: Positive times negative yields a negative. On the one hand, the regression effect tells us that politically interested people read more newspapers but, on the other hand, they use news sites more frequently and for that reason they read less newspapers. The regression effect and indirect correlation clearly contradict each other.

If the confounder—news site use—is not included in the regression model, the standardized regression effect of political interest more or less adds the indirect correlation to the true effect of political interest. Adding a negative amount (indirect correlation), however, is equal to subtracting this amount from the standardized regression coefficient. The true positive effect of political interest on reading time is underestimated.

In this example, the effect of political interest is *suppressed* (*masked*) by the confounder news site use. News site use is a *suppressor variable*. If we include this suppressor variable in our regression model, we eliminate its suppression effect.

A positive regression effect and a negative indirect correlation is just one of two possibilities in which the directions are opposite. The other possibility is that we have a negative regression effect and a positive indirect correlation.

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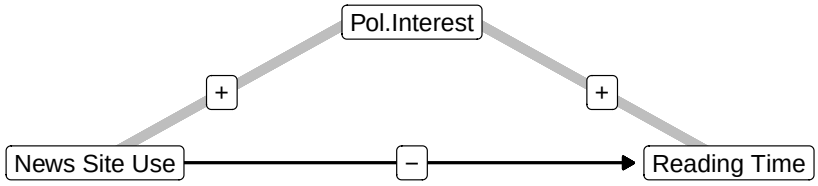

Figure 9.6: Interest in politics as a confounder of the effect of news site use on newspaper reading time.

Just reverse the example and make news site use the predictor and political interest the confounder. The regression effect of news site use on newspaper reading time is negative if people tend to use news sites instead of newspapers as sources of information. The indirect correlation via political interest, however, is positive if politically interested people use news sites more and spend more time on reading newspapers. In this scenario, the negative effect of news site use on newspaper reading is estimated too low if we do not control for political interest.

Suppression can have surprising effects. If the predictor's original effect was close to zero, adding a suppressor variable to the model will strengthen the effect. An effect that we initially believed to be absent may turn out to be substantial and statistically significant. If our regression model tells us that our predictor does not have an effect, we cannot rule out that it does have an effect that is masked by a suppressor variable.

Finally, indirect correlations via other predictors can add so much to the original partial effect of a predictor that the standardized regression coefficient becomes larger than 1 or smaller than -1. This clearly illustrates that standardized regression coefficients are not correlations in multiple regression models. Correlations can never be higher than 1 or lower than -1. Note, however, that the standardized regression coefficient in a simple regression model is equal to the correlation between predictor and outcome. Isn't that confusing?

9.3.2 Reinforcement and spuriousness

Adding a new predictor to a regression model may weaken the effects of other predictors. This happens if the indirect correlation due to a confounder has the same direction (sign) as the regression effect of the predictor.

Here, regression effects are initially overestimated because the predictors cover part of the effect of an important variable that had not yet been added to the regression model. The part of the effect that is due to the confounding variable is called *spurious*. The confounding variable is called a *reinforcer* because it makes an effect appear stronger than it really is.

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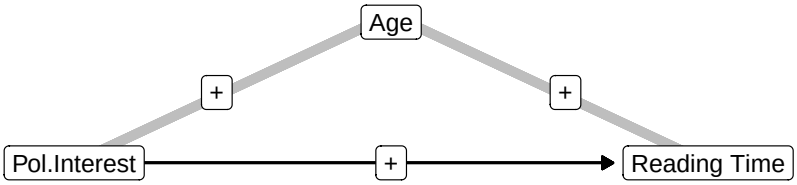

Figure 9.7: Age as a confounder of the effect of interest in politics on newspaper reading time.

As an example, the effect of political interest on newspaper reading time may include the effect of age on newspaper reading. If older people are more interested in politics and do more newspaper reading, age creates a positive indirect correlation between political interest and newspaper reading.

If age is not included as a predictor in the regression model, the indirect correlation is mistakenly attributed to the effect of interest in politics. The estimated effect is too strong. Once we include age as a predictor, the effect of political interest is cleansed of the age effect, so the effect size decreases.

In Figure 9.7, age is positively correlated with both political interest and newspaper reading. But a confounder that is negatively correlated to predictor and outcome has the same impact. Political cynicism, for instance, can be negatively correlated with both interest in politics and newspaper reading. Similar scenarios are available if the regression effect is negative.

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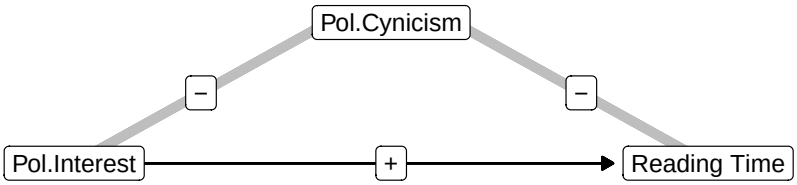

Figure 9.8: Political cynicism as a confounder of the effect of interest in politics on newspaper reading time.

As with suppression, spuriousness can have surprising results. It may happen that the entire estimated effect of a predictor is spurious. Adding a suppressor variable to the regression model may make the entire effect of a predictor disappear. In other words, an effect that we initially thought was substantial may turn out to be too weak to be of interest.

Actually, the indirect correlation between a predictor and outcome via a confounding variable can be so strong that a positive effect in a model without the confounder changes into a negative effect in a model that includes the variable. The opposite may happen as well: A formerly negative effect may become positive if a strong positive reinforcer variable is added to the model.

The bottom line is simple: We can only trust the results if all important confounders are included in the model.

9.4 Comparing Regression Models in SPSS

9.4.1 Instructions

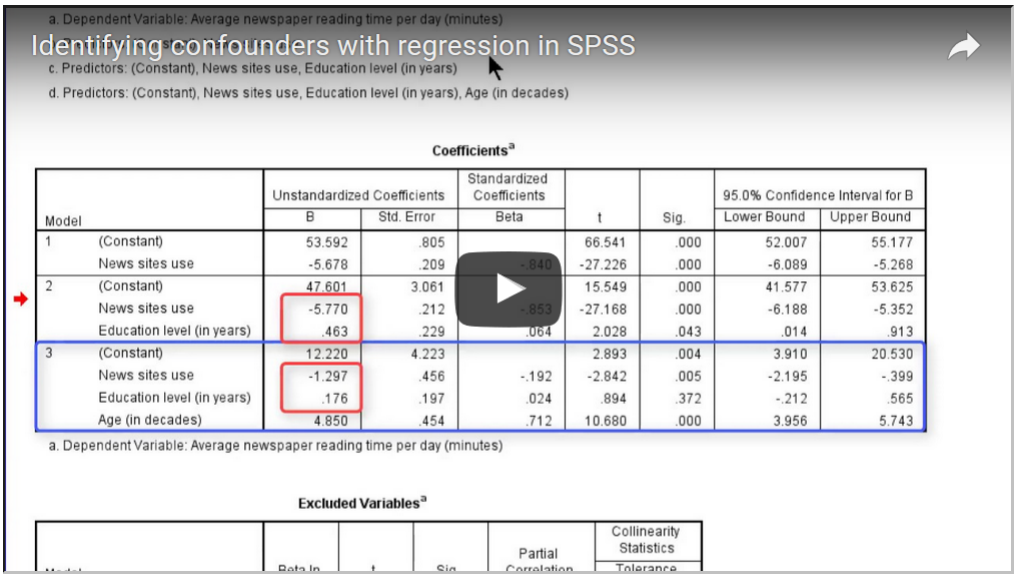

Figure 9.9: Identifying confounders with regression in SPSS.

9.4.2 Exercises

1. The file readers.sav contains the data on newspaper reading time that we have used as example in this chapter. Predict average newspaper reading time by education, interest in politics, news site use, and age. Add the predictors one by one to the regression model in the order specified in the preceding sentence. How do the partial effects change when new predictors are added?
2. In the series of models that you estimated in Exercise 1, for which predictors is age a suppressor or reinforcer? For advanced understanding: Use the correlations between the variables to justify your answers.
3. Predict average newspaper reading time from education, political cynicism, news site use, and age. Add the predictors one by one to the regression model in the order specified in the

preceding sentence. Does suppression occur here? If so, for which predictor and confounder and in which model(s)?

9.5 Mediation as Causal Process

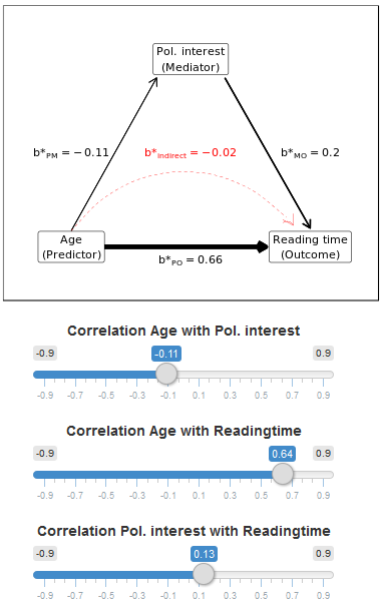

Figure 9.10: How does a common cause affect regression coefficients? The values in this path diagram represent standardized regression coefficients.

1. In Figure 9.10, what does the long, curved arrow represent? Can you motivate your answer with the values that are linked to the arrows?
2. In a mediation model such as Figure 9.10, which standardized effects are always equal to the correlation between the corresponding variables? Explain why this is so.
3. Adjust the correlations in such a way that the effect of age on reading time is fully mediated by political interest. How can we see that the effect is fully mediated?

9.5.1 Criteria for a causal relation

Researchers are usually interested in causal effects, so let us theorize a causal order between age and reading newspapers. From previous research and personal experience, we strongly suspect that older people spend more time on reading newspapers than young people. In statistical language, we expect a positive correlation between age and newspaper reading time. Can age be a cause of current newspaper reading?

Correlation is the first criterion. A causal relation implies correlation or another type of statistical association. If newspaper reading is not correlated with age, it is hard to imagine that age affects newspaper reading. But correlation does not imply causation, as the saying goes. Correlated variables need not be causally related. We need additional arguments to add plausibility to a causal relation.

The second criterion is the time order between cause and consequence A consequence must appear after the cause. In our example, a person's age must be fixed before she displays the behaviour that we want to explain, namely reading newspapers. The time order is very plausible here because age stands for the moment a person was born, which must be prior in time to reading newspapers. If there is a causal relation between age and reading newspapers, age must be the cause and newspaper reading the consequence.

A third criterion for causality is that the correlation is not spurious. In Section 9.3.2, we have encountered a spurious effect as an effect that incorrectly includes the effect of a confounder.

In the context of causality, spuriousness is linked to a confounder that is a *common cause* to both the assumed cause (predictor) and consequence (outcome). Age, for instance, can be a common cause both to having (grand)children and reading newspapers. Older people tend to have more (grand)children and they read more newspapers. If we do not control for age when we regress newspaper reading time on the number of (grand)children a person has, we may find a positive effect.

This effect is probably not causal: We do not spend more time reading newspapers because we have more (grand)children. Unless we use newspaper reading to ignore our children and grandchildren when they are around. Most if not all of the effect of (grand)children on newspaper reading is spurious because it results from a common cause, namely age or the habits and opportunities represented by age.

To interpret the effect that we find as causal, then, we must ensure that there are no confounding variables that are common causes to both our predictors and outcome. Including them as controls in the regression model is a way to solve the problem. Unfortunately, we can never be sure that we have included all common causes in our model.

9.5.2 Mediation as indirect effect

A common cause need not remove the entire effect between a predictor and outcome. Even if part of newspaper reading is caused by age, another part can be caused by a variable related to age, for example, interest in politics. During their lifetime, people may gain more experience with politics and, for that reason, become more interested in reading about politics. This may cause them to invest more time in reading newspapers for collecting information.

Not all people become more interested in politics as they age and their interest need not grow regularly during all of their lifetime. The relation between age and interest in politics, therefore, will not be perfect. This allows us to technically distinguish between the effect of age and the effect of interest in politics.

If we include both age and interest in politics as predictors in a regression model for newspaper reading time, the partial effect of interest in politics is corrected for the spurious correlation between interest in politics and newspaper reading caused by age as their common cause. The partial effect of political interest can be interpreted as causal if current interest in politics was attained before the

newspaper readings that we measure (very plausible) and age is the only common cause of interest in politics and newspaper reading (highly questionable).

[htbp]

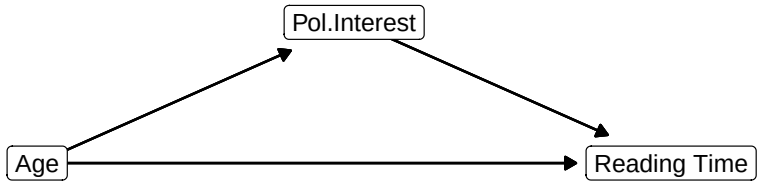

Figure 9.11: Causal diagram for the effects of age and interest in politics on newspaper reading time.

Now let us draw the *causal diagram* for this simple example (Figure 9.11). A causal diagram contains the names of the variables with arrows pointing from causes to consequences. The causal order of variables is represented from left to right. In Figure 9.11, the very first cause (age) is at the left, the final consequence (newspaper reading time) is at the right, and interest in politics is placed in the middle. In this layout, the arrows always point to the right.

In the causal order that we theorize, age is causally prior or *antecedent* to interest in politics, which is antecedent to current newspaper reading time. We have an *indirect effect* of age on newspaper reading by way of interest in politics. When adults grow older, they tend to be more interested in politics and because of this, they tend to spend more time on reading newspapers. We say that interest in politics *mediates* the effect of age on newspaper reading time. Interest in politics is a *mediator*, an *intermediary variable*, or an *intervening variable* in this causal diagram.

A causal diagram like Figure 9.11 is also called a *path diagram*. Each indirect effect is a sequence of direct effects. Each direct effect is a "step" from one variable to another variable, represented by an arrow. An indirect effect, then, can be regarded as a *path* that we can follow to "travel" from one variable to another variable.

[htbp]

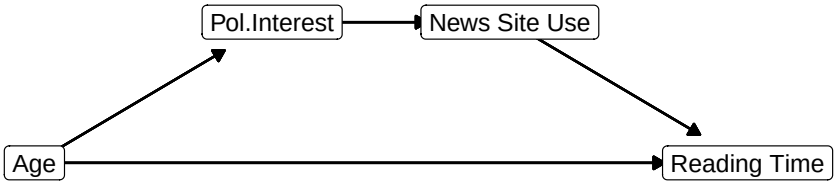

Figure 9.12: Causal diagram for the effect of age on newspaper reading time mediated by interest in politics and news site use.

An indirect effect may contain more than one step or mediator. If we include news site use in the model (Figure 9.12), we would have an indirect effect from age to interest in politics to news site use and finally to newspaper reading time.

9.5.3 Causal process

In our example (Figure 9.12), age has a direct effect on newspaper reading time. What does the direct effect mean? If we start thinking about why older people spend more time on reading newspapers, we soon realize that this is probably not some biological process. It is hard to believe that an ageing human body directly requires more newspaper reading time. The effect is more likely to be social.

In the middle of the 20th century, newspapers were among the most important sources of information. A person who was born and grew up in that period is accustomed to using newspapers as main information source. For later generations, however, news sites on the internet have become important sources of information. Newspapers being less important to them, they are less oriented and accustomed to reading newspapers.

This line of reasoning shows us two things. First, we discover that our common cause may actually represent different things. Age, for instance, refers to life experience in its effect on interest in politics. In contrast, it relates to the period of coming of age in its direct effect on newspaper reading time.

Our second discovery is that we usually look for mediators if we want to understand a direct effect. Date of birth affects exposure to people using newspapers as information sources, which affects the habit of reading newspapers, which finally affects the time spend on reading newspapers later on. Exposure and habit are mediators here. A direct effect of age on newspaper reading merely replaces a causal process that may contain many intermediary steps. Adding mediators to our model is a way of getting more insight in the causal process.

9.6 Path Model with Regression Analysis

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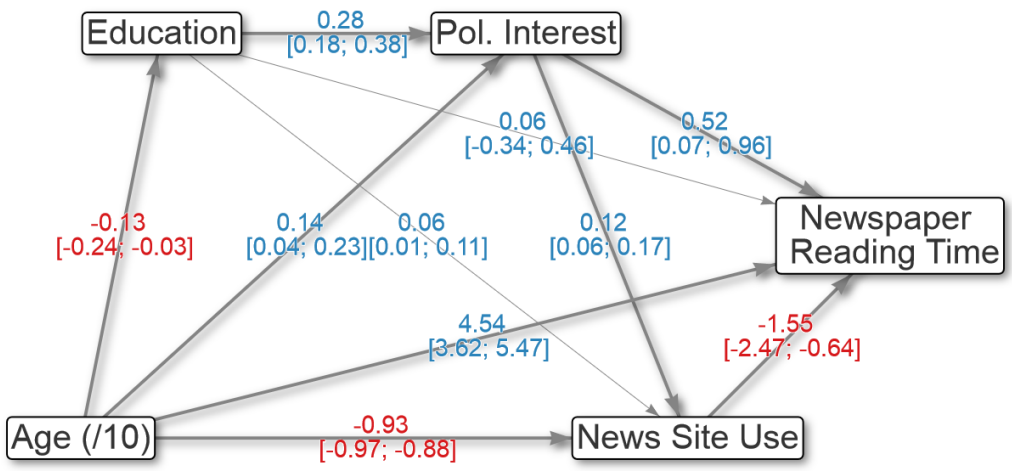

Figure 9.13: Path diagram with unstandardized effect sizes and their 95% confidence intervals.

1. In the causal diagram depicted in Figure 9.13, click on a variable name to highlight the effects in a regression analysis with this variable as the outcome. How many regression analyses can you execute and what do the results mean?
2. The fat arrows were hypothesized whereas the thin ones were not. Why are the thin ones included in the regression analyses (they have coefficient estimates too)?
3. Which effect sizes with their confidence intervals cannot be obtained with regression analyses?

Mediation or, more generally, path models can be estimated with a series of regression models. Every variable in the path diagram with at least one predictor (or incoming arrow) is an outcome variable, so for each of them, we estimate a regression model. The regression model contains all variables as predictors that may cause changes in the outcome variable. In other words, all variables that are causally antecedent to the outcome are used as predictors. In a well-designed causal diagram, all variables to the left of the outcome are antecedent to it.

In the path diagram displayed in Figure 9.13, we would regress newspaper reading time, the final outcome variable, on all other variables. As a next step, we would predict news site use as outcome using all variables except reading time.

Note that we include education level as predictor of news site use and newspaper reading even if we did not draw a direct arrow. Education level is theorized to be causally prior to news use site, so it can have a direct effect. We hypothesized that it did not have a direct effect on news site us and reading time, so we omitted arrows in our hypothesized model. We must include education as a predictor to check that it does not have these direct effects.

A third regression model would predict political interest from education level and age. The final regression model predicts education level from age .

9.6.1 Requirements

We can estimate mediation and path models with regression analysis if we meet the following requirements:

1. Each variable used as an outcome is numeric. This is a general requirement of a linear regression model. In a path diagram, it means that all mediators and outcome variables must be numeric.

   For detail lovers: Variables with only incoming arrows may be dichotomous but that requires logistic regression, which we do not discuss.

2. Each variable used as predictor must be a numeric or dichotomous (dummy) variable. Again, a general requirement of regression models.

3. There are no causal feedback loops. Causality must work in one direction. It must be impossible to travel from a variable back to it while following the direction of the arrows. Note that it can be difficult to assign a causal order. For example, does political interest cause (low) political cynicism or the other way around? Or are they not causally related?

4. All regression models meet the assumptions for regression analysis. Check if the residuals are normally distributed, centered around zero for all levels of the predicted outcome, and that all outcome levels are predicted equally well (see Section 8.1.5).

9.6.2 Size of indirect effects

The regression results tell us the sizes and statistical significance of all direct partial effects on the outcome variable. Both unstandardized and standardized regression coefficients can be used to interpret effects in the usual way. But how do we obtain the size, confidence interval, and statistical significance of indirect effects?

The size of an indirect effect is calculated in exactly the same way as the size of indirect correlations (Section 9.2): Just multiply the size of direct effects. This can be done with either the standardized regression coefficients, as we do for indirect correlations, or the unstandardized regression coefficients.

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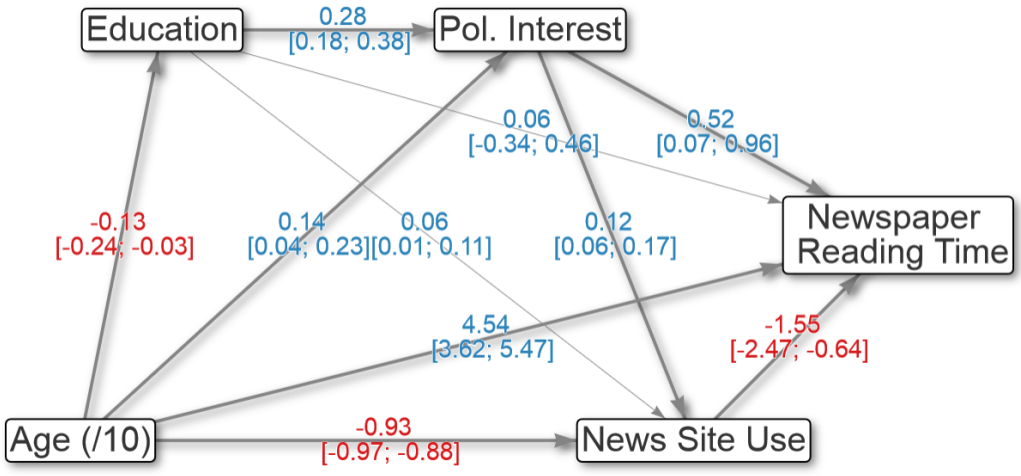

Figure 9.14: Path diagram with unstandardized effect sizes and their 95% confidence intervals.

It may sound weird that we can multiply the unstandardized regression coefficients but it really works. In Figure 9.14, for instance, the unstandardized partial effect of age (measured in tens of years) on interest in politics is 0.14. This means that an additional 10 years of life predict an average increase in interest in politics of 0.14.

In its turn, interest in politics has an unstandardized effect of 0.52 on reading time. An additional unit of interest in politics predicts an average increase in reading time of 0.52 minutes.

Ten additional years of life only predict an increase of 0.14 in political interest, not a full unit increase. As a result, the additional ten years of life predict 0.14 * 0.52 = 0.07 minutes of additional newspaper reading time.

Note that the indirect effect is interpreted in terms of the measurement units of the initial predictor (age in tens of years) and the final outcome (reading time): A difference in years predicts a difference in reading time. As a consequence, we can directly compare unstandardized indirect effect sizes, as we will see in the next section.

9.6.3 Direction of indirect effects

Multiplication of direct effects assigns the right direction (positive or negative) to indirect effects. In the example above, age has a positive effect on interest in politics, which has a positive effect on newspaper reading time. If age goes up, interest in politics goes up and if interest in politics goes up, reading time increases. Thus, higher age is indirectly associated with more reading time through interest in politics: Plus times plus yields a plus.

If people with more interest in politics use news sites more frequently, there is a positive regression effect. If more news site use is associated with less newspaper reading (a negative effect), the indirect effect of interest in politics on reading time via news site use is negative. People with more interest

in politics spend less time on reading newspapers because they use news sites more: Positive times negative yields a negative.

9.6.4 Parallel and serial mediation

If the indirect effects of an antecedent variable on an outcome variable contain at most one mediator, we have *single mediation* or *parallel mediation*. Figure 9.15 illustrates single and parallel mediation.

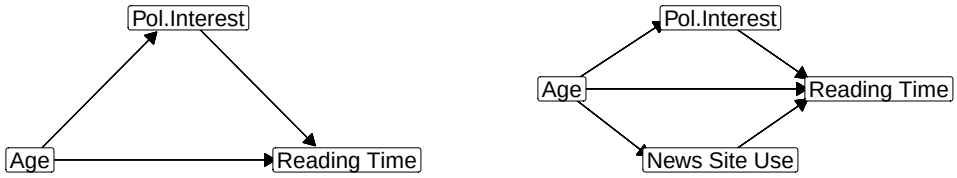

Figure 9.15: Causal diagrams for single (left) and parallel mediation (right).

If any of the indirect effects between an antecedent and outcome variable contains two or more mediators, we are dealing with serial mediation. Figure 9.16 illustrates serial mediation. It contains an indirect effect from age to reading time with two mediators: Age > Political Interest > News Site Use > Reading Time. The distinction between parallel and serial mediation is relevant to the software (PROCESS) that we will use to estimate indirect and total effects (Section 9.9).

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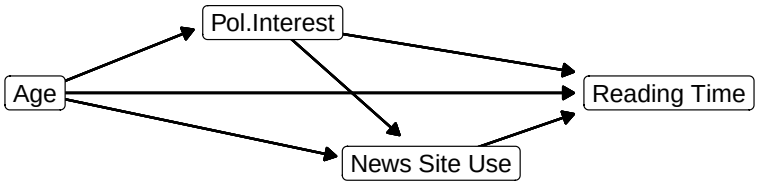

Figure 9.16: Causal diagram for serial mediation.

9.6.5 Partial and full mediation

Table 9.1 lists all direct and indirect effects of age on newspaper reading time in Figure 9.14. We can trace eight different paths from age to newspaper reading time. For each path, we multiply the

Table 9.1: All effects of age on newspaper reading time.

	Effect		Effect		Effect		Effect		Total size
1	Age - Reading Time								
	4.54							=	4.54
2	Age - Education		Education - Reading Time						
	-0.13	*	0.06					=	-0.007
3	Age - Education		Education - Pol. Interest		Pol. Interest - Reading Time				
	-0.13	*	0.28	*	0.52			=	-0.02
4	Age - Education		Education - Pol. Interest		Pol. Interest - News Sites		News Sites - Reading Time		
	-0.13	*	0.28	*	0.12	*	-1.55	=	0.01
5	Age - Education		Education - News Sites		News Sites - Reading Time				
	-0.13	*	0.06	*	-1.55			=	0.01
6	Age - Pol. Interest		Pol. Interest - Reading Time						
	0.14	*	0.52					=	0.07
7	Age - Pol. Interest		Pol. Interest - News SItes		News Sites - Reading Time				
	0.14	*	0.12	*	-1.55			=	-0.02
8	Age - News Sites		News Sites - Reading Time						
	-0.93	*	-1.55					=	1.44
	Total Effect							=	6.03

unstandardized effect sizes.

The unstandardized indirect effects between the same predictor and outcome can be compared directly because they are all expressed in the same measurement units, namely the predicted change in the outcome for a difference of one unit in the predictor (Section 9.6.2). The unstandardized direct effect is expressed in the same measurement units, so it can be compared to the indirect effect. In addition, we can sum the unstandardized direct and indirect effects to obtain the total unstandardized effect.

With this in mind, we see that the relation between age and newspaper reading time is dominated by the positive direct effect ($b = 4.54$) and the positive indirect effect via news site use ($b = 1.44$). The remaining indirect effects are relatively small as indirect effects usually are.

Summing all effects, we obtain a *total effect* of age on newspaper reading time around 6 ($b = 6.03$). A person who is ten years older but in other respects the same as another person, is predicted to spend on average 6 additional minutes on reading newspapers per day.

If the direct effect of a predictor on the outcome is zero in a model with mediators, the predictor's effect is *fully mediated*. This clearly is not the case in our example: There still is a substantial direct effect of age on newspaper reading time. This is what we usually encounter; it is called *partial mediation*.

Sometimes, researchers decide that an effect is fully mediated if the direct effect is no longer statistically significant once a mediator is added to the model. This strategy is contestable because a statistically non-significant direct effect does not mean that the effect is absent (zero) in the population. It can be absent but it is much more likely to be present but just too small to be picked up by our significance test (see Chapter 6).

The distinction between full and partial mediation is a little bit problematic. From a substantive point of view, we may argue that direct effects are probably mediated. As we have seen in Section 9.5.2, a direct effect usually summarizes a causal process that consists of intermediary steps, which is mediation. We may wonder whether it makes theoretical sense to talk about unmediated effects. From a technical point of view, we should realize that a direct effect is not mediated by the mediators that are included in the model. However, it may well be mediated by other variables.

9.6.6 Significance of indirect effects

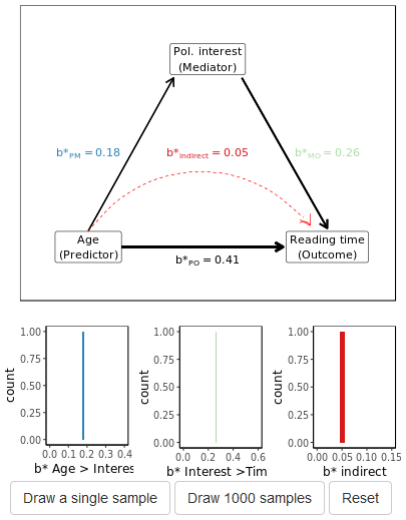

Figure 9.17: Does the sampling dsitribution of an indirect effect resemble the sampling distributions of its direct effects?

1. How is the sampling distribution of indirect effect size created? Before, simultaneously, or after the sampling distributions of direct effect sizes are created? Check your answer using the **Draw a single sample** button in Figure 9.17 repeatedly.
2. Do all three sampling distributions have the same shape?

SPSS does not calculate the size of indirect effects for us or their confidence intervals and p values. It is easy to calculate the sizes of indirect effects, as we have seen in a preceding section: just take the product of direct effects. In contrast, it is not possible to calculate the confidence interval or p value of an indirect effect in a reliable way from the confidence intervals or p values of the direct effects (see Hayes, 2013: Section 4.4 for a detailed discussion of different approaches).

For statistical inference on the indirect effect, we need the sampling distribution of the size of the indirect effect. This sampling distribution is not the same as the product or some other combination of the sampling distributions of the direct effects that make up the indirect effect. The situation is similar to the sampling distribution of the difference of two sample means (independent-samples t test), which is not equal to the difference between the sampling distribution of one mean and the sampling distribution of the other mean (Section 2.5.4).

We use bootstrapping to create the sampling distribution of indirect effect size. We have learned the principles and limitations of bootstrapping in Section 2.1, so we need not go into details here. Suffice it to repeat that our original sample must not be too small and it must be quite representative of the population if we apply bootstrapping.

The confidence interval of an indirect effect can be calculated from its bootstrapped sampling distribution. Table 9.2 shows bootstrap results for the indirect effects in a model with age as predictor, newspaper reading time as outcome, and interest in politics and news site use as mediators.

Table 9.2: Bootstrap results for unstandardized indirect effects in a model with two mediators. Effect size, standard error, lower and upper levels of the 95% confidence interval.

	Effect	Boot SE	BootLLCI	BootULCI
Total indirect effect	1.47	.42	.62	2.25
Age - Pol. Interest - Reading Time	.05	.03	.01	.14
Age - Pol. Interest - News Site Use - Reading Time	-.02	.01	-.05	.00
Age - News Site Use - Reading Time	1.44	.42	.60	2.23

In total, there is a substantive indirect effect of age on newspaper reading time in this model. We are confident that this effect is positive (b = 1.47, 95%CI[0.62, 2.25]). It is easy to see that the indirect effect of age via news site use on reading time is by far the most important indirect effect. On its own, it is responsible for almost the total indirect effect (b = 1.44, 95%CI[0.60, 2.23]).

It may happen that an indirect effect is not statistically significant whereas both direct effects are statistically significant. This sounds like a paradox but it should not upset you. The unstandardized indirect effect tends to be weaker than the direct effects, that is, closer to zero (for instance, see Table 9.1). In this situation, it is more difficult to reject the null hypothesis that the indirect effect is zero in the population. This is all that statistical significance tells us. We need a larger sample to reject null hypotheses for smaller effects (see Chapter 5 on power).

9.7 Controlling for Covariates

We usually have theoretical reasons to expect mediation between one pair of variables, for example, political interest as mediator between age and newspaper reading time. At the same time, we know that our outcome variable and perhaps our mediator may depend on other variables. Newspaper reading time, for instance, may also depend on education. In this situation, we would use the other variables as covariates for which we want to control statistically.

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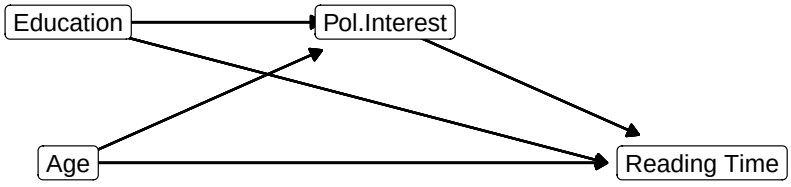

Figure 9.18: Causal diagram for interest in politics as mediator between age and newspaper reading time with education as covariate.

Figure 9.18 represents a model in which education is used as a covariate in a model with political interest mediating the effect of age on newspaper reading time. Education is probably causally

antecedent to both political interest and newspaper reading time, so it is allowed to have an effect on both variables. In this way, we control for education and remove spurious correlation between political interest and newspaper reading time due to education as a common cause.

If education is allowed to predict both political interest and newspaper reading time as in Figure 9.18, political interest mediates the effect of education on newspaper reading time. We are, however, not interested in mediation in the case of a covariate, so we do not estimate or report the indirect effects of education. In other words, a *covariate* is a predictor for which we do not investigate if its effect is mediated.

Note that covariates should only be allowed to have an effect on variables that can be caused by the covariate. We should not include effects of a covariate on a variable that is causally antecedent to the covariate. If a control is a consequence rather than a cause of a mediator, it had better be used as another mediator in the model. If, for instance, political cynicism may affect newspaper reading time but it is a consequence of political interest, it should be included as a second (serial) moderator instead of a covariate.

9.8 Reporting Mediation Results

We analyse a path model as a series of regression models, so the general rules for reporting mediation are the same as for reporting regression analyses (see Section 8.6). If you summarize results in a table, make sure that it includes:

1. The unstandardized regression coefficients for all direct and indirect effects tested in the regression models.

2. The confidence intervals and significance levels of the unstandardized effects.

3. The F test and measure of model fit (R^2) for each regression model.

A path model may yield a lot of direct effects, so it is good practice to present results as a path diagram with the values of the standardized or unstandardized regression coefficients as labels to the arrows. A path model conveniently summarizes the results for the reader (Figure 9.19). Remember that we don't use standardized regression coefficients if the predictor or a covariate is dichotomous or a set of dummy variables (see Section 8.1.3).

Table 9.3: Unstandardized effects in a model regressing newspaper reading time on age with one mediator (News Site Use) and two covariates (Education, Political Interest). OLS estimates for direct effects, bootstrap results for indirect effects, using 5,000 bootstraps and a bias-corrected method.

	B		95% CI
Outcome: News Site Use			
constant	6.62	***	[5.92; 7.31]
age	-0.93	***	[-0.97; -0.88]
education	0.06	*	[0.01; 0.11]
pol.interest	0.12	***	[0.06; 0.17]
R^2	0.86		
F (3, 308)	617.40	***	
Outcome: Newspaper Reading Time			
constant	13.59	***	[5.26; 21.93]
age	4.55	***	[3.62; 5.47]
education	0.06		[-0.34; 0.46]
pol.interest	0.52	*	[0.07; 0.96]
newssite	-1.55	**	[-2.47; -0.64]
R^2	0.79		
F (4, 307)	290.85	***	
Indirect Effect			
age > pol.interest > reading time	1.44		[0.61; 2.17]

[htbp]

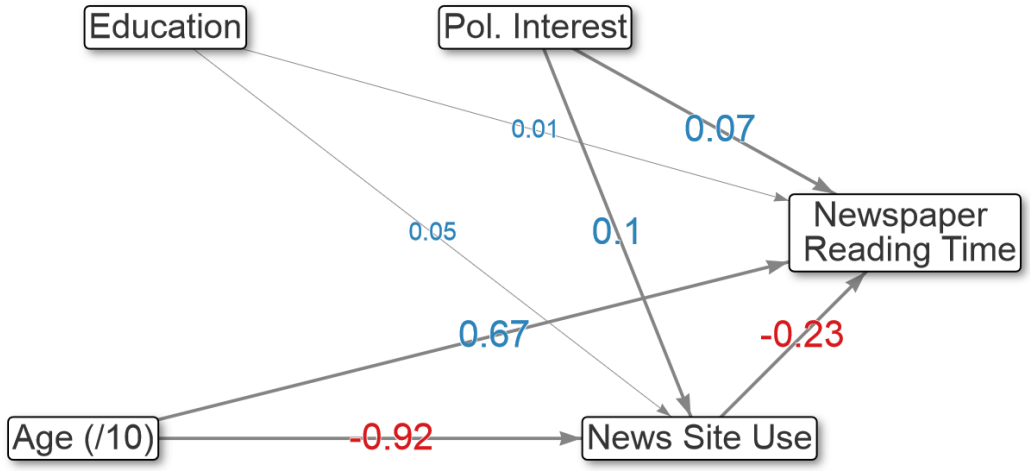

Figure 9.19: Unstandardized direct effects for a path model with one mediator.

If effect mediation is central to your report, focus your presentation and interpretation on the indirect effects. Report the size and confidence interval of each indirect effect estimated with PROCESS. If possible, add both the direct and indirect effect to a diagram such as Figure 9.19.

Interpret the indirect effect just like any regression effect, namely, as the predicted difference in the outcome for a one unit difference in the predictor. It is usually interesting to compare the sizes of the direct and indirect effects. Is the effect predominantly mediated in the model or is only a minor part of the effect mediated in the model?

Inform the reader that you bootstrapped the indirect effect and report the settings in PROCESS that you have used for bootstrapping: the number of bootstrap samples and the method used for the confidence intervals. For a more elaborate discussion of reporting mediation, see (Hayes, 2013: 198-202).

9.9 Mediation with SPSS and PROCESS

9.9.1 Instructions

SPSS cannot apply statistical inference to indirect effects, so we use the PROCESS macro developed for this purpose (Hayes, 2013). If correctly installed (see below), the macro can be used from within the SPSS Regression menu. Please note that you had better not paste the PROCESS commands to the SPSS syntax because it produces a lot of code that is difficult to understand. Instead, run the PROCESS command directly from the menu and manually add a comment to your SPSS syntax file reminding yourself of the model that you estimated with PROCESS.

Download the PROCESS macro and install the SPSS custom dialog file. Check the FAQ at the PROCESS website if installation is not successful. If PROCESS is successfully installed, it can be found in the Analyse > Regression menu.

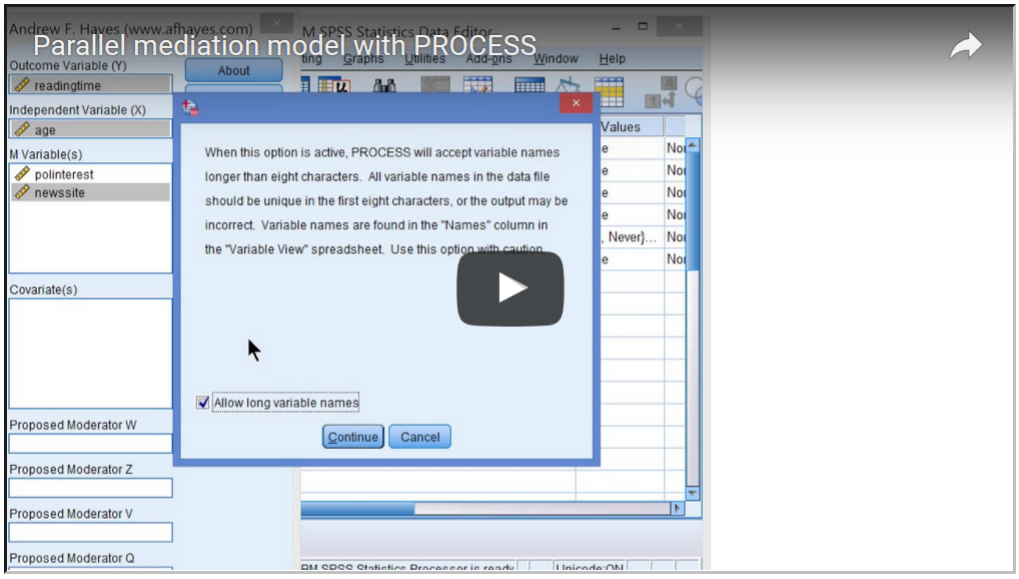

Figure 9.20: Estimating a single or parallel mediation model with PROCESS (Model 4).

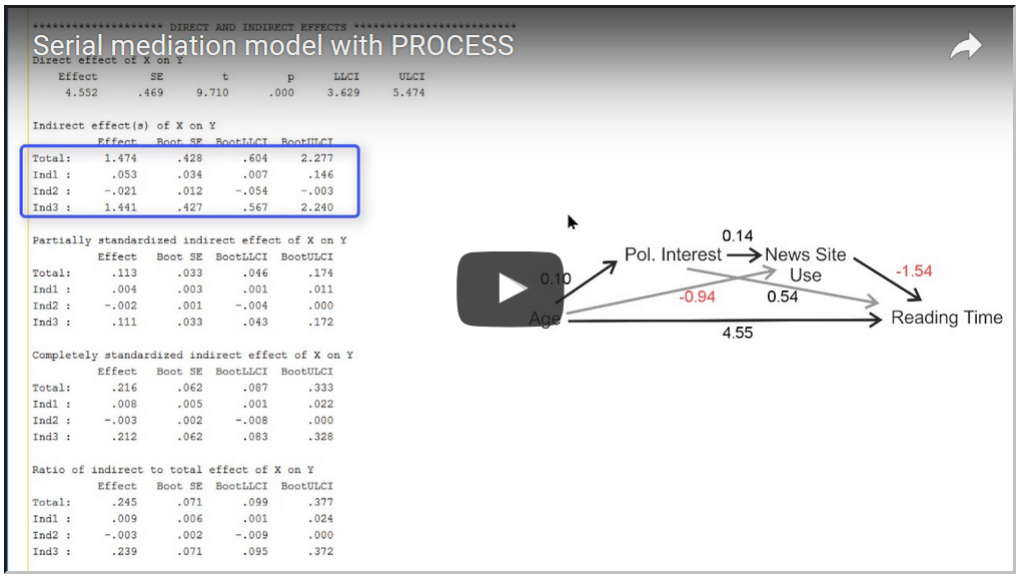

Figure 9.21: Estimating a serial mediation model with PROCESS (Model 6).

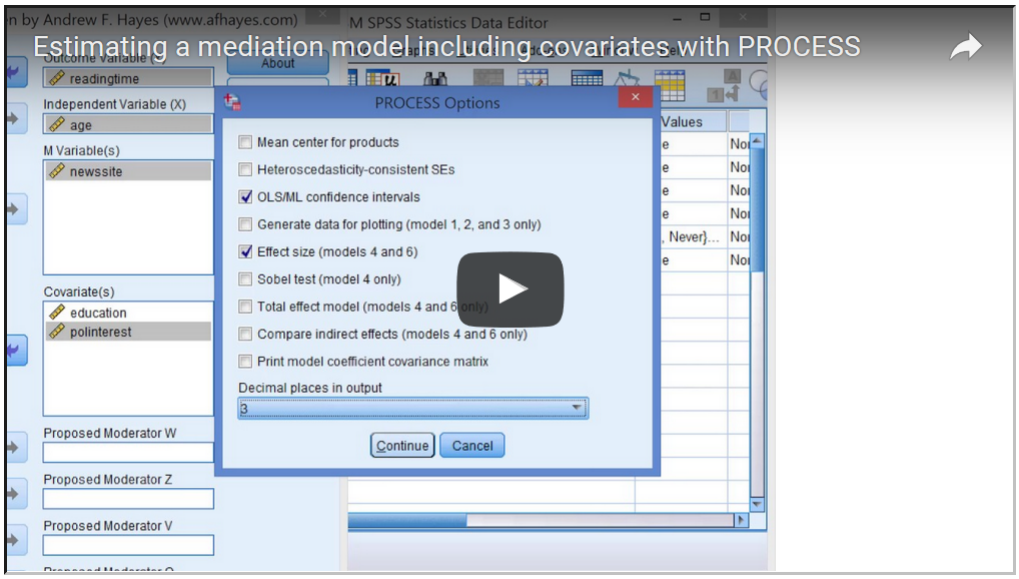

Figure 9.22: Estimating a mediation model including covariates with PROCESS.

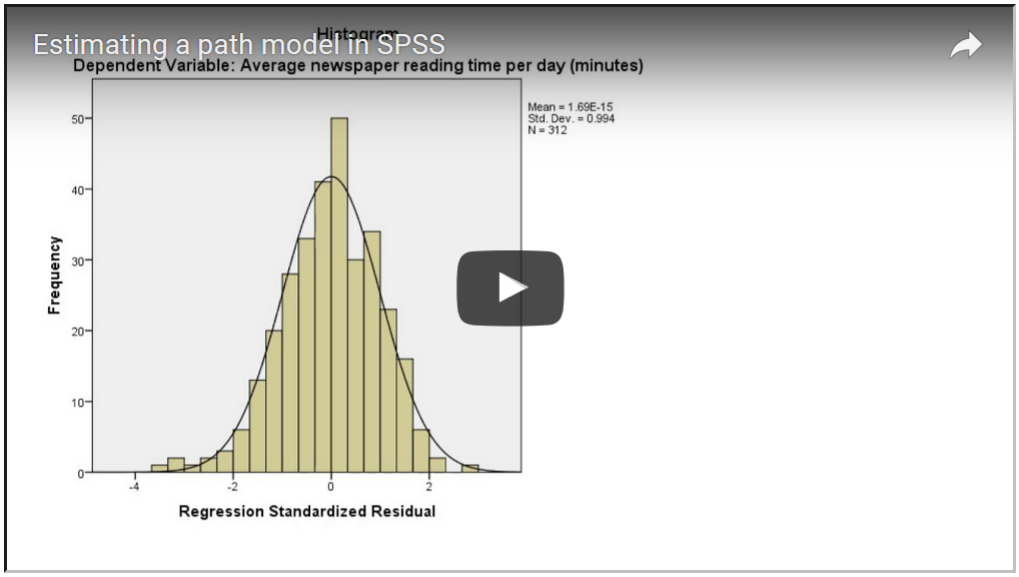

Figure 9.23: Estimating a path model in SPSS.

9.9.2 Exercises

1. Use readers.sav to analyze the causal model depicted in Figure 9.14 with a series of regression models in SPSS. Create a table and draw a path diagram to present the direct effects.
2. To what extent is the effect of age on newspaper reading time mediated by news site use? Use the data of Exercise 1 and PROCESS to estimate both the unstandardized and standardized indirect effect in a model containing only these three variables. Interpret the results.
3. Add interest in politics as a covariate to the model of Exercise 2. Are you going to use it as a covariate for the mediator (news site use), the outcome (newspaper reading time), or both? Motivate your choice. Present the unstandardized effects as a path diagram and add the indirect effect to it. Which direct effects are not present in this model?
4. Add political interest to the model of Exercise 2 such that it mediates the effect of age on news site use: Age > Political Interest > News Site Use > Reading Time. Estimate the model with PROCESS. Report the unstandardized indirect effects as a table and interpret them.
5. The data set children.sav contains information about the media literacy of children and parental supervision of their media use. Is the effect of age on media literacy fully or partially mediated by parental supervision? Use PROCESS and SPSS to estimate the model and check the assumptions. Motivate your answer to the question.

9.10 Criticisms of Mediation

If we think of causality, we usually think of a process in which one thing leads to another thing, which leads to something else, and so on. This is apparent if we want to explain why we think that one phenomenon causes another (see Section 9.5.2). Mediation, however, is difficult to establish with regression analysis and, as some argue, perhaps impossible to establish.

9.10.1 Causal order assumed

It is paramount to note that the regression approach to mediation and path models does not tell us anything about the causal order of the variables. The causal order is purely an assumption that we make. The plausibility of the assumptions depends on how well we can argue the time order of the variables and the absence of common causes for cause-consequence pairs (see 9.5.1).

9.10.2 Time order

To establish the time order of variables, we must think about the time at which the behaviours or opinions that we measure took place. This is what matters, not the time at which we make the measurement. After all, we can collect information on behaviour a long time after the fact, for example by asking respondents when they started using news sites or checking internet use logs.

The more time has passed between the occurrence of the behaviour or opinion that we think is the cause and the occurrence of the one we think is the consequence, the more plausible the causal order. If cause and consequence appear very close in time, it may be difficult to argue that one precedes the other.

9.10.3 Causality or underlying construct?

For causes and consequences that appear nearly simultaneously, we should take into account that the two measurements may measure the same underlying construct. Think of the way we construct a scale from items: We assume that the items measure the same underlying attitude, for instance, interest in politics.

The indicators of a scale are correlated because they have a common cause, namely, the underlying attitude. But it does not make sense to interpret the correlation as a sign of mediation. One item does not trigger another item, and so on. A mediator must be theoretically and conceptually different from both the predictor and outcome. We have to provide arguments that they are really different.

An underlying construct such as an attitude is just one example of a common cause that undermines the conclusion that an effect is mediated. Any common cause of predictor and mediator or of mediator and outcome that is not included in the model renders all or part of the correlations spurious, that is, non-causal. If we doubt the causality of any effect in the path constituting the indirect effect, we must doubt the causality of the indirect effect as well. Without causality, there is no mediation. So we should think hard of common causes and include them in our model.

9.10.4 Statistical control is not experimental control

In a strict interpretation, mediation cannot be established with regression models. To understand this, let us look very carefully at the statistical meaning of direct and indirect effects.

A direct effect of age on newspaper reading time refers to changes in reading time that depend on changes in age but not on changes in the mediator, for instance, interest in politics. Strictly speaking, age should change and interest in politics should not change for a person to detect the direct effect of age on reading time. But interest in politics depends on age if it mediates the effect of age, so it tends to change if age changes. That is a problem.

In an experiment, we would have to manipulate the value of the mediator to ensure that it does not change. If we succeed in doing this, which is difficult to imagine, the effect is really a direct effect. For example, interest in politics is manipulated to be the same for some participants. Then, a change in newspaper reading time due to age change would indeed represent the direct effect for these participants.

Controlling the effect of a predictor on an outcome for the mediator in a regression model, however, is not the same as experimental control as described above. In a regression model, the mediator values vary among persons. The statistical trick is that we only compare people who have the same mediator score when we calculate the direct effect. But even for these people, the effect of the predictor on the mediator may have done it's work: Their actual interest in politics is affected by their age. As a result, the effect of age on newspaper reading time includes an effect of age on interest in politics, so the mediator (interest in politics) is not completely excluded from the direct effect.

9.10.5 Recommendations

All in all, mediation is an intuitively simple and appealing concept. Unfortunately, it is very difficult to substantiate the claim that indirect effects in path models represent mediation. Mediation

assumes causal effects and causality is difficult to establish.

If you plan to investigate mediation:

1. Justify that the mediator is theoretically and conceptually different from the predictor and outcome.
2. Motivate the time order between variables in the model.
3. Include variables that can be common causes to predictor, mediator, or outcome in your research project and in the regression models that you are going to estimate.

An experimental design with randomization helps with Recommendations 2 and 3.

9.11 Combining Mediation and Moderation

Mediation and moderation (Chapter 8) can occur in the same model. For example, the effect of age on newspaper reading time mediated by interest in politics can be different for females and males. In other words, the indirect effect is different for females and males.

If the indirect effect is different for females and males, at least one of the two direct effects (predictor on mediator or mediator on outcome) must be different for females and males. This direct effect is moderated and as a consequence, indirect effects including this effect are moderated. This is called *moderated mediation*. In the example, sex is the moderator and interest in politics is the mediator of the indirect effect of age on newspaper reading time.

Several models with more than one mediator or with moderated mediation can be estimated with PROCESS. For an overview of the models, see http://www.afhayes.com/public/templates.pdf or Appendix A in Hayes (2013). The models, however, are quite complex, so we leave them for enthusiasts.

9.12 Take-Home Points

- In a multiple regression model, a regression coefficient represents the predictive effect of a variable while controlling for the effects of all other predictors. It is called a *partial effect*: the predictions of the outcome that cannot be predicted by the other predictors.
- If a new predictor is added to a regression model, the regression coefficient of an old predictor changes if the new predictor is correlated with both the old predictor and the outcome. If the old predictor's effect becomes stronger, the new predictor was a suppressor. If it becomes weaker or changes direction (sign), the new predictor was a reinforcer and the old effect was (partially) spurious.
- An estimated regression coefficient only shows the true effect of a predictor if all suppressors and reinforcers are included in the model.
- A causal or path model without causal feedback loops can be estimated as a series of regression models: one regression model for each variable that has at last one predictor in the path model.
- Unstandardized regression coefficients, standardized regression coefficients, and correlations can be multiplied to obtain indirect effects or indirect correlations.

- An indirect effect is a mediated effect. Variables that are at the same time predicted and predictors in an indirect effect are *mediators*, *intermediary variables*, or *intervening variables*.
- Statistical inference on an indirect effect—its confidence interval and significance level—requires a sampling distribution of the indirect effect's size. This distribution can be bootstrapped with the PROCESS macro (Hayes, 2013).
- Mediation is an intuitively appealing concept but it is difficult to establish with regression models. A causal interpretation requires a clear time order between predictor, mediator, and outcome, a clear theoretical and conceptual difference between these three variables, and the inclusion of all common causes of predictor, mediator, and outcome in the regression models.

Read the little but very helpful book on the logic of causal order by James A. Davis (1985) for more information on causality and correlational analysis.

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