



A minimal introduction to probability theory, statistical inference & hypothesis testing

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Preface

The purpose of these notes

In the following pages one will find an introductory course to the theory of probability and statistical inference, aiming to cover both foundations and basic mathematical concepts, but also practical tools to deal with real data science problems, such as bayesian probability and hypothesis testing. The text is composed by seven chapters, together with some appendix sections reviewing basic mathematical notions, and a bibliographic note. The purpose of these lecture notes is to make both probability and statistical analysis an easy, engaging and exciting topic for anyone interested, without the need for prior experience.

Both, predictive probability and descriptive statistics have deep historical roots, from ancient works on chance and divination to modern scientific topics oriented towards information theory, modelling and data analysis. As one could guess, rivers of ink have been written about such topics, and endless literature sources are available. However, after following many different courses at both bachelor and postgraduate levels, and teaching such topics myself during the last three years, I have found that most resources belong, almost certainly, to one of the next three classes. Either (i) deeply mathematical, and hence out of reach for most experimental or clinically oriented scientists, (ii) laboratory oriented, focusing on inference and experimental design, and hence missing most of the mathematical background, or (iii) with a direct focus towards programming and computation, relying on domain specific notebooks (Python, R, Matlab, SPSS, etc), and online resources with precompiled libraries for simulation, which again miss most of the mathematical and formal intuitions. Indeed, the misuse of statistics in experimental sciences is a critical topic in modern times, as mathematicians have extensively discussed during the last decades. The well-known article by John P. A. Ioannidis, "*Why most published research findings are false*" [1], serves as a prominent example, and it may serve as motivation for a rigorous study.

As a matter of fact, when it comes to modern statistics, data analysis or experimental design, concepts like *stochasticity*, *randomness*, *sampling*, *hypothesis*, *significance*, *statistic test*, *p-value*—just to mention some of them—are frequently used, but for most bachelor and even master's level degrees they are rarely introduced or properly defined. Indeed, for most experimental and clinically oriented degrees, they are not introduced at all, leaving the student with just a superficial knowledge relying on intuition about some particular cases. Hence, developing high-quality, simple, and accessible open source material for present and future generations, covering both probability and statistical inference from both a fundamental *and* applied level, remains an urgent task for scientists and educators.

This is intended to be a complete introductory course, and no previous mathematical background is required. By keeping the theory simple and always followed by examples, we will build the definitions and quantities from simple to more complex. All mathematical formulas will be introduced with rigorous notation, but keeping in mind that it is not the symbols or the numbers, but the intuitions and the general understanding, what we are after. Additionally, all topics will be introduced alongside with some short historical discussion and context, as we believe that a purely technical knowledge just grasps the complexity—and beauty—of scientific topics. As one

could anticipate already, a proper understanding of ideas such as uncertainty, variation, chance, probability, inference, etc, can be applied to describing a vast amount of real-world phenomena, ranging from gambling and games of chance to data analysis and modelling in physics, biology, machine learning and quantum mechanics, among many others.

As mentioned, the course is organised in seven chapters, covering the topics listed below:

- Chapter 1: The Statistical theory of sampling, data types, estimators of central tendency and variation, and data visualization.
- Chapter 2: Fundamentals of probability theory and random variables. Discrete and continuous events, cumulative probabilities, the idea of expected value.
- Chapter 3: Estimation, confidence intervals and critical regions [...].
- Chapter 4: Introduction to hypothesis testing [...].
- Chapter 5: Modelling, dependence and correlation [...].
- Chapter 6: Introduction to Bayesian probability [...].
- Chapter 7: Introduction to stochasticity and Markov processes [...].

At the end of each chapter there will be a series of exercises and coding examples to illustrate and demonstrate the concepts discussed. To avoid misconceptions, let us emphasize here that both, probability and statistics are just branches of mathematics dealing chance and information in random events, *much earlier* than computers, coding languages, Python, R or P-values were even conceived. The data-oriented, practical ways in which probability and statistics are usually taught, relying heavily on computation, is just a consequence of the fact that automatized measurements are nowadays available and trendy in modern times, with simulation at our reach.

Example textbooks covering introduction to probability and statistical inference, for further reading:

- A simple, intuitive introduction to statistics with few mathematical concepts is provided in Spiegelhalter's "*The Art of Statistics: How to Learn from Data*" [2].
- A more foundational textbook, with more advanced mathematical approach, can be found at DeGroot and Schervish's "*Probability and Statistics*" [3].
- For a philosophical and historical perspective on probability and statistics, please find Forster and Bandyopadhyay's handbook "*Philosophy of Statistics*" [4].
- A comprehensive introduction with focus on practical applications and modern data analysis tools is can be found at Diez, Barr & Mine "*OpenIntro Statistics*" [5].
- For fundamental concepts in probability and statistics, including random variables, distributions and statistical inference, with practical examples and exercises follow Hossein Pishro-Nik's "*Probability, Statistics & Random Processes*" [6].

Introduction

Even fire obeys the laws of numbers.

— J.B. Joseph Fourier

A bit of history

As one might expect, the origins of probability and related concepts can be traced back to very ancient times. Civilizations such as the Babylonians, Egyptians, and Greeks already encountered uncertainty in various aspects of life, including commerce, games of chance, and divination. Consequently, notions of randomness and stochasticity have deep historical roots. For instance, archaeological findings suggest that the earliest known dice date back over 5,000 years, reflecting humanity's early fascination with chance and unpredictability [7]. Although these cultures had not yet developed a formal mathematical theory of probability, they recognized recurring patterns in random events and attempted to anticipate outcomes through either empirical observation or superstition. For a detailed historical overview, see Florence Nightingale's 1962 manuscript "*Games, Gods and Gambling*" [8].

While classical Greek and Roman philosophers frequently discussed the nature of chance, necessity, and determinism, their inquiries remained primarily philosophical rather than mathematical. From Aristotle to Cicero, many have distinguished between events occurring by chance and those determined by fate, foreshadowing later developments in probability theory [9]. These early ideas, though lacking quantitative formalism, provided the intellectual foundation for later scientific inquiry into randomness and causality.

A significant shift occurred during the late medieval and early Renaissance periods, when more rigorous mathematical ideas began to shape. Italian mathematician and gambler Gerolamo Cardano (1501–1576) is normally credited as making the first substantial contributions to the mathematical analysis of chance. His work "*Liber de Ludo Aleae (Book on Games of Chance)*" [10], posthumously published in 1663, is one of the earliest known texts to explore probability through the analysis of gambling problems. However, Cardano's reasoning, while insightful, lacked the symbolic clarity and mathematical rigour of modern probability theory. Readers consulting the original manuscript will notice an ambiguous and sometimes inconsistent symbolic system, quite unlike the formal structures we use nowadays.

The formalization of probability as a mathematical discipline did not occur until the 17th century, most notably through the seminal correspondence between Blaise Pascal and Pierre de Fermat. Their work, motivated by problems such as finding a fair division of stakes in interrupted games of chance, introduced foundational concepts such as combinatorics, expected values, and variance [11]. These developments paved the way for later contributions by Christiaan Huygens, who in 1657 wrote the first published textbook on probability "*De Ratiociniis in Ludo Aleae (On Reasoning in Games of Chance)*" [12], and Jacob Bernoulli, whose 1713 "*Ars Conjectandi (The Art of Conjecturing)*" remains among the most influential early texts in the field. Their works, along with many others, collectively laid the groundwork for the probabilistic and statistical

methods that foreshadow modern scientific reasoning [13, 14].

From the 19th century onwards, probability theory became increasingly intertwined with statistics and inference, giving rise to the mathematical and empirical frameworks that led to modern scientific analysis of uncertainty. Building on the analytical foundations laid by Laplace—who unified probability with inference through inverse probability—and Gauss’s theory of errors, Adolphe Quetelet—Belgian astronomer and mathematician—played a decisive role in extending probabilistic reasoning to social and biological phenomena. His notion of the statistical individual, or *homme moyen*, framed variation not as noise to be eliminated, but as a fundamental object of study, helping to establish statistics as a distinct discipline concerned with populations rather than isolated events [15, 16, 17].

Within this emerging landscape, Florence Nightingale stands as a central figure in the practical and institutional adoption of statistical reasoning. Through her innovative use of graphical representations and her advocacy for quantitative evidence in public health policy, she demonstrated the power of statistical methods as tools for decision-making under uncertainty [18]. In parallel, Joseph Fourier’s work on heat conduction introduced series expansions and integral transforms that, while originally developed in the context of mathematical physics, would later become indispensable in the study of random processes, signal analysis, noise, and diffusion. Although Nightingale and Fourier approached uncertainty from fundamentally different directions—one through empirical data and social reform, the other through mathematical analysis of physical systems—their contributions expanded the scope of probabilistic thinking and helped prepare the intellectual ground for the later development of stochastic processes and statistical physics.

A further conceptual leap occurred in the early 20th century with the work of Andrey Markov, a Russian mathematician working at a time when probability theory was still largely built on the assumption of independent events. Markov was interested in understanding whether the familiar regular patterns of probability—such as averages stabilizing over time—could still arise when events influenced one another. To explore this question, he studied sequences in which the outcome of each step depends only on the immediately preceding one, rather than on the entire past.

This simple idea, later formalized as what are now called Markov chains, showed that randomness and order need not rely on complete independence. Even when successive events are linked, long-term statistical patterns can still emerge under suitable conditions. Markov’s work, developed within the strong Russian tradition of rigorous analysis, opened the door to the modern study of systems that evolve over time under uncertainty, from physical processes to language, biology, and many contemporary data-driven models [19].

Markov’s investigations inaugurated the systematic study of dependence in stochastic processes and laid the groundwork for much of modern probability theory. By showing that long-run behavior could be analyzed without recourse to independence, his work opened new avenues in the mathematical treatment of dynamical systems subject to randomness. The conceptual framework he introduced has since become central to a wide range of disciplines, including statistical mechanics, linguistics, finance, and more recently, machine learning and data science, where Markovian models serve as fundamental tools for modeling sequential and temporal data [20].

As a final note, the modern axiomatic formulation of probability was introduced in the early 20th century by the Russian mathematician Andrey Kolmogorov. In his 1933 monograph "*Grundbegriffe der Wahrscheinlichkeitsrechnung (Foundations of the Theory of Probability)*" [21], Kolmogorov synthesized classical and frequentist ideas into a rigorous mathematical framework based on measure theory. His axioms remain the standard foundation for probability theory to this day. It may seem surprising that a concept with such ancient origins was not formally axiomatized until relatively recent times, and we will return to Kolmogorov’s formulation

and its implications in greater detail in further chapters. Nevertheless, philosophical discussions about the interpretation of probability and its relation to the physical sciences—especially in the context of determinism, epistemology, and modern topics such as quantum mechanics—predate Kolmogorov’s formulation and continue to evolve to this day.

Chapter 1

Descriptive statistics

Statistics is the grammar of science.

— Karl Pearson

As a first approach to probability and statistics, we should properly define both topics and their main fields of study. Although deeply related, and both historically rooted in *combinatorics*—the mathematical study of counting discrete structures, and how they change—they constitute well-differentiated fields of mathematical analysis. A clear distinction often made is that probability is a *predictive* branch of mathematics, dealing with random events, and aiming to compute expected values for unknown outcomes. On the other hand, statistics can be viewed as a *descriptive* approach to uncertainty, based on sampling finite sets of observations from a given population and constructing informative quantities, called *estimators*, to explore central tendency and variation. Such distinctions have been extensively debated by mathematicians, experimental scientists, and philosophers of science [22].

As a rule of thumb, probability provides a formal language for modelling uncertainty, whereas statistics concerns the epistemic problem of learning from data. In this chapter, we introduce basic ideas of statistical inference such as population, sampling, and estimators of central tendency and variation, together with notions of representation and visualization. The foundations of probability theory, rooted in the works of Bernoulli, Laplace, and Gauss, among others, will be covered in Chapter 2.

A philosophical position often adopted is that statistics is essentially the study of uncertainty, and that the statistician’s role is to assist other fields that encounter uncertainty in their work. In practice, statistics is ordinarily associated with data, and it is the link between the variability in the data and the uncertainty inherent in the phenomenon under study that has occupied statisticians [23].

As a final note, let us emphasize how these two approaches can and do coexist in science. It is often said that science proceeds by formulating hypotheses and making predictions, which are then compared and benchmarked against experimental results. While this description applies well to many areas, it is a simplification and not universally accurate. Some sciences—such as Newtonian mechanics, much of physics, and chemistry—rely on building precise models that generate quantitative predictions later tested by experiment. A clear example is the use of Newtonian mechanics to predict where and when a stone will fall when thrown, followed by experimental measurement.

By contrast, a paradigmatic example of an inference-driven scientific theory is Darwinian evolution, which does not aim primarily to predict individual outcomes but rather to reconstruct and explain observed patterns from available evidence. This distinction is worth emphasizing, as definitions of science that focus exclusively on predictive power can be misleading. Different sciences may differ substantially in methods, instrumentation, and conceptual tools, yet they

are all equally legitimate in their aims and explanatory roles [24, 25].

1.1 Population and sampling

A large part of the history of science can be seen as a continuous effort to translate observations of reality into precise mathematical terms. Describing natural phenomena in numerical language requires tools that relate one or more relevant quantities—often called *variables*—and explain how they change with respect to one another. The goal of modelling may be, for example, to determine the distance from the Earth to the Sun, estimate the number of stars in the observable universe, or relate the incidence of lung cancer to environmental or behavioral factors, such as smoking.

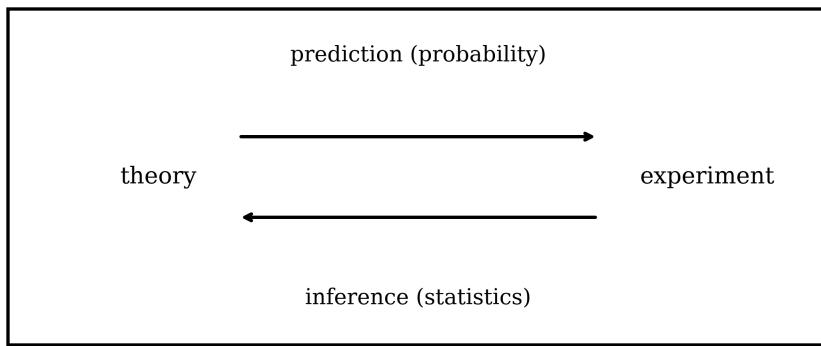


Figure 1.1: Representation of two complementary approaches to randomness and variability: a predictive, theory-driven path from model to experiment, and a descriptive, inference-based path from data to explanation. Probability and statistics are normally framed as the branches of mathematics addressing both ways.

In the same way mathematics is often summarized as the tasks related to *count*, *measure*, and *sort*, statistical problems can be grouped into three broad categories. *Sampling* concerns the selection of a finite set of observations from a larger, typically unknown population. *Estimation* involves constructing numerical summaries that describe how the data are distributed, while *visualization* addresses how observations are represented and how such representations influence interpretation. All three are fundamentally concerned with uncertainty and variability.

Hence, all statistical inquiries begin with observations and measurements, which we normally refer to as *data*. And data begins with the act of selection, or *sampling*. The natural world offers a vast abundance of phenomena, with endless opportunities for observation, but only a finite subset can ever be recorded. This distinction gives rise to two central notions: the *population*, which we denote by \mathcal{P} , represents the complete set of all possible observations under study. We will write it as

$$\mathcal{P} = \{x_1, x_2, \dots, x_N\}. \quad (1.1)$$

The *sample* \mathcal{S} , on the other hand, is the finite subset actually collected. For a series of N observations x_1, x_2, \dots, x_N , a sample of just n elements—less than the total, which is denoted by the upper case N —is defined as

$$\mathcal{S} = \{x_1, x_2, \dots, x_n\}, \quad n < N, \quad (1.2)$$

The population represents the ideal object of inference, while the sample is the concrete, finite evidence available to us. As an example, if I want to study some disease and its relation smokers in a given country, the behavior of a specific population, or the active genes in the genome, I will never have access to the *complete population*, but only to the amount of them that I am able to

question, measure, or survey. This distinction is far from trivial. A poorly chosen sample often misrepresents the population and may induce bias, whereas a carefully constructed one mirrors its essential features, and can be used to describe the underlying nature.

Equally important is the recognition that not all data is equal, neither behaves in the same way. A common distinction is to consider *categorical* and *numerical* data. Categorical—or *qualitative*—data describes qualities or labels such as the eye colour of students in a classroom (blue, brown, green), the brand of a purchased smartphone, etc. Sometimes they are further divided into *nominal* categories, with no natural order, like the eye colour or the smartphone brand, and *ordinal* categories with a meaningful order. Examples of these would be the finishing places in a race (first, second, third), survey responses ranging from *strongly disagree* to *strongly agree*, etc.

The other big family is normally referred to as numerical—or *quantitative*—data. It represents numerical quantities and is often subdivided into *discrete*, countable numbers, such as the number of books on a shelf (4, 5, 6) or the number of goals scored in a match, and *continuous* values that can take any number within a range, such as the time a sprinter takes to run 100 meters, or the height of a person measured with some arbitrary precision.

Distinguishing between these types is no mere slang; different types of observations require different mathematical tools, and will be described in different ways. For example, it would not make sense to compute a mean out of smartphone brands, but to compute the mean of their prices is informative. Similarly, the distribution of finishing places after a race might be summarized by a median position, whereas heights of athletes could be studied with averages and measures of spread. A correct classification of data is thus a safeguard against misuse and a guide toward insight.

As a summary, sampling and proper description of data establish the ground upon which statistics is built. Before calculating, summarizing, or diving into inference, one must ensure that the information collected is both *representative* and *properly understood*. Without these foundations, descriptive measures risk floating unmoored, detached from the reality they claim to represent. Accurate sampling and rigorous description will lead to a faithful representation of the phenomena under study and their relationships, detecting anomalies, and even building accurate predictions.

Let's end this section with a historical note. As we have mentioned, uncertainty has long been associated with games of chance and gambling, but it was not addressed as a statistical problem until much later. The Royal Statistical Society, founded in 1834, together with many other early statistical organizations, was originally established to gather and publish data, with the aim of informing social and economic questions through systematic measurement. It did not take long before statisticians began to ask how such data might best be analyzed and interpreted, and modern *statistical inference* gradually emerged. Among the Society's influential early figures were Adolphe Quetelet, whose work helped establish statistics as a tool for studying social phenomena, and Charles Babbage, who advocated quantitative approaches to scientific and administrative problems.

Among its most famous members was Florence Nightingale, admitted in 1858 as the Society's first female member, whose work exemplified the practical use of statistical reasoning in policy and public health. In the early 20th century, foundational questions concerning probability and inference were further clarified through the work of thinkers such as Frank P. Ramsey, who connected probability with rational belief and decision-making [26]. Other notable presidents of the Royal Statistical Society have included William Beveridge and Ronald Fisher, whose contributions will be discussed in Chapter 4.

Andrew Lang's famous quote "*most people use statistics as a drunken man uses lamp-posts—for support rather than illumination*", highlights the tendency to use statistics as a crutch,

relying on them for validation rather than seeking genuine understanding. Lang's observation serves as a cautionary reminder to approach statistical data with critical thinking and not merely as a tool to bolster preconceived notions.

1.2 Central tendency and variation

Once we have drawn a clear distinction between the population under study and the selected sample, we immediately face a fundamental problem. Neither the population mean—often referred to as the *true* mean and usually denoted by μ —nor the population variance, known as the *true* variance and written as σ^2 , are directly available to us. As we have seen, the only information at our disposal is the finite set of observations contained in our sample. From this limited information, we therefore seek to construct quantities that provide insight into key features of the population, such as its central value or its variability. These quantities are known as *statistical estimators*. Common examples include the *sample mean*, the *median*, the *variance* and the *standard deviation*.

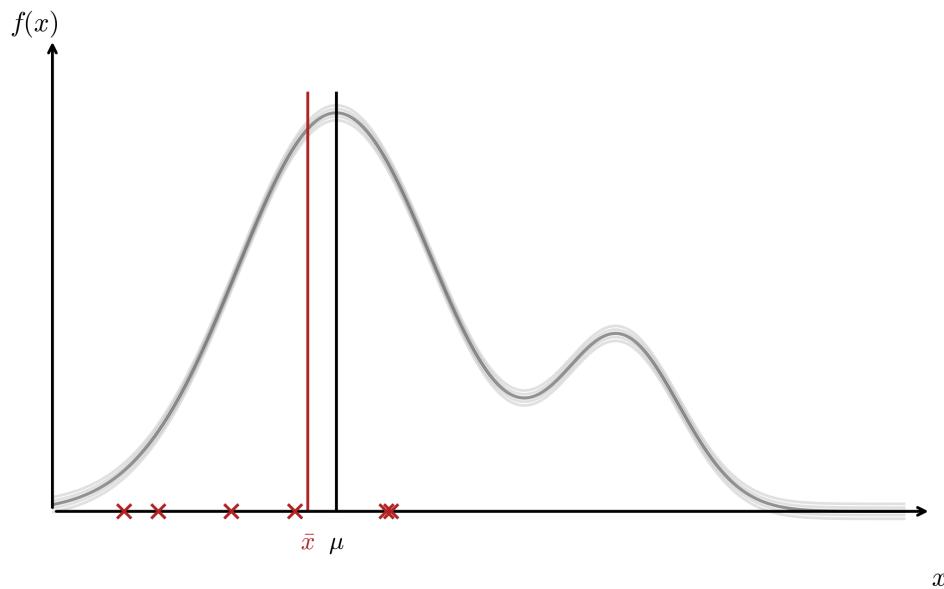


Figure 1.2: Representation of the *true* population mean μ , in black, and the observed *sample* mean \bar{x} . The true mean is an ideal and inaccessible quantity, while the sample mean can be computed as an estimator of the finite sample.

Once observations have been collected, a natural question arises: what is the *center*, or *typical*, value of this data set? Measures of central tendency address this question by summarizing the data with a single representative number, offering an immediate sense of where the observations are located within the distribution.

The sample mean:

The *sample mean*, or *average* is perhaps the most familiar measure of central tendency. Imagine we are doing an experiment where we measure some variable, and let's call it x for simplicity. x can be anything we could measure, like position at a given time, energy of some system, concentration of a specific substance, etc. Let's imagine we repeat the measurement n times, and we obtain the values x_1, x_2, \dots, x_n . That will be our set of observations—our *sample*— \mathcal{S} . We could simply write it as a list—or a *vector*—in the following way:

$$\mathcal{S} = \{x_1, x_2, \dots, x_n\} .$$

Keep in mind that from the mathematics perspective the word *vector* has a slightly different meaning, with subtleties related to algebraic operations and relations they should satisfy, but for the purpose of this course, where we prioritize above all simplicity, a vector and a list of numbers will be essentially the same thing.

We can define the sample mean of an arbitrary large sample of n observations, as the sum of all elements divided by the total. We will write it as \bar{x} , and define it as follows:

$$\bar{x} = \frac{1}{n}(x_1 + x_2 + \dots + x_n) . \quad (1.3)$$

We can write this in a slightly more compact way as a *summation*, as follows:

$$\bar{x} = \frac{1}{n} \sum_{i=1}^n x_i . \quad (1.4)$$

Here we denote the sum of all elements x_i with the greek letter \sum , starting with the first one (x_1 , for $i = 1$) and until the last one (x_n , for $i = n$). The expressions (1.3) and (1.4) mean *exactly* the same thing, just written in different ways.

Let's illustrate with an example. Suppose we repeat a measurement three times, obtaining the results $x_1 = 1$, $x_2 = 2$, and $x_3 = 3$. Our sample is then $\mathcal{S} = \{1, 2, 3\}$, and the sample mean is

$$\bar{x} = \frac{1}{3} \sum_{i=1}^3 x_i = \frac{1}{3}(1 + 2 + 3) = 2 .$$

As a warm-up exercise, try computing the same mean value for a second sample, let's say $\mathcal{S} = \{4, 5, 6\}$. Substituting into the general expression (1.4) gives

$$\bar{x} = \frac{1}{3} \sum_{i=1}^3 x_i = \frac{1}{3}(4 + 5 + 6) = 5 .$$

As we see, the sample mean captures information about the "central" value, where most events cluster. Although useful, it is sensitive to extreme values—often called *outliers*—which motivates the definition of additional, more robust measures of central tendency.

The median:

The *median* represents similar information, as the value that splits the ordered data set in half. For an ordered sample $x_{(1)} \leq x_{(2)} \leq \dots \leq x_{(n)}$, the median M is defined as

$$M = \begin{cases} x_{(k+1)} , & \text{if } n = 2k + 1 \text{ (odd) ,} \\ \frac{x_{(k)} + x_{(k+1)}}{2} , & \text{if } n = 2k \text{ (even) .} \end{cases} \quad (1.5)$$

Note that here k is just an integer that helps locate the middle position of an ordered data set of size n . If the sample size n is even, we write $n = 2k$, while for n odd, we write $n = 2k + 1$. In the case of an odd-sized sample, the median is just the middle-point, while for an even size, it is computed as the average of the two middle points.

The mathematical definition (1.5) may seem a bit unnatural at first, so let's navigate it with a couple of examples. Consider the sample $\mathcal{S} = \{1, 2, 3, 5, 3, 2, 7\}$. First, we order the data:

$$\mathcal{S}_{\text{ordered}} = \{1, 2, 2, 3, 3, 5, 7\} .$$

Since the sample has an odd number of elements ($n = 7$), the median is just the middle value:

$$M = x_{(4)} = 3 .$$

Now consider an even-sized sample $\mathcal{S} = \{1, 2, 3, 5, 4, 3, 2, 7\}$. Ordering the data gives

$$\mathcal{S}_{\text{ordered}} = \{1, 2, 2, 3, 3, 4, 5, 7\}.$$

Which has now an even number of elements ($n = 8$). Hence, applying such case in (1.5), the median is the average of the two middle values

$$M = \frac{x_{(4)} + x_{(5)}}{2} = \frac{3 + 3}{2} = 3.$$

Unlike the mean, the median is robust to outliers and skewed data, capturing the central position of the dataset even with repeated values. To illustrate that, let's have a look at the following sample $\mathcal{S} = \{1, 2, 3, 3, 4, 4, 200\}$, which contains the value 200 as a huge outlier. The sample mean would be

$$\bar{x} = \frac{1}{7}(1 + 2 + 3 + 3 + 4 + 4 + 200) = \frac{217}{7} = 31.$$

While the median, given a size $n = 7$ would just be the middle (4th) value

$$M = 3.$$

For instance, the data represented in LHS of Figure 1.4 will be accurately described by computing the mean, given its symmetric behaviour, while the one in the RHS will be better addressed with a median, accounting for the skewness and the presence of outliers.

The sample variance:

Beyond central location, it is important to understand the *spread* of the data. We define the *sample variance* s^2 of a data set as a quantity that captures how far the elements are from the mean value:

$$s^2 = \frac{1}{n-1} \sum_{i=1}^n (x_i - \bar{x})^2. \quad (1.6)$$

The factor $n-1$ in the denominator of (1.6) is called the *Bessel correction factor*. A technical explanation is that this correction ensures that s^2 is an *unbiased estimator* of the population variance, a concept we will discuss in Chapter 3. In particular, it reflects the fact that the sample mean \bar{x} is itself estimated from the data.

Note that the variance is obtained by summing the squared differences between each observation and the mean. The differences are squared so that positive and negative deviations do not cancel and the result is always non-negative. If all elements in the sample are very close to the mean, the variance s^2 will be small; if the elements are widely spread, the variance will be larger.

Let us illustrate this definition with an example. For the sample $\mathcal{S} = \{1, 2, 3\}$, which has $n = 3$ observations and sample mean $\bar{x} = 2$, the variance is

$$s^2 = \frac{1}{3-1} \sum_{i=1}^3 (x_i - \bar{x})^2 = \frac{1}{2} ((1-2)^2 + (2-2)^2 + (3-2)^2) = \frac{1}{2} (1+0+1) = 1,$$

which we could interpret as, on average, the elements of the list being *one unit* away from the mean.

As a warm-up exercise, try to compute the variance for a second sample, let's say $\mathcal{S} = \{4, 5, 6\}$. By substituting in the general expression (1.6) you should get the result

$$s^2 = \frac{1}{3-1} \sum_{i=1}^3 (x_i - \bar{x})^2 = \frac{1}{2} ((4-5)^2 + (5-5)^2 + (6-5)^2) = \frac{1}{2} (1+0+1) = 1.$$

We obtain again a variance $s^2 = 1$, indicating as in the previous example, that the elements of this sample \mathcal{S} are also *one unit* away from the mean.

The standard deviation:

Another useful quantity used to characterize variability is the so-called *standard deviation*, which is simply the square root of the variance,

$$s = \sqrt{\frac{1}{n-1} \sum_{i=1}^n (x_i - \bar{x})^2}, \quad (1.7)$$

and therefore has the same units as the original data. While the variance measures spread in squared units, the standard deviation provides a more interpretable measure of how far, on average, observations lie from the mean.

At a glance, variance and standard deviation both quantify how much the elements of a data set deviate from the mean, capturing the notion of *spread*.

Quantiles:

Finally, *quantiles* provide another way to describe the distribution of data by dividing an ordered data set into equal proportions. The p -th quantile Q_p is defined as the value below which a fraction p of the data lies. Common special cases include the *first quartile* (Q_1 , corresponding to the 25th percentile), the *median* (Q_2 , the 50th percentile), and the *third quartile* (Q_3 , the 75th percentile). Informally, they answer questions of the form: “*What value separates the lowest $p\%$ of observations from the rest?*” They are particularly useful for describing skewed data and for comparing distributions without relying solely on the mean. To illustrate this idea with a simple example, consider the ordered sample

$$\mathcal{S} = \{1, 2, 3, 4, 5, 6, 7, 8\}.$$

Since there are $n = 8$ observations, the median Q_2 lies halfway between the fourth and fifth elements and is therefore

$$Q_2 = \frac{4+5}{2} = 4.5.$$

The first quartile Q_1 separates the lowest 25% of the data and lies between the second and third elements, while the third quartile Q_3 lies between the sixth and seventh elements. In this way, quartiles summarize the distribution by marking its lower tail, central region, and upper tail.

A rigorous definition of quantiles requires the notion of a distribution function and cumulative probability, which we will introduce in the next chapter. For a continuous cumulative distribution function (CDF) F , the p -th quantile satisfies

$$Q_p = \inf\{x : F(x) \geq p\}. \quad (1.8)$$

In summary, the mean, median, mode, variance, standard deviation, and quantiles provide a rich and complementary view of a data set’s central tendency and variability. Together, they allow for both numerical and graphical summaries that capture essential features of the data.

Variation is not merely a technical detail; it is the essence of uncertainty. Without spread, probability would be trivial, as every outcome would be identical. It is precisely in the differences among observations that statistical inquiry finds its substance. Central tendency and variation thus form complementary lenses through which data become intelligible: they allow us to assess whether groups are similar or different, whether an observation is ordinary or surprising, and whether observed variation can plausibly be attributed to chance. In this sense, descriptive statistics foreshadows the inferential methods to come, hinting at deeper regularities beneath the numbers.

1.3 Data visualization

While numerical summaries are useful, the human mind often grasps patterns much more quickly through vision than through calculation. By *data visualization* we mean a family of techniques used to transform numbers and sequences into shapes, colours, and spatial structures that are easier to interpret and can often be understood at a glance. Visualization turns abstraction into perception and frequently reveals regularities that remain hidden when data are examined only through formulas or numerical summaries. Today, a broad range of disciplines grouped under the name of data visualization—or data *representation*—have become central pillars of scientific practice and data-driven inquiry.

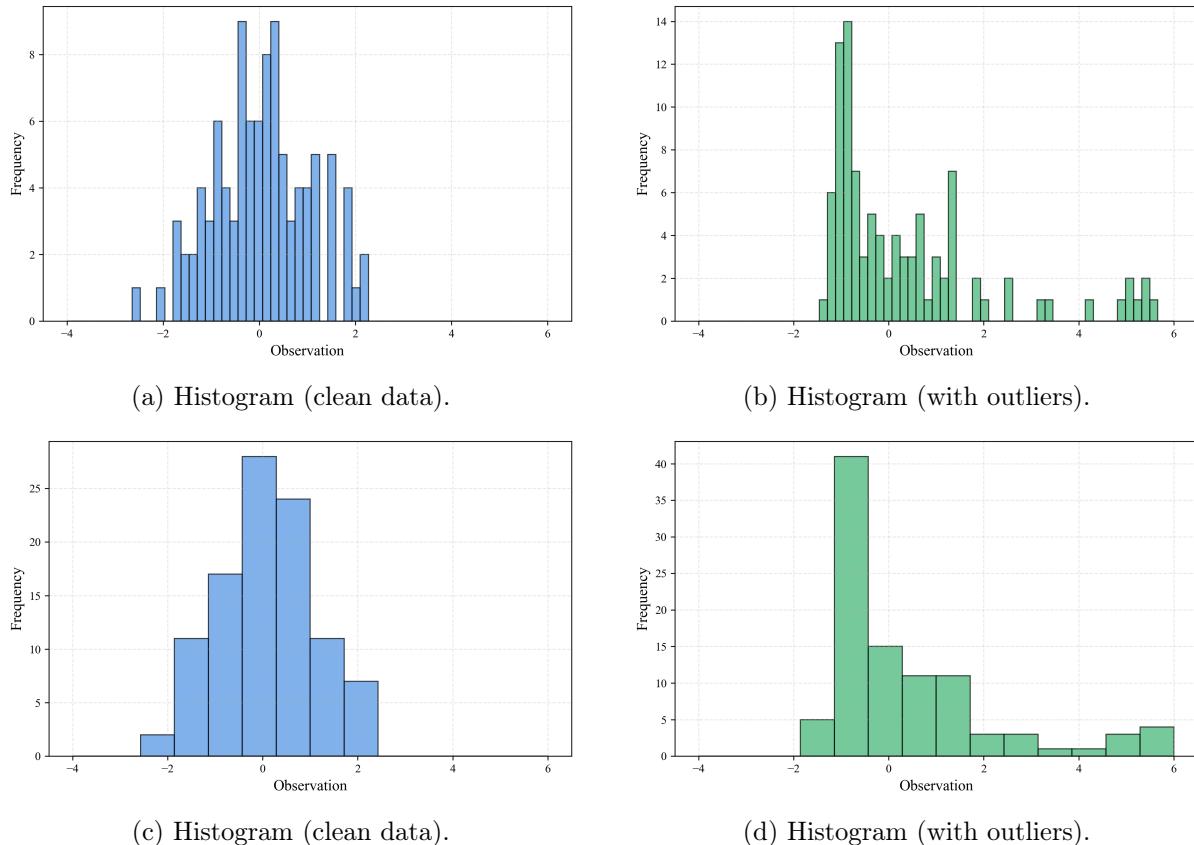


Figure 1.3: Comparison of graphical summaries for $n = 100$ observations drawn from a Gaussian distribution. Left column: uncontaminated data, with both small and large binning size. Right column: data affected by outliers, with both small and large binning size. Figure shows how a small bin size may give lead to resolution, but also introduce noise.

Among the oldest and most fundamental visualization tools is the *histogram*. The idea of dividing data into intervals in order to visualize frequency dates back to the late 19th century, when Karl Pearson formalized the histogram as a graphical representation closely connected to probability distributions [27, 28]. A histogram divides the range of a data set into consecutive intervals, or *bins*, and represents the number—or relative *frequency*—of observations falling within each bin by the height of a bar. This simple yet powerful plot provides an immediate visual impression of the distribution, allowing one to identify symmetry, skewness, concentration of values, and potential gaps. For instance, a symmetric histogram suggests a roughly balanced distribution around the mean, whereas a right-skewed histogram indicates that large values are less frequent but may still exert a strong influence on measures such as the mean. Histograms are therefore widely used in the physical sciences and in contexts where data are compared to

theoretical or mathematical predictions.

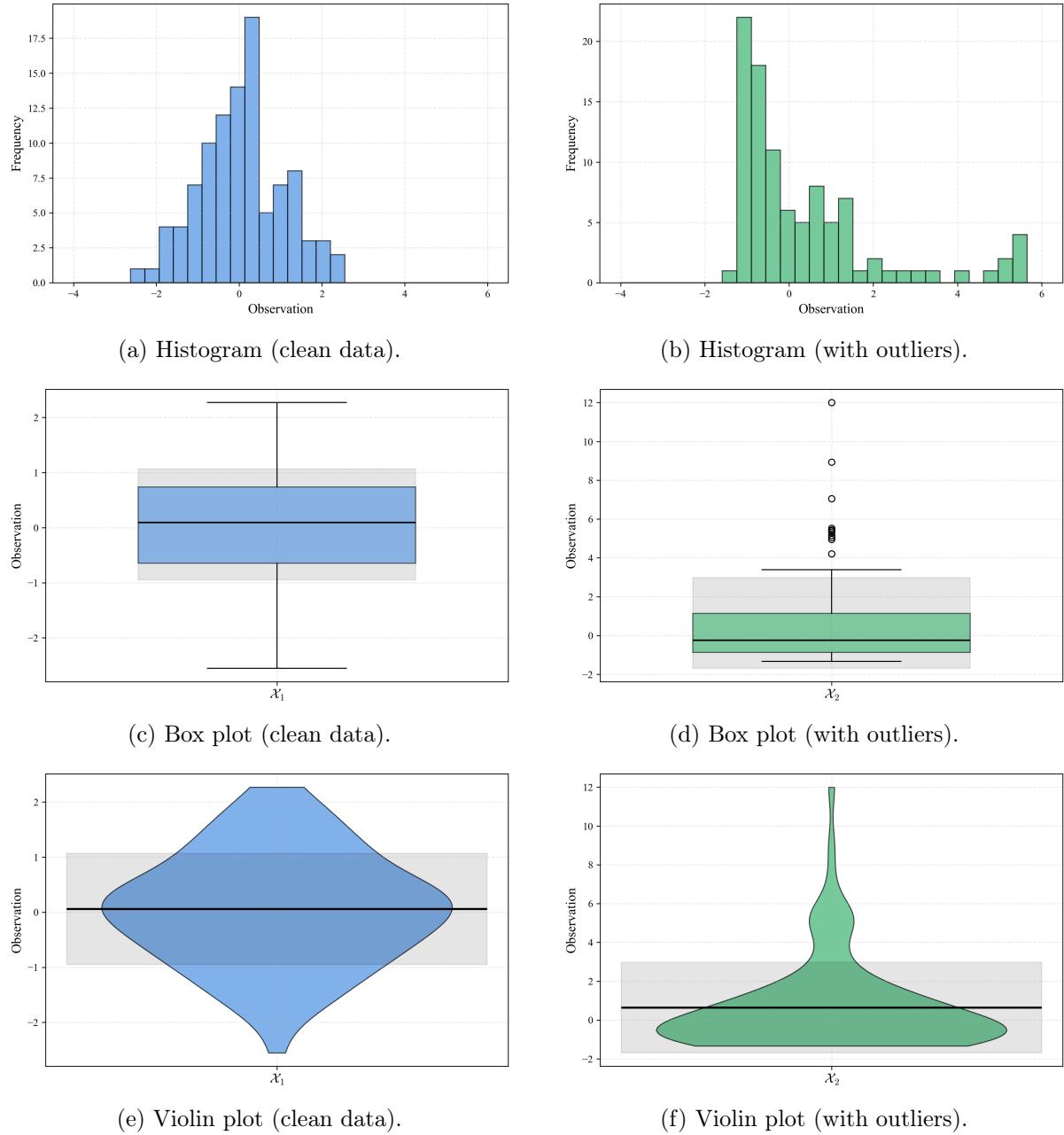


Figure 1.4: Comparison of graphical summaries for $n = 100$ observations drawn from a Gaussian distribution. Left column: uncontaminated data. Right column: data affected by outliers. The rows show, respectively, histograms, box plots, and violin plots, illustrating how different visualization techniques respond to skewness and extreme observations.

Constructing an informative histogram requires some care. As a general rule, bins should be of equal width and together cover the entire range of the data, while reflecting natural groupings when possible. The choice of bin width plays a crucial role: using many narrow bins increases resolution but can introduce spurious fluctuations, especially in the presence of outliers, whereas using a small number of wide bins produces a smoother and more robust picture at the cost of detail. Because extreme values can strongly affect the appearance of a histogram, they must be handled thoughtfully. For highly skewed distributions, numerical summaries such as the median and the interquartile range (IQR) often provide a more stable description than the mean.

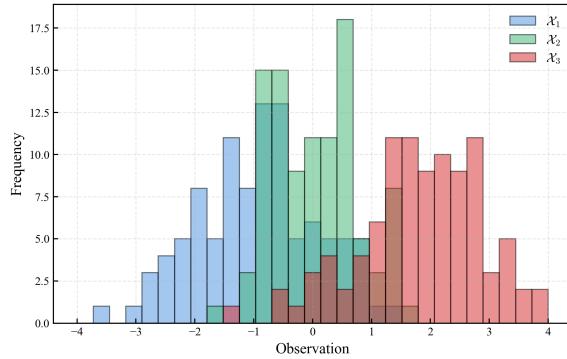
Another widely used visualization is the *box plot*, also known as the *box-and-whisker* plot, introduced by John Tukey in 1970 as part of his work on exploratory data analysis [29]. The box plot offers a compact summary of a data set's central tendency, spread, and potential outliers. It is constructed from five key statistics: the minimum, first quartile (Q_1), median (Q_2), third quartile (Q_3), and maximum. The box itself represents the interquartile range ($IQR = Q_3 - Q_1$), while observations lying more than 1.5 times the IQR from the quartiles are typically flagged as outliers. Box plots allow for rapid comparisons across multiple groups and are particularly effective at revealing asymmetry and variability without being overly influenced by extreme values. For this reason, they are especially common in biological, medical, and clinical sciences, where experiments are often repeated many times with relatively small sample sizes.

More recently, the *violin plot* has emerged as a refinement of the box plot, combining summary statistics with a smooth representation of the distribution's shape. Although its precise origin is less sharply documented, the violin plot gained prominence in the late 20th century with the development of statistical software environments such as R and Python, particularly following the work of Hintze and Nelson in the 1990s [30]. A violin plot augments the box plot by incorporating a kernel density estimate of the data, producing a mirrored shape that reflects the underlying distribution. In addition to displaying the median and quartiles, violin plots reveal features such as skewness and multimodality that may be obscured in simpler summaries, making them especially useful for comparing several groups side by side.

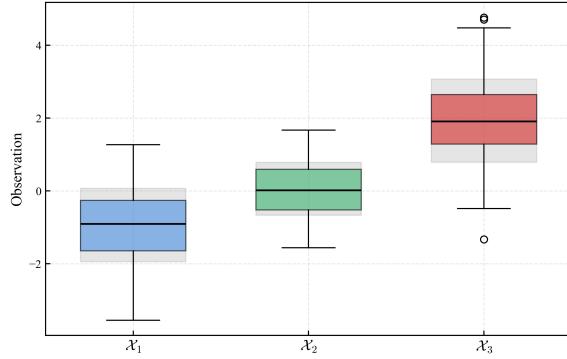
The importance of visualization extends beyond convenience. Early work by Spearman on association [31] and later demonstrations such as Anscombe's quartet [32] highlighted a crucial lesson: data sets with nearly identical numerical summaries can exhibit dramatically different graphical structures. Visualization is therefore not merely a tool for presentation, but a fundamental instrument of statistical reasoning. By complementing numerical summaries, graphical representations help guard against misinterpretation and deepen our understanding of variability, structure, and uncertainty in data.

As a note, let us emphasize that the roots of data visualization can be traced back well before modern statistics, to the early development of analytical geometry in the 17th century. A decisive step was taken by René Descartes, whose introduction of coordinate systems in "*La Géométrie*" (1637) provided a systematic way to represent numerical relationships geometrically [33]. By associating quantities with positions in space, Descartes established the conceptual framework underlying graphs, curves, and plots as representations of functional relationships. Although his work was not statistical in intent, it laid the mathematical foundation upon which later visual representations of empirical data would be built. Over the following centuries, this geometric perspective was gradually adapted to observational and social data, culminating in the 19th-century development of statistical graphics—such as frequency plots and histograms—as tools for exploring variability, association, and uncertainty.

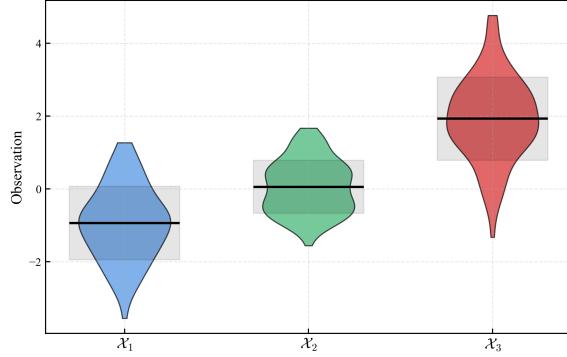
Following Descartes' geometric framework, graphical representations of data evolved through the work of figures such as William Playfair, who in the late 18th century introduced line and bar charts to depict economic time series, and Adolphe Quetelet, who applied statistical regularities to social phenomena. In the 19th century, visualization became both an analytical and persuasive tool, exemplified by Florence Nightingale's use of statistical graphics in public health and Charles Joseph Minard's multivariate maps. These developments established visualization as a central instrument for exploring, communicating, and reasoning about data, long before the formalization of modern statistical theory [34, 35].



(a) Three sets of observations χ_1, χ_2, χ_3 of sample size $n = 100$ drawn from a Gaussian distribution, with the mean value and standard deviation represented as a histogram.



(b) Three sets of observations χ_1, χ_2, χ_3 of sample size $n = 100$ drawn from a Gaussian distribution, with the mean value and standard deviation represented as a box plot.



(c) Three sets of observations χ_1, χ_2, χ_3 of sample size $n = 100$ drawn from a Gaussian distribution, with the mean value and standard deviation represented as a violin plot.

Figure 1.5: Comparison of three visualization methods—histogram, box plot, and violin plot—showing the mean and variability of three samples of size $n = 100$ drawn from a Gaussian distribution.

Chapter 2

Foundations of Probability

It is through the calculation of probabilities that the divine order becomes visible.

— Jacob Bernoulli

At its heart, probability is nothing more—and nothing less—than a branch of mathematics developed to describe random phenomena, also referred to as *stochastic*. The word “stochastic” comes from the Greek *στοχαστικός*, literally meaning “to guess” or “to aim.” Probability thus provides a numerical language for uncertainty, allowing us to quantify how surprising or plausible an outcome is before it is observed.

The study of probability, though having very ancient roots, began its modern development in the 17th century through the famous correspondence between Blaise Pascal and Pierre de Fermat. Their discussion about games of chance, and in particular the “problem of the division of stakes”, laid the groundwork for a systematic mathematical analysis of uncertain events. A few decades later, Jacob Bernoulli’s *“Ars Conjectandi”* provided the first sustained theoretical treatment of probability, including an early formulation of the law of large numbers [13, 14]. Subsequent refinements by Abraham de Moivre, particularly his work on normal approximation, and by Pierre-Simon Laplace transformed probability into a powerful analytical theory, while its fully axiomatic structure only crystallised in the 20th century, as we will see [16].

Beyond games of chance, probability rapidly became essential for the understanding of natural phenomena and human affairs. Astronomy, population studies, and various physical problems required tools to reason quantitatively about variability, error, and incomplete information. During the 19th century, thinkers such as Cournot emphasized the connection between probabilistic laws and empirical regularities, arguing that probability acquires meaning through its relation to observable frequencies in the world. In this sense, probability emerged not merely as a mathematical curiosity, but as a response to practical problems involving uncertainty and regularity in the empirical world.

As we have mentioned already, a decisive step toward mathematical rigor was taken by Andrey Kolmogorov in 1933. In his *“Grundbegriffe der Wahrscheinlichkeitsrechnung”* [21], Kolmogorov showed that probability could be treated as a branch of measure theory, independent of any specific interpretation. This formulation built directly on earlier developments in analysis, most notably Henri Lebesgue’s theory of integration, which provided the mathematical language needed to define probabilities as measures on sets [36]. Rather than defining probability through intuition, symmetry, or frequency, Kolmogorov postulated a small set of axioms from which the entire formal theory follows.

The measure-theoretic approach introduced by Kolmogorov was later systematized and widely disseminated through modern mathematical treatments of probability, most famously

in Patrick Billingsley's *Probability and Measure* [37]. These works established the now-standard framework in which random variables, expectations, and convergence are treated using the tools of modern analysis.

From a philosophical point of view, two influential strands in the interpretation of probability emerge from these debates. On the one hand, the frequentist program, most clearly articulated by Richard von Mises, grounded probability in long-run relative frequencies of repeatable experiments. On the other hand, approaches originating with Thomas Bayes and later developed in the twentieth century interpreted probability as a rational degree of belief. Both perspectives play an important role in modern probability and statistics, and their mathematical and philosophical foundations will be examined in detail in Chapter 6.

Parallel developments in the early 20th century focused on statistical inference from data rather than individual decision-making. These approaches emphasized long-run frequency properties, error control, and sampling distributions, leading to the classical framework of statistical inference that still underlies much of modern applied statistics.

2.1 Probability and random events

In modern mathematics, probability is defined axiomatically following Kolmogorov's axioms [21]. Without much technicality, probability \mathbb{P} is a number we associate to each event, satisfying three fundamental rules:

- Probabilities are never negative: $\mathbb{P}(A) \geq 0$ for any event A .
- The probability of a certain event is 1.
- If two events cannot occur together, the probability that one or the other occurs is the sum of their probabilities.

For a discrete set of all possible outcomes $\{x_1, x_2, \dots, x_n\}$, these rules imply the normalization condition

$$\sum_{i=1}^n \mathbb{P}(x_i) = 1 ,$$

also referred to as *unitarity*, which simply states that *something must happen*.

The numerical value of a probability reflects how surprising an outcome would be. For a given event A , such as observing heads in a coin toss, or a specific face in a dice roll, when $\mathbb{P}(A) \rightarrow 0$, the event is almost impossible; observing it would be highly surprising. On the contrary, when $\mathbb{P}(A) \rightarrow 1$, the event is almost certain; its occurrence carries little surprise. For anything in between, there is a level of *uncertainty*, or *surprise*, where probability quantifies degrees of expectation, rather than absolute certainty or impossibility.

Why, for example, do we say that a fair coin has probability 1/2 of landing heads, or that a fair die has probability 1/6 of showing a given face? These numbers are not empirical facts but modeling assumptions based on symmetry. When all outcomes are assumed to be equally possible and indistinguishable before observation, probability assigns equal weight to each outcome. Probability theory then explores the logical consequences of these assumptions.

This idea, that half of the times we toss a coin we obtain heads, hence we assign 1/2 probability, or that one every six times we roll dice we see a specific face, hence we assign 1/6 probability, leads to common interpretation of probability known as the *frequentist* view, developed most clearly by von Mises in his *"Probability, Statistics and Truth"* [38]. In this perspective, probability is identified with the long-run relative frequency of an event in repeated, identical experiments. Saying that a coin has probability 0.5 of landing heads means that, over

many tosses, roughly half will result in heads. And as we increase the number of observations, at higher *frequencies*, we expect that number to converge to a perfect half.

An alternative interpretation is the *Bayesian* view, originating with Thomas Bayes [39] and developed further by Laplace and later authors such as de Finetti [40] and Jaynes [41]. Here, probability quantifies uncertainty or degree of belief rather than long-run frequency, and probabilities are updated as new information becomes available using Bayes' theorem.

Both interpretations use the same mathematical rules and rely on Kolmogorov's axioms. The difference lies not in the calculations, but in how probability statements are interpreted. Again, Bayesian methods and their practical consequences will be introduced formally in Chapter 6.

2.2 Discrete events

With this simple definition of probability, we can now start categorizing event based on how their probabilities are *distributed*. By *discrete* events we mean those where the set of possible outcomes is finite or countably infinite. From coins and dice to counting, discrete models are particularly useful when outcomes correspond to counts, successes and failures, or categorical observations. In such cases, probability distributions will represent exact probabilities to individual outcomes and are therefore called probability *mass* functions.

Mathematically, a discrete probability distribution assigns a probability $\mathbb{P}(x_i)$ to each possible outcome x_i , such that

$$\mathbb{P}(x_i) \geq 0, \quad \sum_{\forall i} \mathbb{P}(x_i) = 1. \quad (2.1)$$

where the \forall symbol is just a mathematical character meaning "for all".

2.2.1 Bernoulli trials

The Bernoulli trial was formalized by Jacob Bernoulli in "*Ars Conjectandi*" (1713) [13]. His motivation was to understand how regularity emerges from randomness when an experiment with two outcomes is repeated many times.

A Bernoulli random variable x takes only two values, usually 1 (success) and 0 (failure). Its probability mass function is

$$\mathbb{P}(x; p) = \begin{cases} p, & x = 1, \\ 1 - p, & x = 0, \end{cases} \quad 0 \leq p \leq 1. \quad (2.2)$$

Bernoulli trials are used whenever an experiment has exactly two possible outcomes. Typical examples include the heads and tails of the coin, success or failure of a medical treatment, or whether a user clicks on a digital advertisement. In all these cases, the outcome is binary, even if the underlying process is complex.

Example: A single coin toss of a fair coin can be modeled as a Bernoulli trial, with $x = 1$ representing heads and $x = 0$ tails. For a fair coin, symmetry suggests $p = 1/2$.

Example: A single coin toss of a biased coin can be modeled as a Bernoulli trial, with $x = 1$ representing heads and $x = 0$ tails, but now the probability of success would be, for instance $p = 2/3$.

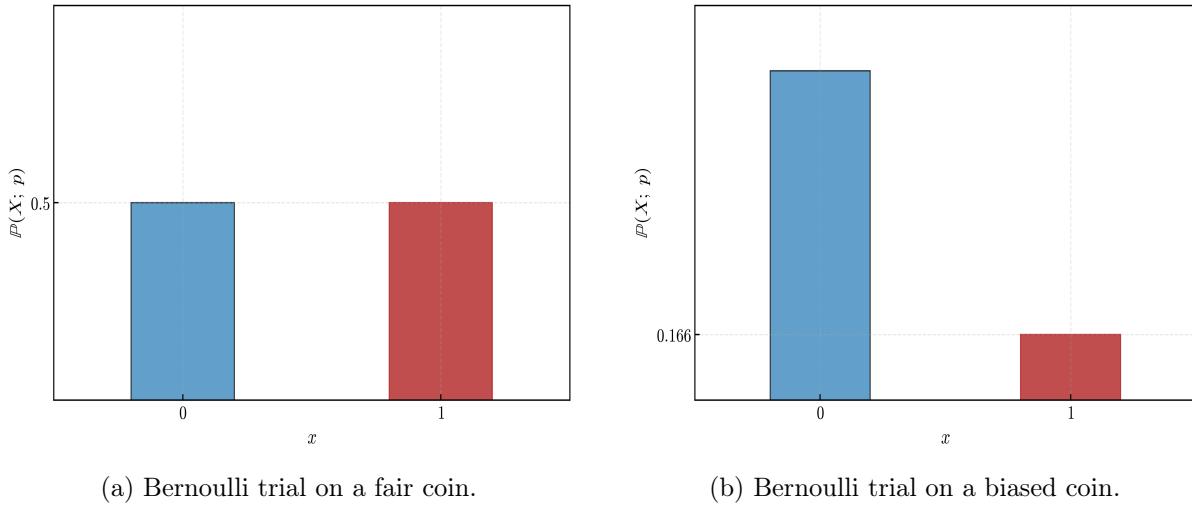


Figure 2.1: Bernoulli probability distribution

2.2.2 Discrete uniform distribution

The discrete uniform distribution has its roots in classical symmetry arguments used in early probability theory. It formalizes the idea that, in the absence of distinguishing information, all outcomes should be treated equally. This idea reflects a principle already present in early probability theory: when no outcome can be distinguished from another based on available information, they should be treated symmetrically. Laplace formalized this reasoning as "the principle of insufficient reason".

If a random variable x can take n distinct values $\{x_1, \dots, x_n\}$, the discrete uniform distribution assigns

$$\mathbb{P}(x; n) = \frac{1}{n}, \quad i = 1, \dots, n. \quad (2.3)$$

Discrete uniform distributions appear whenever outcomes are assumed to be equally likely. Examples include faces of dice, card draws from a well-shuffled deck, or randomized experimental assignments where each category is given equal probability.

Example: Rolling a fair six-sided die can be modeled as a discrete uniform distribution on $\{1, 2, 3, 4, 5, 6\}$, where each face has probability $1/6$.

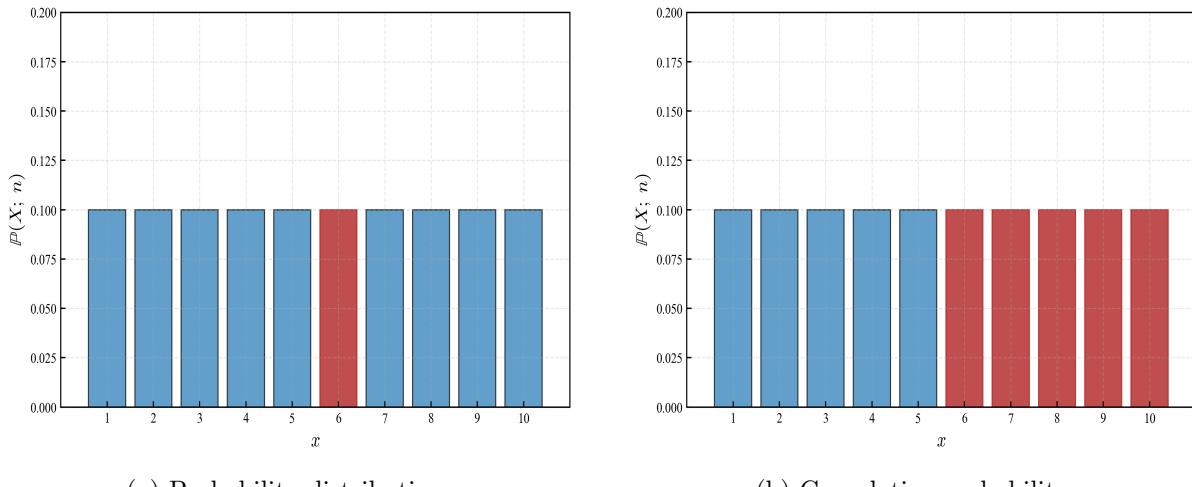


Figure 2.2: Discrete uniform probability distribution

2.2.3 Binomial distribution

The binomial distribution was systematically studied by Abraham de Moivre in the early 18th century. His analysis of repeated Bernoulli trials led not only to the binomial formula but also to the first appearance of the normal approximation. De Moivre introduced the binomial distribution while studying games of chance, but its importance quickly extended far beyond gambling. By considering repeated trials under identical conditions, the binomial distribution became a central model for understanding variability in counting processes.

The binomial distribution models the number of successes in n independent Bernoulli trials with success probability p . Its probability mass function, given a total number of attempts n , and the individual probability p of each success, is

$$\mathbb{P}(x; n, p) = \binom{n}{x} p^x (1-p)^{n-x}, \quad x = 0, 1, \dots, n. \quad (2.4)$$

Binomial models naturally arise when we count how many times a certain event occurs in a fixed number of attempts. Examples include the number of defective items in a batch, the number of patients responding to a treatment, or the number of voters favoring a candidate in a survey.

Example: The number of heads obtained when tossing a fair coin 10 times follows a binomial distribution with $n = 10$ and $p = 1/2$.

Example: The number of 4s obtained when rolling a fair dice 10 times follows a binomial distribution with $n = 10$ and $p = 1/6$.

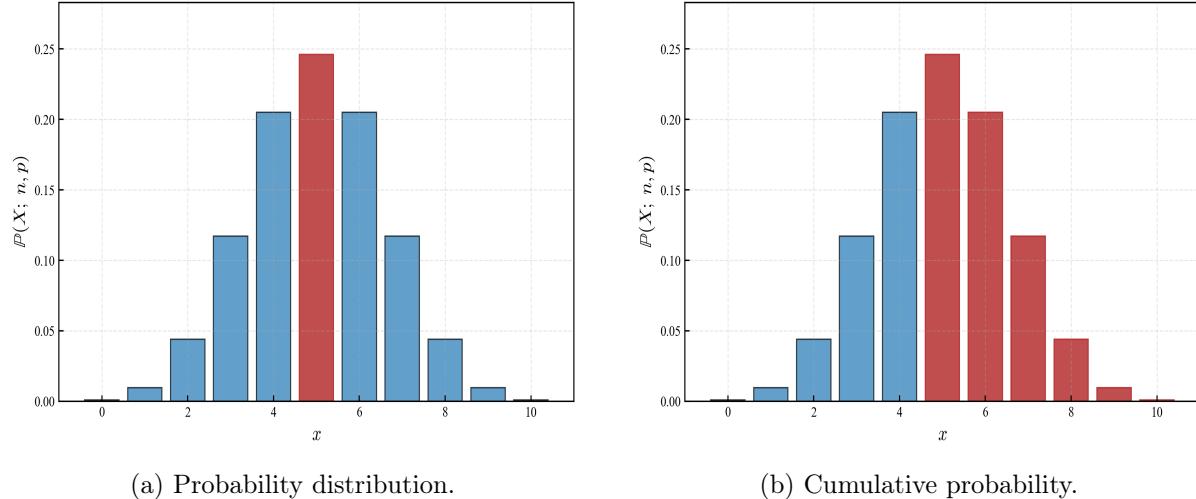


Figure 2.3: Binomial probability distribution

2.2.4 Poisson distribution

The Poisson distribution was introduced by Siméon Denis Poisson in 1837 while studying rare events in judicial statistics. It arises as a limiting case of the binomial distribution when events are rare but opportunities are numerous. Poisson originally introduced this distribution to study rare events, such as wrongful convictions in court cases. Its mathematical simplicity and clear interpretation soon made it a fundamental model for random counts occurring over time or space.

The Poisson distribution models the number of events occurring in a fixed interval of time or space. Its probability mass function, known the observed historical average λ , also known as

"rate of occurrence", is

$$\mathbb{P}(x; \lambda) = \frac{\lambda^x e^{-\lambda}}{x!}, \quad x = 0, 1, 2, \dots, \quad (2.5)$$

Poisson distributions are commonly used to model events that occur independently and sporadically. Typical examples include the number of phone calls received by a call center, the number of typing errors on a page, or the number of decay events detected by a sensor during a fixed time interval.

Example: The number of emails received in one hour, when messages arrive independently at an average rate of $\lambda = 5$ per hour, can be modeled using a Poisson distribution.

Example: The number of cancer patients observed in a hospital over a week, when the average patients happen at a rate of $\lambda = 7$ per week, can also be modeled using a Poisson distribution.

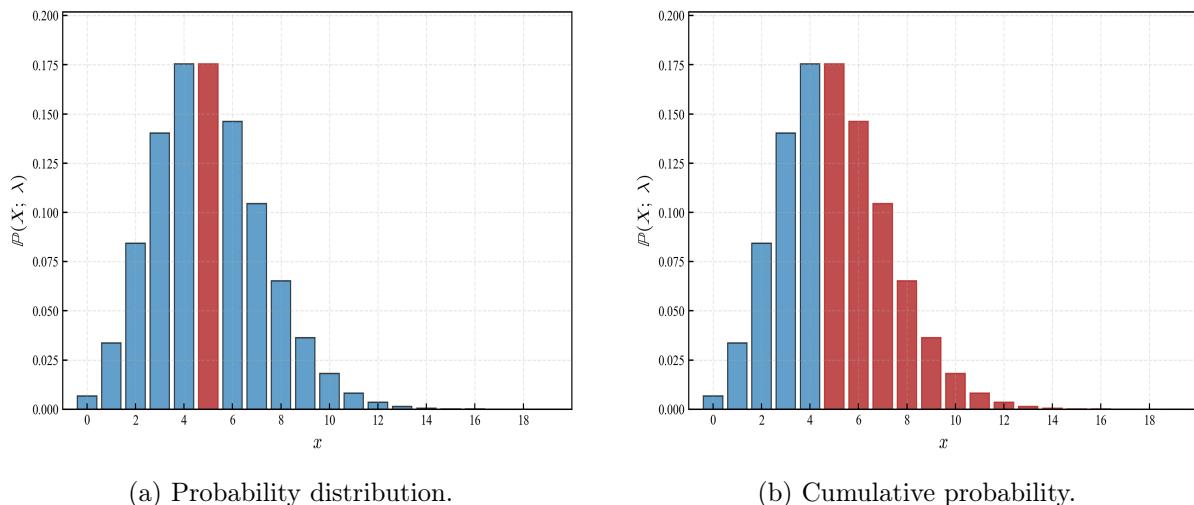


Figure 2.4: Poisson probability distribution

Cumulative probabilities:

So far, we have described probability distributions by assigning probabilities to individual outcomes. While this is natural for discrete models, it is often more informative to consider the probability that a random variable takes a value *up to*, greater or smaller than a given threshold. This leads to the notion of *cumulative probability*.

As a note, it is common notation to use uppercase letters (such as X) to denote random variables, and lowercase letters (such as x) to denote their possible values. For a discrete random variable X , the *cumulative distribution function* (CDF) is defined as

$$F(x) = \mathbb{P}(X \leq x), \quad (2.6)$$

that is, the probability that the outcome of the experiment is strictly smaller than x .

If the possible values of X are $\{x_1, x_2, \dots\}$, the cumulative probability at a point x is obtained by summing the probabilities of all outcomes less than or equal to x :

$$F(x) = \sum_{x_i \leq x} \mathbb{P}(X = x_i). \quad (2.7)$$

The cumulative distribution function provides a global view of the distribution. While the probability mass function tells us how probability is assigned locally to each outcome, the CDF tells us how probability accumulates as we move along the real line.

Several important properties follow immediately from the definition:

- $F(x)$ is non-decreasing.
- $0 \leq F(x) \leq 1$ for all x .
- $\lim_{x \rightarrow -\infty} F(x) = 0$ and $\lim_{x \rightarrow +\infty} F(x) = 1$.

Example. For a fair six-sided die, the probability that the outcome is *at most* 4 is

$$\mathbb{P}(X \leq 4) = \mathbb{P}(1) + \mathbb{P}(2) + \mathbb{P}(3) + \mathbb{P}(4) = \frac{4}{6}.$$

The corresponding cumulative distribution function increases in steps of size $1/6$ at each integer outcome.

Cumulative probabilities play a central role in probability theory because they naturally generalize to the continuous case, where individual outcomes no longer carry positive probability.

2.3 Continuous events

By *continuous* events, in contrast to the discrete case, we mean that the set of possible outcomes is uncountably infinite, typically forming an interval of real numbers. In such cases, individual outcomes have zero probability, and uncertainty is described using probability *densities*. Probabilities are obtained by integrating the density over ranges of values.

When moving from discrete to continuous outcomes, the frequentist intuition that works well for counting events begins to break down. In a discrete setting, probabilities can be interpreted as long-run relative frequencies of individual outcomes. For example, the probability of rolling a 3 with a fair die can be understood as the fraction of times the outcome 3 appears when the die is rolled repeatedly. Each outcome has a positive probability, and frequencies converge to these values as the number of trials grows.

In a continuous setting, this interpretation can no longer be applied directly. If outcomes lie on a continuous interval, such as all real numbers between 0 and 1, the probability of observing any exact value is zero. No matter how many times the experiment is repeated, the relative frequency of obtaining exactly 0.37 will be zero. Same would happen with the probability of measuring a specific temperature in a room, let's say 25.0 degrees. Since there is an infinite, continuous amount of values from 24.999... to 25.000, and from 25.000 to 25.001, the probability of measuring a single value would also be mathematically zero. This does not mean that the outcome is impossible, but rather that probability must now be assigned to *ranges* of values rather than to individual points. We just need a new mathematical object that represents this information.

The concept of a probability *density* is introduced precisely to resolve this issue: densities describe how probability is distributed locally, while actual probabilities are obtained by integrating the density over intervals. In this way, the frequentist idea of long-run relative frequency is preserved, but it applies to intervals of outcomes rather than to single values.

Mathematically, a continuous probability distribution is described by a density function $f(x)$ such that

$$f(x) \geq 0, \quad \int_{-\infty}^{\infty} f(x) dx = 1. \tag{2.8}$$

The probability that a random variable lies in an interval $[a, b]$ is then given by the area under the density curve between a and b .

2.3.1 Gaussian distribution

The Gaussian distribution emerged from the work of Abraham de Moivre in the early 18th century and was later developed systematically by Pierre-Simon Laplace. Its physical interpretation was provided by Carl Friedrich Gauss in "*Theoria Motus Corporum Coelestium*" (1809) [15], in the context of measuring errors of astronomical observations, where repeated measurements of the same quantity produced small deviations around a central value. This interpretation linked probability theory directly to experimental science.

The Gaussian distribution models the accumulation of many small, independent effects. Its central role in probability theory is explained by the central limit theorem, which establishes it as a universal limiting distribution, and that we will cover in Chapter 3.

The probability density function of a Gaussian random variable x with mean μ and variance σ^2 is

$$f(x; \mu, \sigma) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{(x-\mu)^2}{2\sigma^2}\right), \quad x \in \mathbb{R}. \quad (2.9)$$

Gaussian distributions are used to model many natural and social phenomena where values cluster around an average, and it appears incredibly often. Examples include measurement errors, biological traits such as height, and aggregated effects of many small influences acting together. Why so many physical phenomena tend to appear centered around a mean value (μ), with some notion of spread (σ), and converging to a perfect Gaussian bell-shape as the number of observations increase, is still an open question which triggers various philosophical debates.

Example: Measurement errors in physical experiments are often modeled as Gaussian, with $\mu = 0$ representing no systematic bias and σ describing measurement precision.

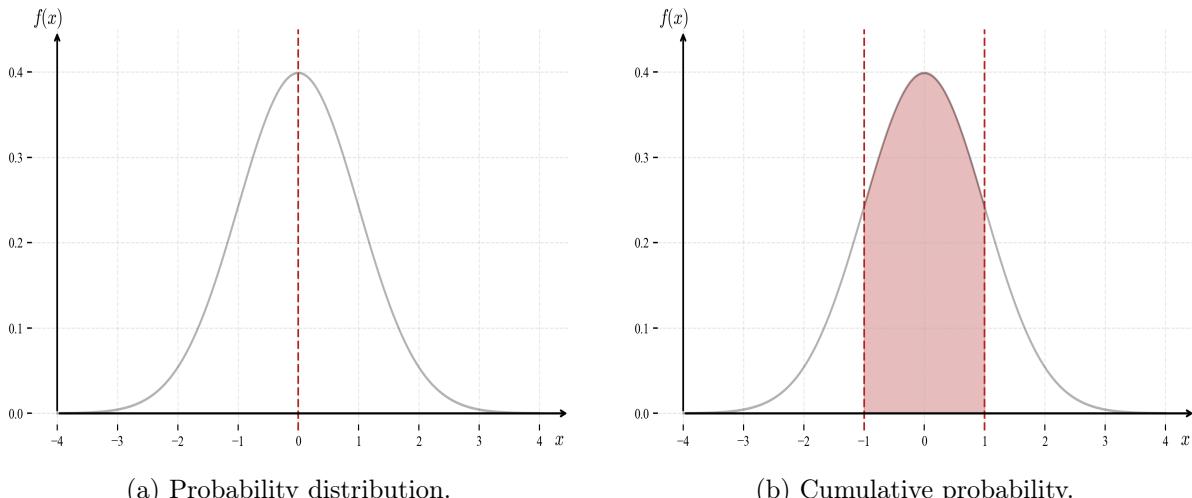


Figure 2.5: Gaussian probability density distribution

2.3.2 Exponential distribution

The exponential distribution arose in the 19th century in the study of waiting times and decay processes, closely connected to Poisson's work on random events and later developments in queueing theory [42, 20]. The exponential distribution emerged naturally from the study of random event timing, particularly in physics and telecommunications. Its mathematical form reflects the assumption that events occur independently and at a constant average rate.

It naturally models the time until the first occurrence of a random event and is characterized by the absence of memory: the future waiting time does not depend on how much time has already elapsed.

The probability density function of an exponential random variable X with rate $\lambda > 0$ is

$$f(x; \lambda) = \lambda e^{-\lambda x}, \quad x \geq 0. \quad (2.10)$$

Exponential models are appropriate for waiting-time phenomena. Examples include the time until a machine fails, the time until the next customer arrives, or the time between successive radioactive decay events.

Example. The time until the next phone call arrives at a call center, assuming calls arrive independently at a constant average rate, is often modeled using an exponential distribution.

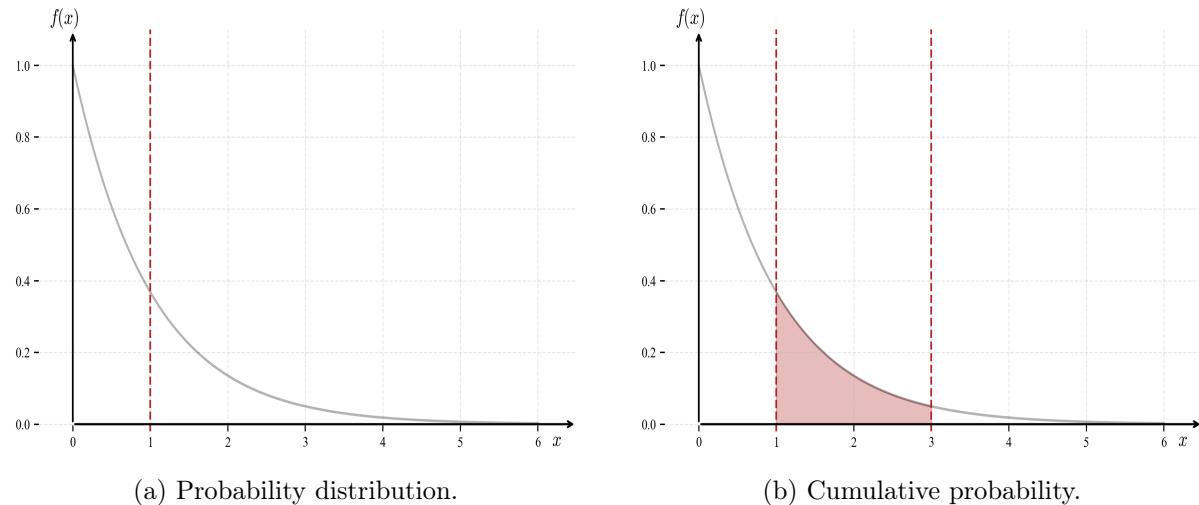


Figure 2.6: Exponential probability density distribution

2.3.3 Continuous uniform distribution

The continuous uniform distribution, also called flat distribution, extends classical symmetry arguments already present in Laplace's *Théorie Analytique des Probabilités* (1812) [16]. It represents complete ignorance about where within a bounded interval an outcome may fall. The continuous uniform distribution formalizes the idea of complete uncertainty over a bounded range. Unlike other distributions, it does not privilege any value within the interval, making it a neutral reference model.

If a random variable x is uniformly distributed on an interval $[a, b]$, its probability density function is

$$f(x; a, b) = \frac{1}{b - a}, \quad a \leq x \leq b. \quad (2.11)$$

Continuous uniform distributions are often used in simulations and random sampling. They arise, for example, when generating random starting points, choosing random times within a fixed interval, or modeling unknown quantities constrained only by upper and lower bounds.

Example: If a random number generator produces values evenly between 0 and 1, the outcome can be modeled as a continuous uniform distribution on $[0, 1]$.

Cumulative probability in the continuous case:

When outcomes are continuous, individual values have zero probability and probability is described using densities rather than masses. Nevertheless, the idea of cumulative probability

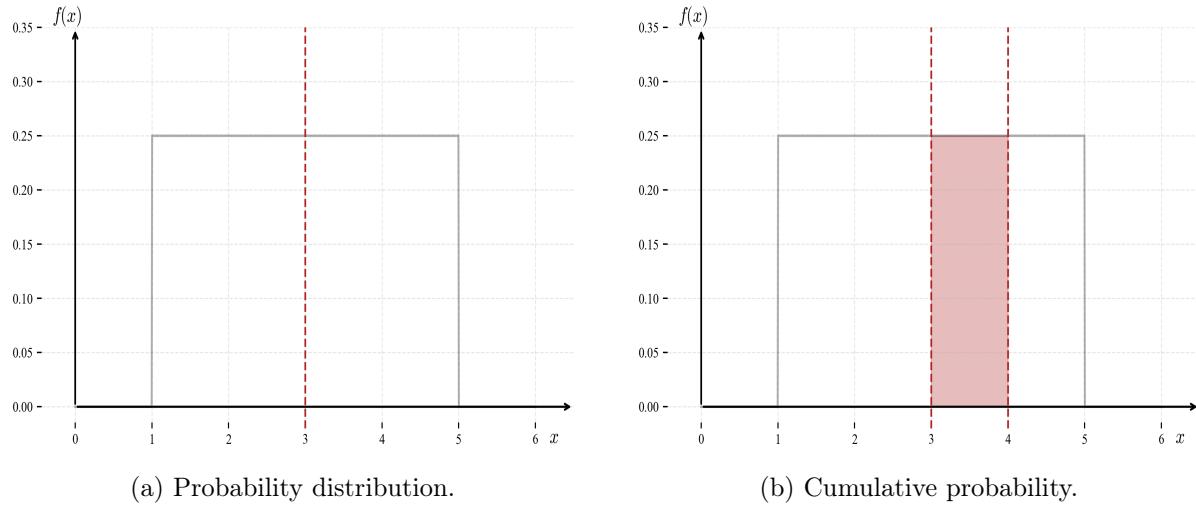


Figure 2.7: Continuous uniform probability density distribution

remains fundamental. As before, to get used to standard notation, we use uppercase letters (such as X) to denote random variables, and lowercase letters (such as x) to denote their possible values.

For a continuous random variable X with probability density function $f(x)$, the cumulative distribution function is defined in exactly the same way:

$$F(x) = \mathbb{P}(X \leq x). \quad (2.12)$$

The difference lies in how this probability is computed. Since probability is distributed continuously, cumulative probability is obtained by integrating the density:

$$F(x) = \int_{-\infty}^x f(t) dt. \quad (2.13)$$

In this setting, the density $f(x)$ does not represent probability itself, but rather the *rate at which probability accumulates*. The probability that X lies in an interval $[a, b]$ is given by

$$\mathbb{P}(a \leq X \leq b) = \int_a^b f(t) dt = F(b) - F(a). \quad (2.14)$$

Thus, while probability mass functions assign probabilities to individual points, probability density functions describe how probability is spread across the real line. In both discrete and continuous cases, the cumulative distribution function provides a unified description of uncertainty and serves as the primary object connecting probability to integration.

2.4 Expected values

Probability distributions describe uncertainty, but to summarize and compare them we often want a small number of representative quantities. The most important of these are the *moments* of a random variable. Moments capture different aspects of a distribution such as its location, spread, and shape.

Throughout this section, we will again denote random variables by uppercase letters, such as X . In the discrete case, probabilities are assigned to individual values via $\mathbb{P}(X = x_i)$, while in

the continuous case probabilities are assigned to intervals and described through a probability density function.

Mean as expected value:

The most fundamental moment is the *expected value*, also called the mean. Naming here may seem misleading, as this mean is not to be confused with the sample mean we discussed in previous chapter. One thing is the mean and variance as *expected values of random variables*, and a different one is as a number that summarizes a sample, which we referred in last chapter as *sample mean*. Informally, the expected value represents the long-run average outcome of a random experiment repeated many times. It answers the question: *where is the distribution centered?*

For a discrete random variable X taking values $\{x_i\}$ with probabilities $\mathbb{P}(X = x_i)$, the expected value is defined as

$$\mathbb{E}[X] = \sum_i x_i \mathbb{P}(X = x_i). \quad (2.15)$$

For a continuous random variable with probability density function $f(x)$, the expected value is defined analogously by replacing the sum with an integral:

$$\mathbb{E}[X] = \int_{-\infty}^{\infty} x f(x) dx. \quad (2.16)$$

The expected value is a *first-moment* quantity: it captures the location of a distribution but provides no information about its variability. A key property of expectation is linearity. For any random variables X_i ,

$$\mathbb{E}\left[\sum_i X_i\right] = \sum_i \mathbb{E}[X_i], \quad (2.17)$$

regardless of whether the variables are independent.

Variance as expected value:

The second moment of central importance is the *variance*, which measures how spread out the distribution is around its mean. Variance is defined as the expected squared deviation from the mean:

$$\text{Var}(X) = \mathbb{E}[(X - \mathbb{E}[X])^2]. \quad (2.18)$$

An equivalent and often more convenient expression for the variance is

$$\text{Var}(X) = \mathbb{E}[X^2] - (\mathbb{E}[X])^2. \quad (2.19)$$

For a discrete random variable, this corresponds to

$$\text{Var}(X) = \sum_i (x_i - \mu)^2 \mathbb{P}(X = x_i), \quad \mu = \mathbb{E}[X], \quad (2.20)$$

while for a continuous random variable it is given by

$$\text{Var}(X) = \int_{-\infty}^{\infty} (x - \mu)^2 f(x) dx. \quad (2.21)$$

More generally, the k -th *moment* of a random variable describes higher-order features of its distribution:

- The *first moment*, referred to as the *mean*, describes central location.

- The *second moment*, referred to as the *variance*, describes spread.
- The *third moment* is related to *skewness*, measuring asymmetry.
- The *fourth moment* is related to *kurtosis*, measuring tail heaviness.

In practice, mean and variance already provide a powerful summary of most distributions. Classical statistical inference—such as confidence intervals, hypothesis tests, and error propagation—relies heavily on estimators of these two quantities and on their sampling distributions.

2.5 Mean and variance of common distributions

We conclude this chapter by collecting the expected value and variance of the probability distributions introduced earlier. These results provide concrete examples of the abstract definitions given in the previous section and will be used repeatedly in later chapters.

Bernoulli distribution:

Let $X \sim \text{Bern}(p)$, with $\mathbb{P}(X = 1) = p$ and $\mathbb{P}(X = 0) = 1 - p$. Then

$$\mathbb{E}[X] = p, \quad (2.22)$$

$$\text{Var}(X) = p(1 - p). \quad (2.23)$$

The mean equals the success probability, while the variance is largest when $p = 1/2$.

Binomial distribution:

Let $X \sim \text{Bin}(n, p)$ represent the number of successes in n independent Bernoulli trials. Then

$$\mathbb{E}[X] = np, \quad (2.24)$$

$$\text{Var}(X) = np(1 - p). \quad (2.25)$$

Both the mean and variance scale linearly with the number of trials.

Poisson distribution:

Let $X \sim \text{Pois}(\lambda)$, where $\lambda > 0$ is the average rate of occurrence. Then

$$\mathbb{E}[X] = \lambda, \quad (2.26)$$

$$\text{Var}(X) = \lambda. \quad (2.27)$$

A defining feature of the Poisson distribution is that its mean and variance coincide.

Discrete uniform distribution:

Let X be uniformly distributed on the set $\{1, 2, \dots, n\}$. Then

$$\mathbb{E}[X] = \frac{n + 1}{2}, \quad (2.28)$$

$$\text{Var}(X) = \frac{n^2 - 1}{12}. \quad (2.29)$$

The mean lies at the center of the interval, while the variance depends only on its width.

Gaussian distribution:

Let $X \sim \mathcal{N}(\mu, \sigma^2)$. Then

$$\mathbb{E}[X] = \mu, \quad (2.30)$$

$$\text{Var}(X) = \sigma^2. \quad (2.31)$$

The parameters μ and σ^2 directly control the location and spread of the distribution.

Exponential distribution:

Let $X \sim \text{Exp}(\lambda)$, with $\lambda > 0$. Then

$$\mathbb{E}[X] = \frac{1}{\lambda}, \quad (2.32)$$

$$\text{Var}(X) = \frac{1}{\lambda^2}. \quad (2.33)$$

Larger values of λ correspond to shorter expected waiting times and reduced variability.

Continuous uniform distribution:

Let $X \sim \text{Unif}(a, b)$. Then

$$\mathbb{E}[X] = \frac{a + b}{2}, \quad (2.34)$$

$$\text{Var}(X) = \frac{(b - a)^2}{12}. \quad (2.35)$$

As in the discrete case, the mean lies at the midpoint of the interval and the variance depends only on its length.

These examples illustrate how mean and variance summarize probability distributions in concrete terms. In later chapters, we will study how these quantities are estimated from data and how their sampling variability affects statistical inference.

Chapter 3

Estimation, variability and confidence

The development of mathematics is a continuous process of abstraction.

— Emmy Noether

In the previous chapters, we described data using summary statistics and introduced probability models to represent uncertainty. In this chapter, we connect these two perspectives. Estimation is the process through which data are used to learn about unknown features of a population, while probability provides the language to quantify how reliable such learning is.

As we discussed already, a crucial distinction must be made between *prediction* and *inference*. Prediction focuses on forecasting future observations, whereas inference aims to draw conclusions about underlying parameters or mechanisms that generate the data. Estimation lies at the heart of inference: it transforms random samples into numerical statements about unknown quantities.

Because data are inherently variable, different samples lead to different estimates. Understanding how estimates behave across repeated samples is therefore essential. The main goal of this chapter is to explain how probability theory allows us to quantify this variability and to construct principled measures of uncertainty such as confidence intervals.

3.1 The Law of Large Numbers

Historically, the Law of Large Numbers was first proved by Jacob Bernoulli in his posthumously published *Ars Conjectandi* (1713). Bernoulli's motivation was not purely mathematical: he sought to justify how stable numerical patterns could emerge from seemingly random individual events. His theorem provided the first rigorous foundation for interpreting probability in terms of long-run relative frequencies and marked a decisive step in connecting abstract probability with empirical observation [13, 14].

The Law of Large Numbers formalizes the intuitive idea that averages stabilize when more data are collected. While individual observations may be highly variable, their average becomes increasingly predictable as the sample size grows.

Historically, this result was first articulated by Jacob Bernoulli in the early eighteenth century. It provided the first rigorous justification for interpreting probability as long-run relative frequency and established a bridge between theoretical probability and empirical observation.

Let X_1, X_2, \dots be independent and identically distributed random variables with expected value μ . The Law of Large Numbers states that the sample mean

$$\bar{X}_n = \frac{1}{n} \sum_{i=1}^n X_i \tag{3.1}$$

converges to μ as the sample size n increases.

Example. When repeatedly tossing a fair coin, individual outcomes are unpredictable, but the proportion of heads approaches $1/2$ as the number of tosses grows.

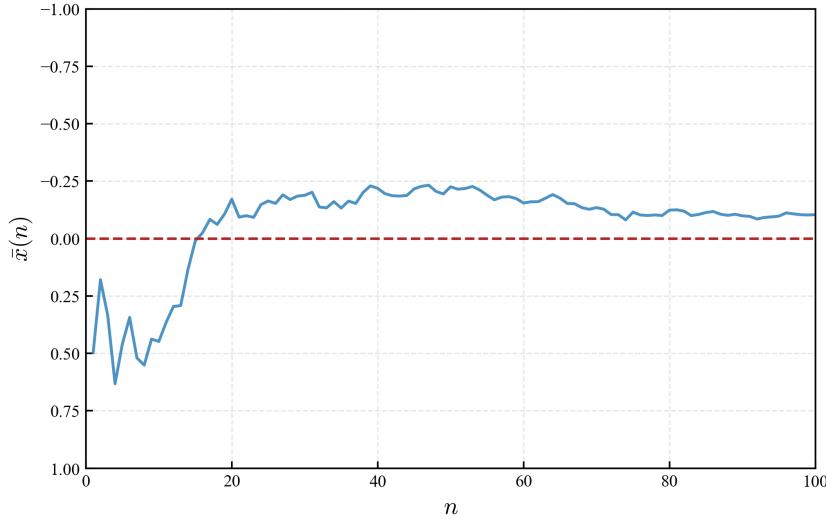


Figure 3.1: The Law of Large Numbers.

3.2 The Central Limit Theorem

The origins of the Central Limit Theorem can be traced to the work of Abraham de Moivre in the early eighteenth century, who discovered that binomial distributions with large numbers of trials could be approximated by a normal curve. This insight was later generalized by Pierre-Simon Laplace, who showed that the normal distribution arises broadly from the aggregation of many independent random effects. The modern formulation of the theorem, with precise conditions and convergence statements, was completed only in the late nineteenth and early twentieth centuries [16, 24].

While the Law of Large Numbers explains where averages converge, it does not describe how they fluctuate around their limiting value. The Central Limit Theorem answers this question by describing the distribution of fluctuations.

One of the most remarkable results in probability theory, the Central Limit Theorem explains why the Gaussian distribution appears so frequently in statistical practice. It shows that many different random processes give rise to approximately normal behavior when aggregated.

Let X_1, \dots, X_n be independent and identically distributed with mean μ and variance σ^2 . The Central Limit Theorem states that the standardized sample mean

$$\frac{\bar{X}_n - \mu}{\sigma/\sqrt{n}} \tag{3.2}$$

approaches a standard normal distribution as n becomes large.

Example. Even if individual measurements are skewed, the distribution of their average over many observations is often approximately Gaussian.

3.3 Bias, variance and Mean Squared Error

The systematic study of estimators and their properties developed alongside the rise of mathematical statistics in the late nineteenth and early twentieth centuries. Early statisticians recognized that good estimation procedures must balance systematic error and random variability. This insight led to the decomposition of mean squared error into variance and squared bias, a framework that remains central in both classical statistics and modern machine learning [24, 3].

An estimator is a rule that assigns a numerical value to an unknown parameter based on observed data. Because estimators depend on random samples, they are themselves random variables.

The *bias* of an estimator measures systematic error: it quantifies whether the estimator tends to overestimate or underestimate the true parameter. The *variance* measures how much the estimator fluctuates from sample to sample.

If $\hat{\theta}$ is an estimator of a parameter θ , its bias is defined as

$$\text{Bias}(\hat{\theta}) = \mathbb{E}[\hat{\theta}] - \theta, \quad (3.3)$$

and its variance is

$$\text{Var}(\hat{\theta}). \quad (3.4)$$

A common way to combine these two sources of error is the mean squared error (MSE):

$$\text{MSE}(\hat{\theta}) = \mathbb{E}[(\hat{\theta} - \theta)^2] = \text{Var}(\hat{\theta}) + \text{Bias}(\hat{\theta})^2. \quad (3.5)$$

Example: The sample mean and variance

Let X_1, X_2, \dots, X_n be independent and identically distributed random variables with

$$\mathbb{E}[X_i] = \mu, \quad \text{Var}(X_i) = \sigma^2.$$

The *sample mean*

$$\bar{X} = \frac{1}{n} \sum_{i=1}^n X_i$$

is an estimator of the population mean μ . Taking expectations,

$$\mathbb{E}[\bar{X}] = \frac{1}{n} \sum_{i=1}^n \mathbb{E}[X_i] = \mu,$$

so the sample mean is an *unbiased* estimator of μ . Its variance is

$$\text{Var}(\bar{X}) = \frac{\sigma^2}{n},$$

which decreases as the sample size increases, explaining why larger samples yield more precise estimates.

By contrast, consider the *sample variance*

$$s^2 = \frac{1}{n-1} \sum_{i=1}^n (X_i - \bar{X})^2,$$

which estimates the population variance σ^2 . The factor $n-1$ in the denominator is chosen so that

$$\mathbb{E}[s^2] = \sigma^2,$$

making s^2 an unbiased estimator. If instead the denominator n were used, the resulting estimator would be biased downward. This correction illustrates how bias and variance depend on the precise form of an estimator.

3.4 Confidence intervals and critical regions

Confidence intervals emerged as a practical response to the limitations of point estimation. Rather than asking for a single best value, statisticians sought procedures that quantify uncertainty in a repeatable and operational way. The concept was formalized in the early twentieth century as part of the frequentist framework, emphasizing long-run coverage properties under repeated sampling. This interpretation remains foundational in applied statistics and experimental science [3, 4].

Point estimates summarize data with a single number, but they do not convey uncertainty. Confidence intervals address this limitation by providing a range of plausible values for an unknown parameter. A confidence interval is constructed so that, in repeated sampling, it contains the true parameter a fixed proportion of the time. This proportion is called the confidence level and is typically expressed as a percentage.

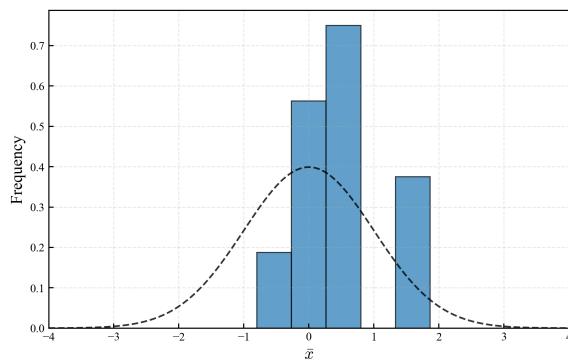
For a population with mean μ and known variance σ^2 , an approximate $100(1-\alpha)\%$ confidence interval for μ is given by

$$\bar{X}_n \pm z_{\alpha/2} \frac{\sigma}{\sqrt{n}}, \quad (3.6)$$

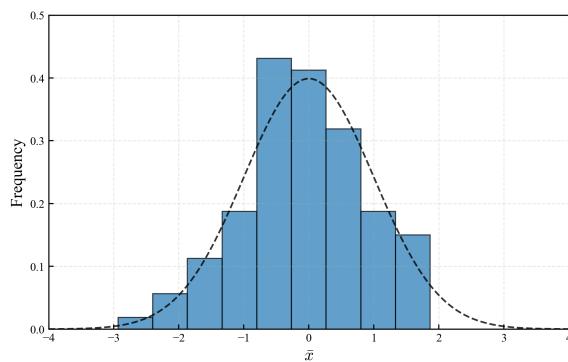
where $z_{\alpha/2}$ is a quantile of the standard normal distribution.

Confidence intervals are closely related to hypothesis testing. The set of parameter values not rejected by a statistical test forms a confidence region. This duality provides a unified framework for estimation and decision-making.

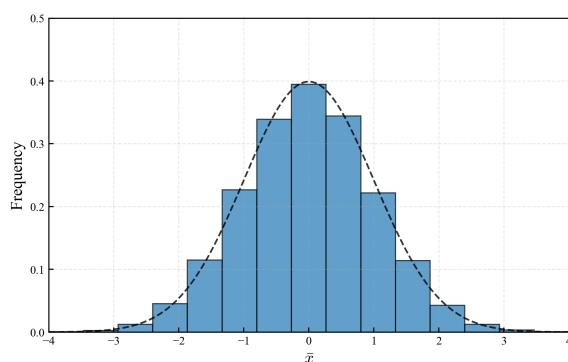
Example. A 95% confidence interval for the mean expresses the range of values that are consistent with the observed data under repeated sampling.



(a) The Central Limit Theorem 1



(b) The Central Limit Theorem 2



(c) The Central Limit Theorem 3

Figure 3.2: The Central Limit Theorem

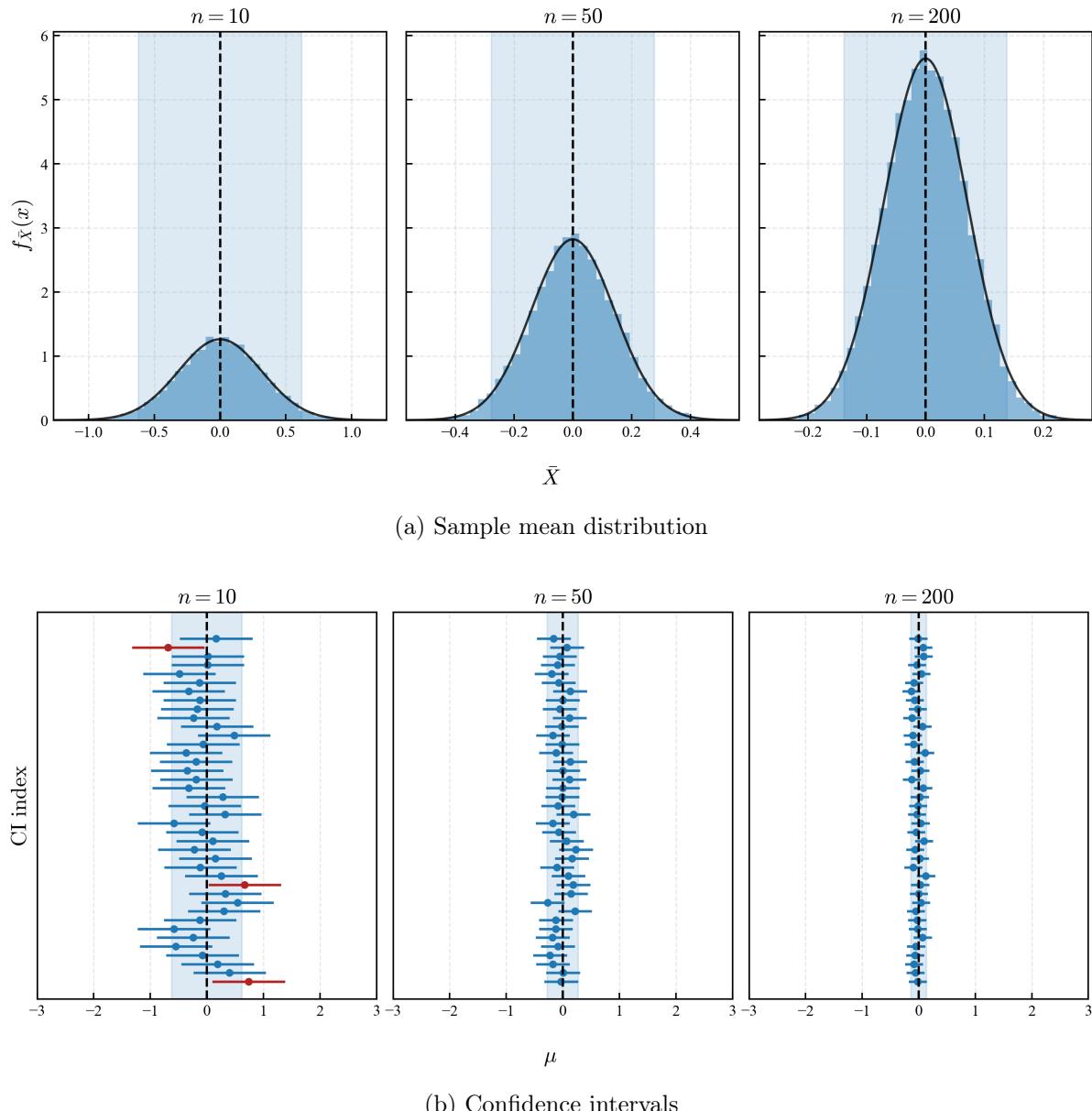


Figure 3.3: Confidence intervals and critical regions

Chapter 4

Introduction to hypothesis testing

The object of statistical science is the reduction of data to relevant information.

— Ronald A. Fisher

The term *hypothesis testing* lies on top of the two pillars we have mentioned in previous chapters. From statistical analysis, as discussed in Chapter 1, we will use sampling, estimators, and graphical summaries to describe data. From probability theory, as discussed in Chapter 2, we will rely on probability distributions and expected values to model random variation and uncertainty. Throughout this chapter, we will mostly work in a *parametric* setting, where data is assumed to follow a simple, smooth, and well-behaved distribution—most often the Gaussian distribution. Under these assumptions, and supported by the Law of Large Numbers and the Central Limit Theorem, estimators such as the sample mean and variance provide reliable information about the true population parameters. Confidence intervals and critical regions, introduced in Chapter 3, formalize this idea of reliability.

Within this framework, we introduce the notion of *test statistic*, also referred to as *statistic*, or *statistic test*: a numerical quantity computed from data, designed to measure how close our observations are to what we would expect under a given hypothesis. Statistical tests are built by comparing such quantities—such *statistics*—to their behavior under an assumed model. In modern hypothesis testing, this comparison is often summarized through the *p-value*, which quantifies how unusual the observed data would be if the null hypothesis were true. We will discuss such topics in detail in the throughout the chapter.

Let us begin with a brief historical note, often skipped. The ideas behind hypothesis testing did not emerge all at once. While the general notion of testing expectations against observations is very old, the mathematical tools required for modern statistical testing are relatively recent. As we have seen, systematic use of estimators and probability models developed gradually during the 19th and early 20th centuries, and the axiomatic foundations of probability were only formalized in 1933 with Kolmogorov's work [21].

The first statistical tests were developed in the early 20th century by researchers such as Pearson and Fisher, among many others, and were originally designed to measure discrepancies between data and theoretical expectations, not to support automatic accept–reject decisions. The formal structure of hypothesis testing, including the very idea of null and alternative hypotheses, error rates, and decision rules, was later introduced by Jerzy Neyman and Egon Pearson, son of Karl Pearson. Because these ideas developed in stages, their interpretation requires some care. Throughout this chapter, we will emphasize both the practical use of statistical tests and the assumptions on which they are based.

It is worth noting, already at this stage, that the interpretation of statistical tests is not purely technical, but also deeply philosophical. Fisher's original conception of significance testing

treated the p -value as a flexible measure of evidence against a null hypothesis, while the Neyman-Pearson framework emphasized long-run error control and decision rules [43]. These distinct viewpoints connect more broadly to 20th century debates about scientific inference, prediction, and falsification, notably in the work of mathematicians and philosophers such as Reichenbach, Popper, and, more recently, de Finetti and Mayo.

All these philosophical issues provide important context for understanding both the strengths and the limitations of modern hypothesis testing, and will be discussed at the end of the chapter, to motivate and introduce the very idea of Bayesian probability.

4.1 Prediction vs inference revisited

As we saw in previous chapters, when formulating hypotheses about natural phenomena, it is important to recall the distinction between population and sampling. On the one hand, we consider an idealized and generally inaccessible population, characterized by true but unknown quantities such as the mean and variance (μ , σ^2). Mathematical prediction, in this context, refers to the computation of expected values—also known as statistical moments—defined for a random variable together with its probability distribution. For a review on random variables and probability distributions, please go back to Chapter 2.

Given a random variable, expected values (or moments) can be computed directly from its probability distribution.

Population mean for a discrete random variable x and possible outcomes $\{x_i\}$:

$$\mu = \mathbb{E}[x] = \sum_i x_i \mathbb{P}(x = x_i) \quad (4.1)$$

Population variance for a discrete random variable x and possible outcomes $\{x_i\}$:

$$\sigma^2 = \mathbb{E}[(x - \mu)^2] = \sum_i (x_i - \mu)^2 \mathbb{P}(x = x_i) \quad (4.2)$$

Population mean for a continuous random variable x with density $f(x)$:

$$\mu = \mathbb{E}[x] = \int_{-\infty}^{\infty} x f(x) dx \quad (4.3)$$

Population variance for a continuous random variable x with density $f(x)$:

$$\sigma^2 = \mathbb{E}[(x - \mu)^2] = \int_{-\infty}^{\infty} (x - \mu)^2 f(x) dx \quad (4.4)$$

In any of these cases, we compute cumulative probabilities as the sum of all cases above / below a certain value, or in a given range. In the case of continuous random variables, following density distributions, this sum is computed as the definite integral of the distribution.

Hypotheses are therefore always formulated in terms of mathematical predictions about the *population-level parameters*. For example, under Newtonian mechanics, a hypothesis may consist of Newton's second law, from which predictions can be made about the position of a falling object as a function of time. In biology, a hypothesis may concern the effect of a gene on a disease or on stress response, formulated in terms of expected expression levels or count. In epidemiology or medical sciences, about the relationship between smoking prevalence and lung cancer risk. In all such cases, hypotheses concern population properties, while access to them is obtained only through finite samples of observations, collectively referred to as *data*. Out of that data, we compute estimators such as the sample mean and sample variance (\bar{x} , s^2). For a review on describing populations and statistical estimators, please go back to Chapter 1.

Observed sample mean for a sample $\mathcal{X} = \{x_1, x_2, \dots, x_n\}$

$$\bar{x} = \frac{1}{n} \sum_{i=1}^n x_i \quad (4.5)$$

Observed sample variance for the same sample

$$s^2 = \frac{1}{n-1} \sum_{i=1}^n (x_i - \bar{x})^2 \quad (4.6)$$

Hypothesis testing formalizes this comparison between population-level predictions and sample-based estimates by quantifying how compatible the observed data are with a hypothesized model.

4.2 General approach to hypothesis testing

When dealing with hypotheses, predictions, experiments, and data, there exist many approaches and formulations, as many as instruments, scales, and fields of study. These approaches change from one field to another, and they also change over time. Our very ideas of hypothesis, prediction, measurement, and scientific law have evolved historically. Nowadays, when people refer to *hypothesis testing*, they usually mean a very specific approach: an almost algorithmic set of rules applied broadly to inference and data analysis problems. In this chapter, we will define such approach as the *modern* or *general* approach to hypothesis testing. It assumes basic notions of probability theory, randomness, and probability distributions, together with statistical concepts such as estimators and sample-based descriptions. The core ideas of statistical tests, *p*-values, and significance that we discuss here are relatively recent, tracing back to the work of Pearson, Fisher, and Neyman in the early 20th century [43].

The general approach to hypothesis testing can be summarized in the following steps:

- **Formulate hypotheses.** One specifies a *null hypothesis* H_0 , representing the expected or reference case, and an *alternative hypothesis* H_1 , representing a departure from H_0 that would be considered scientifically relevant or surprising.
- **Experiment, measurement, observation.** Any process—regardless of instrumentation or field of study—that produces measurements or observations, resulting in one or more samples of data.
- **Compute a statistic or test statistic.** From the observed data, one computes an informative quantity, which may be a simple estimator such as the sample mean or variance, or a more elaborate statistic designed to quantify how far the observed data deviate from what is expected under H_0 .
- **Compute a *p*-value.** The *p*-value is the probability that, assuming the null hypothesis and its associated population parameters are true, one would obtain a value of the statistic at least as extreme as the one observed.
- **Interpret the result.** The *p*-value is compared to a chosen significance level, leading to a decision or conclusion, commonly phrased as rejecting or not rejecting the null hypothesis. This is already a subtle topic with open philosophical questions, as we will see.

A few remarks are in order regarding this general roadmap. A statistic may be as simple as an estimator, such as the sample mean, or a more abstract quantity derived from the data. Fisher originally introduced the *p*-value as a continuous measure of evidence against the null hypothesis,

rather than as a strict decision rule. The widespread practice of fixed significance thresholds and accept–reject decisions reflects a later synthesis of Fisher’s ideas with the Neyman-Pearson framework. As a result, the modern approach to hypothesis testing combines elements of both traditions, a point we will return to later in this chapter. *Warning.* A p -value *does not* measure the probability that a hypothesis is true or false, but rather how compatible the observed data are with the null hypothesis under the assumed model.

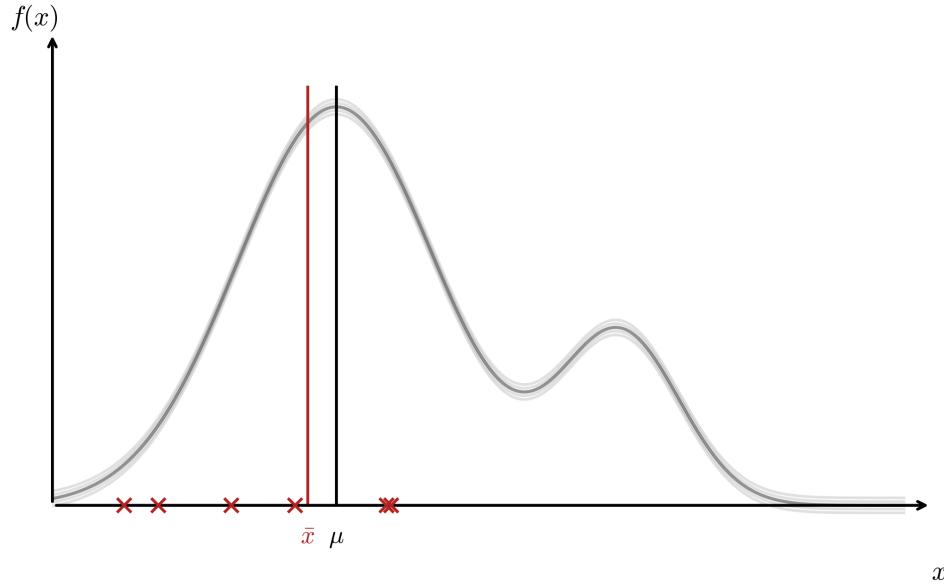


Figure 4.1: Representation of the *true* population mean μ , in black, and the observed *sample* mean \bar{x} . The true mean is an ideal and unaccessible quantity, while the sample mean can be computed as an estimator of the finite sample.

4.3 Statistical tests: common examples

4.3.1 One-sample t -test: compare sample mean with hypothesized value

The one-sample t -test is arguably the simplest example of a statistical test we will discuss. It was developed in 1908 by William S. Gosset, a statistician working at the Guinness brewery in Dublin, who was concerned with accurately estimating the variability of the sample mean when the population variance is unknown, particularly for small sample sizes. Due to restrictions imposed by his employer, Gosset published his work in the *Biometrika* journal under the pseudonym *Student*. For this reason, the test is still widely known as the *Student’s t-test* [44].

The test begins by formulating a null hypothesis about the true population mean *prior to any data collection*. Typically, the null hypothesis is written as

$$H_0 : \mu = \mu_0,$$

where μ denotes the true (and generally inaccessible) population mean, and μ_0 is a hypothesized reference value. As emphasized in Chapter 2, such population-level quantities can be predicted mathematically through expected values, or estimated empirically from observed data.

We then collect a sample of observations

$$\mathcal{X} = \{x_1, x_2, \dots, x_n\},$$

from which we compute the sample mean \bar{x} as an estimator of μ , and the sample standard deviation s as an estimator of the unknown population standard deviation σ .

Combining these elements, we define the one-sample t -statistic as

$$t = \frac{\bar{x} - \mu_0}{s/\sqrt{n}}. \quad (4.7)$$

This statistic quantifies how far the observed sample mean deviates from the hypothesized value, relative to the estimated variability of the data. In particular, as $\bar{x} \rightarrow \mu_0$, we have $t \rightarrow 0$.

Because \bar{x} and s depend on random samples, the statistic t itself is a *real-valued random variable*, and it will follow *some* distribution. Under the null hypothesis H_0 , its probability distribution is given by the *Student's t-distribution*,

$$f(t; \nu) = \frac{\Gamma(\frac{\nu+1}{2})}{\sqrt{\pi\nu}\Gamma(\frac{\nu}{2})} \left(1 + \frac{t^2}{\nu}\right)^{-(\nu+1)/2}, \quad (4.8)$$

where $\nu = n - 1$ denotes the number of *degrees of freedom*. It can be demonstrated that as $\nu \rightarrow \infty$, the t -distribution converges to the standard normal distribution.

Once the distribution of the test statistic is known, we compute the p -value. Following Fisher's original definition, the p -value is the probability of obtaining a value of the statistic at least as extreme as the one observed, assuming that the null hypothesis H_0 is true.

For a one-sided test, this probability is given by

$$p_{\text{one-sided}} = \mathbb{P}(t \geq t_{\text{obs}}) = \int_{t_{\text{obs}}}^{\infty} f(t; \nu) dt,$$

while for a two-sided test,

$$p_{\text{two-sided}} = \mathbb{P}(|t| \geq |t_{\text{obs}}|) = 2 \int_{|t_{\text{obs}}|}^{\infty} f(t; \nu) dt.$$

Example. For a sample of size $n = 10$, with observed mean $\bar{x} = 5.2$, sample standard deviation $s = 1.0$, and hypothesized value $\mu_0 = 5$, the observed statistic is

$$t_{\text{obs}} = \frac{5.2 - 5}{1/\sqrt{10}} \approx 0.63.$$

With $\nu = 9$ degrees of freedom, the corresponding two-sided p -value is approximately $p \approx 0.54$.

4.3.2 Two-sample t -test: compare sample means of two independent groups

The two-sample t -test extends the ideas of the one-sample case to the comparison of two independent samples,

$$\mathcal{X}_1 = \{x_{1,1}, \dots, x_{1,n_1}\}, \quad \mathcal{X}_2 = \{x_{2,1}, \dots, x_{2,n_2}\}.$$

The null hypothesis now concerns the equality of the two population means,

$$H_0 : \mu_1 = \mu_2,$$

where μ_1 and μ_2 denote the true means of the populations from which the samples are drawn.

From the observed data, we compute the sample means \bar{x}_1 , \bar{x}_2 and sample variances s_1^2 , s_2^2 , which serve as estimators of the corresponding population quantities.

A commonly used test statistic for this problem is given by

$$t = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}. \quad (4.9)$$

This statistic measures the difference between the two sample means relative to the estimated standard error of that difference. As $\bar{x}_1 \rightarrow \bar{x}_2$, we again have $t \rightarrow 0$.

This formulation corresponds to *Welch's two-sample t-test*, which does not assume equal population variances. Under the null hypothesis, the statistic approximately follows a Student's *t*-distribution, with degrees of freedom given by the Welch–Satterthwaite approximation. As in the one-sample case, the *p*-value is obtained by integrating the appropriate tail(s) of the *t*-distribution [45].

An alternative formulation is the two-sample *t*-test with *pooled variance*, which additionally assumes that the two populations have the same variance, $\sigma_1^2 = \sigma_2^2$. Under this assumption, the sample variances s_1^2 and s_2^2 are combined into a single pooled estimator of the common variance, leading to a simplified standard error and a Student's *t*-distribution with $\nu = n_1 + n_2 - 2$ degrees of freedom. While this test is exact under normality and equal variances, it is more sensitive to heteroscedasticity than Welch's test and is therefore less robust when the equality of variances is in doubt.

4.3.3 Fisher's *F*-test: compare variances of two independent groups

Fisher's variance-ratio test, commonly known as the *F*-test, was introduced in the 1920s and formally developed in Fisher's foundational works "*Statistical Methods for Research Workers*" (1925) and "*The Design of Experiments*" (1935). Fisher's contributions to statistics, experimental design, and mathematical modelling are widely regarded as, by far, among the most influential of the 20th century [46, 47, 48].

The *F*-test begins by formulating a null hypothesis about the equality of population variances *prior to any data collection*. In its simplest form, the null hypothesis is

$$H_0 : \sigma_1^2 = \sigma_2^2,$$

where σ_1^2 and σ_2^2 denote the true (and generally inaccessible) variances of the two populations under study. As in previous examples, these population-level quantities may be hypothesized based on prior knowledge or theoretical considerations, as discussed in Chapter 2.

We then collect two independent samples

$$\mathcal{X}_1 = \{x_{1,1}, \dots, x_{1,n_1}\}, \quad \mathcal{X}_2 = \{x_{2,1}, \dots, x_{2,n_2}\},$$

from which we compute the sample variances s_1^2 and s_2^2 , serving as estimators of σ_1^2 and σ_2^2 , respectively. The Fisher *F*-statistic is defined as the ratio

$$F = \frac{s_1^2}{s_2^2}. \quad (4.10)$$

By construction, when the sample variances are similar, the statistic remains close to one, and in the ideal case $s_1^2 \rightarrow s_2^2$, we have $F \rightarrow 1$. As in earlier examples, the test statistic is designed so that, under the null hypothesis, it takes a simple and characteristic value.

Unlike the *t*-test, where the null hypothesis appears explicitly as a parameter in the definition of the statistic, the *F*-statistic is defined purely as a ratio of estimators. Historically, this reflects

Fisher's focus on sampling distributions rather than on explicit parameter-based hypotheses. The null hypothesis is encoded implicitly through the condition under which the ratio of sample variances follows a specific probability distribution.

Because the statistic F is computed from random samples, it is itself a real-valued random variable. Under the null hypothesis $H_0 : \sigma_1^2 = \sigma_2^2$, its distribution is given by Fisher's *F-distribution*,

$$f(F; \nu_1, \nu_2) = \frac{1}{B\left(\frac{\nu_1}{2}, \frac{\nu_2}{2}\right)} \left(\frac{\nu_1}{\nu_2}\right)^{\nu_1/2} F^{\nu_1/2-1} \left(1 + \frac{\nu_1}{\nu_2}F\right)^{-(\nu_1+\nu_2)/2}, \quad (4.11)$$

where $\nu_1 = n_1 - 1$ and $\nu_2 = n_2 - 1$ denote the degrees of freedom. Some texts denote the distribution by F_{ν_1, ν_2} ; here we reserve F for the statistic itself and $f(F; \nu_1, \nu_2)$ for its probability density. As both degrees of freedom increase, the distribution becomes increasingly concentrated around $F = 1$, and the logarithm of F is approximately normally distributed.

Once the sampling distribution is specified, the *p*-value is computed by integrating the appropriate tail of the *F*-distribution. For a one-sided test,

$$p_{\text{one-sided}} = \mathbb{P}(F \geq F_{\text{obs}}) = \int_{F_{\text{obs}}}^{\infty} f(F; \nu_1, \nu_2) dF.$$

Because the *F*-distribution is asymmetric, two-sided *p*-values are defined by doubling the smaller tail probability,

$$p_{\text{two-sided}} = 2 \min \left\{ \int_0^{F_{\text{obs}}} f(F; \nu_1, \nu_2) dF, \int_{F_{\text{obs}}}^{\infty} f(F; \nu_1, \nu_2) dF \right\}.$$

Example. If $n_1 = n_2 = 10$, with sample variances $s_1^2 = 4$ and $s_2^2 = 2$, then

$$F_{\text{obs}} = 2, \quad \nu_1 = \nu_2 = 9,$$

yielding a one-sided *p*-value of approximately $p \approx 0.12$.

Remark (Fisher's exact test).

It is worth noting that not all of Fisher's contributions to hypothesis testing rely on continuous distributions or asymptotic arguments. In situations involving small samples and categorical data—most notably 2×2 contingency tables—Fisher introduced what is now known as *Fisher's exact test*. Rather than comparing estimators such as means or variances, this test is based on the exact sampling distribution of cell counts under a fixed-margins assumption, which follows a hypergeometric distribution. As in the variance-ratio test, the null hypothesis is encoded through the conditions under which the observed statistic has a known distribution. We will return to this test later when discussing inference for categorical data and contingency tables.

4.3.4 Fisher's ANOVA: compare variability across multiple groups

Fisher's analysis of variance (ANOVA) generalizes the variance-ratio *F*-test to more than two groups. Developed in the 1920s in the context of experimental design, ANOVA addresses the question of whether observed differences between several group means can plausibly be attributed to random variation alone [47].

In essence, ANOVA compares the variability between group means to the variability within groups.

Consider k independent samples

$$\mathcal{X}_1, \mathcal{X}_2, \dots, \mathcal{X}_k,$$

with sizes n_1, n_2, \dots, n_k , sample means $\bar{x}_1, \bar{x}_2, \dots, \bar{x}_k$, and overall mean \bar{x} . The null hypothesis is

$$H_0 : \mu_1 = \mu_2 = \dots = \mu_k,$$

stating that all groups share the same true population mean.

The ANOVA F -statistic is defined as

$$F = \frac{s_{\text{between}}^2}{s_{\text{within}}^2}, \quad (4.12)$$

where s_{between}^2 and s_{within}^2 represent the variation between samples, and within samples, and are computed as

$$\begin{aligned} s_{\text{between}}^2 &= \frac{1}{k-1} \sum_{i=1}^k n_i (\bar{x}_i - \bar{x})^2, \\ s_{\text{within}}^2 &= \frac{1}{N-k} \sum_{i=1}^k \sum_{j=1}^{n_i} (x_{ij} - \bar{x}_i)^2, \end{aligned}$$

and $N = \sum_{i=1}^k n_i$. When the null hypothesis is true and group means are similar, the ratio remains close to one.

Under H_0 , the ANOVA F -statistic follows a Fisher F -distribution with degrees of freedom $\nu_1 = k-1$ and $\nu_2 = N-k$. The corresponding p -value is obtained by integrating the right tail of this distribution, exactly as in the two-sample F -test.

4.3.5 Pearson's χ^2 test: goodness-of-fit and tests of independence

The chi-square test was introduced by Karl Pearson in 1900 as part of his work on goodness-of-fit and contingency tables [49]. Pearson's original formulation was oriented toward measuring discrepancy between observed and expected frequencies, rather than toward formal decision-based hypothesis testing. Given observed counts $\{O_1, O_2, \dots, O_k\}$ and expected counts $\{E_1, E_2, \dots, E_k\}$, the χ^2 -statistic

$$\chi^2 = \sum_{i=1}^k \frac{(O_i - E_i)^2}{E_i} \quad (4.13)$$

was conceived as a numerical measure of lack of agreement between data and model, with larger values indicating poorer fit.¹

As in the previous examples, the χ^2 -statistic is computed from random data, and repeating the experiment would generally lead to different observed counts and hence a different value of χ^2 . This means that χ^2 is itself a real-valued random variable. Under suitable conditions and sufficiently large samples, it follows a probability distribution known as the Pearson χ^2 -distribution,

$$f(\chi^2; \nu) = \frac{(\chi^2)^{\nu/2-1} e^{-\chi^2/2}}{2^{\nu/2} \Gamma(\nu/2)}, \quad (4.14)$$

defined for $\chi^2 > 0$.

Unlike the t -test, where the degrees of freedom are always $n-1$, the degrees of freedom ν of the χ^2 -test depend on the structure of the data and on how many parameters are estimated under the null hypothesis. In particular:

¹Pearson's original formulation predates the modern null/alternative hypothesis framework and the notion of Type I and Type II errors.

- For a goodness-of-fit test with k categories,

$$\nu = k - 1 - p,$$

where p is the number of parameters estimated from the data.

- For a test of independence in an $r \times c$ contingency table,

$$\nu = (r - 1)(c - 1).$$

In the modern framework, the chi-square test is formulated with an explicit null hypothesis and a p -value. One specifies a null hypothesis H_0 describing the expected distribution or independence structure, derives the asymptotic distribution $\chi^2 \sim \chi_\nu^2$ under H_0 , and computes the p -value as the right-tail probability

$$p = \mathbb{P}(\chi^2 \geq \chi_{\text{obs}}^2) = \int_{\chi_{\text{obs}}^2}^{\infty} f(\chi^2; \nu) d\chi^2.$$

A deeper theoretical connection emerges through likelihood-based testing. Pearson's χ^2 -statistic is asymptotically equivalent to the likelihood-ratio statistic $-2 \log \Lambda$, a result formalized by Wilks in the 1930s. Together with Wald and score tests, this establishes a unifying asymptotic framework for hypothesis testing in parametric models.

Two remarks are in order. First, the validity of the Pearson χ^2 -test relies on large-sample approximations: expected counts should not be too small, and the approximation improves as sample size increases. When these conditions fail—most notably in small samples or sparse contingency tables—exact procedures such as Fisher's exact test provide a more reliable alternative. Second, the appearance of the chi-square distribution in this context is not accidental. Together with the Wald and score (Lagrange multiplier) tests, the likelihood-ratio test forms a triad of asymptotically equivalent procedures. Although these tests differ in construction, all converge to the same χ^2 distribution under the null hypothesis in large samples, providing a unifying framework for parametric inference.

A remark is in order regarding sidedness. Unlike tests such as the t -test, where deviations in either direction from the null hypothesis are meaningful, the χ^2 -statistic is nonnegative by construction and measures the overall discrepancy between observed and expected frequencies. Small values of χ^2 indicate unusually good agreement with the model, whereas large values indicate poor fit. Consequently, evidence against the null hypothesis arises only through large values of the statistic, and hypothesis testing with the χ^2 -distribution is inherently one-sided. While it is mathematically possible to define a two-sided p -value by symmetrizing tail probabilities, such constructions are nonstandard and rarely meaningful in practice, as unusually small values of χ^2 do not correspond to a distinct or interpretable alternative hypothesis.

4.3.6 The Wald test: asymptotic behavior

The Wald test was developed by Abraham Wald in the 1930s as part of a general asymptotic theory of hypothesis testing for parametric models with large samples [50]. Its purpose is to test hypotheses about finite-dimensional parameters using large-sample approximations. Unlike classical tests tailored to specific settings, the Wald test provides a general framework applicable to linear models, generalized linear models, and maximum likelihood estimation.

Conceptually, the Wald test generalizes classical parametric tests such as the t - and F -tests by formulating hypotheses directly in terms of model parameters, and by relying on the asymptotic normality of estimators. In this sense, it unifies earlier procedures within a common large-sample theory.

Let $\hat{\theta}$ be an estimator of a parameter θ . The Wald statistic is defined as

$$W = (\hat{\theta} - \theta_0)^\top \widehat{\text{Var}}(\hat{\theta})^{-1} (\hat{\theta} - \theta_0).$$

Under the null hypothesis and suitable regularity conditions,

$$W \xrightarrow{d} \chi_p^2,$$

where p is the number of tested constraints. Corresponding p -values are obtained from the upper tail of the chi-square distribution.

Example (one-dimensional Wald test). Consider the case $p = 1$, where θ is a scalar parameter and $\hat{\theta}$ is an estimator that is asymptotically normal,

$$\hat{\theta} \stackrel{\sim}{\sim} \mathcal{N}(\theta, \sigma^2).$$

Suppose we wish to test the null hypothesis $H_0 : \theta = \theta_0$. The Wald statistic then reduces to

$$W = \frac{(\hat{\theta} - \theta_0)^2}{\hat{\sigma}^2},$$

which is simply the square of a standardized deviation. Under the null hypothesis, W converges in distribution to a χ_1^2 random variable. Equivalently, the signed statistic

$$Z = \frac{\hat{\theta} - \theta_0}{\hat{\sigma}}$$

is asymptotically standard normal. In this one-dimensional setting, the Wald test therefore coincides with the familiar large-sample z -test, illustrating how classical tests arise as special cases of the general Wald framework.

This one-dimensional Wald formulation is used extensively in applied settings. For example, the `DESeq2` software for differential gene expression analysis models log fold-changes using generalized linear models and tests individual coefficients via Wald statistics, relying on large-sample normal approximations to obtain χ_1^2 or equivalently normal-based p -values [51].

4.4 Parametric and non-parametric tests

Statistical tests are often described as *parametric* or *non-parametric*, a distinction that reflects both historical development and underlying philosophical views about statistical modelling. Parametric tests were developed first, at the beginning of the 20th century, in a context where probability models were seen as idealized descriptions of data. These tests assume that observations come from a distribution which is simple smooth, and described by a small number of parameters, such as the mean and variance. Statistical inference then focuses directly on these parameters.

In practice, parametric tests are frequently associated with the Gaussian, or Normal distribution. This historical association arises because many of the foundational procedures of classical statistics—such as the t -test, the F -test, and analysis of variance—are exact under normality. As a result, the parametric versus non-parametric distinction is often informally described as “Gaussian versus non-Gaussian.” This simplification is useful pedagogically, but it should be remembered that parametric models also include many non-Gaussian distributions, such as the binomial or Poisson.

Non-parametric tests emerged later, largely in the 1940s and 1950s, motivated by the recognition that real data often deviate from idealized models. Rather than assuming a specific

distributional form, these methods aim to remain valid under broad and unspecified distributions. They typically rely on ranks, signs, or empirical distributions, and therefore make fewer assumptions about the shape of the data.

From a historical perspective, the development of statistical testing can be roughly organized as a timeline. Early work by Pearson and Fisher between 1900 and 1930 established the foundations of parametric inference, including the χ^2 -test, the t -test, and analysis of variance. In the mid-20th century, researchers such as Wilcoxon, Mann, and Whitney introduced distribution-free methods to address practical limitations of these classical procedures. Later developments, including asymptotic theory and robust statistics, provided a unifying framework that connects parametric and non-parametric approaches.

To organize the tests presented in this section, it is helpful to focus on their *goal* rather than on their label. Some tests are designed to compare central tendencies between samples, others to assess variability, and others to evaluate the overall agreement between data and a theoretical model. Viewed this way, non-parametric tests are not simply substitutes for parametric ones, but complementary tools that reflect different assumptions, historical traditions, and inferential aims.

4.4.1 Wilcoxon signed-rank test

The Wilcoxon signed-rank test was introduced by Frank Wilcoxon in 1945 as a distribution-free alternative to the one-sample and paired-sample t -tests [52]. It was motivated by situations in which normality could not be assumed but a test of central location was still desired. The parametric analogue is the one-sample or paired t -test, which tests a hypothesis about a mean. By contrast, the Wilcoxon signed-rank test targets symmetry of the distribution about a specified location.

The test statistic is based on the ranks of the absolute deviations $|x_i - \theta_0|$, with signs retained. Under the null hypothesis of symmetry, the statistic has a known finite-sample distribution; for moderate to large samples, it is commonly approximated by a normal distribution, from which p -values are obtained.

More explicitly, let

$$d_i = x_i - \theta_0,$$

and let R_i denote the rank of $|d_i|$ among the nonzero differences. The Wilcoxon signed-rank statistic is defined as

$$W = \sum_{i: d_i > 0} R_i,$$

that is, the sum of the ranks corresponding to positive deviations. Under the null hypothesis of symmetry about θ_0 , the distribution of W is known exactly.

4.4.2 Mann–Whitney U test

The Mann–Whitney U test, introduced by Mann and Whitney in 1947, provides a non-parametric alternative to the two-sample t -test for independent samples [53]. It was designed to compare two populations without assuming normality or equal variances. The parametric analogue is the two-sample t -test, which compares population means. The Mann–Whitney test instead assesses whether one distribution tends to produce larger observations than the other.

The test statistic U is constructed from the ranks of the pooled samples. Under the null hypothesis that the two distributions are identical, U has a known exact distribution and, asymptotically, a normal distribution. p -values are computed either exactly or via the normal approximation.

Let $R_{1,i}$ denote the rank of the i -th observation from sample 1 in the pooled sample. The Mann–Whitney statistic is

$$U = \sum_{i=1}^{n_1} R_{1,i} - \frac{n_1(n_1 + 1)}{2}.$$

Equivalently, U counts the number of pairs $(x_{1,i}, x_{2,j})$ such that $x_{1,i} > x_{2,j}$.

4.4.3 Levene median-based test

Levene's test was proposed by Howard Levene in 1960 as a robust alternative to Fisher's variance-ratio test [54]. The median-based version, later emphasized by Brown and Forsythe, improves robustness against non-normality. The parametric analogue is the classical F -test for equality of variances, which is highly sensitive to departures from normality. Levene's test replaces variances by absolute deviations from group centers.

The statistic is computed by applying a one-way ANOVA to the transformed data $|x_{ij} - \tilde{x}_i|$, where \tilde{x}_i is the group median. Under the null hypothesis of equal spreads, the test statistic follows approximately an F distribution, from which p -values are obtained.

Formally, define the transformed observations

$$z_{ij} = |x_{ij} - \tilde{x}_i|,$$

where \tilde{x}_i is the median of group i . The Levene test statistic is then the usual ANOVA F -statistic computed from the z_{ij} ,

$$F = \frac{s_{\text{between}}^2(z)}{s_{\text{within}}^2(z)},$$

where $s_{\text{between}}^2(z)$ and $s_{\text{within}}^2(z)$ denote the between- and within-group variances of the transformed data.

4.4.4 Kruskal–Wallis test

The Kruskal–Wallis test was introduced in 1952 by Kruskal and Wallis as a non-parametric extension of one-way ANOVA. It was motivated by the need to compare more than two groups without assuming normality. The parametric analogue is Fisher's one-way ANOVA, which tests equality of group means. The Kruskal–Wallis test instead evaluates whether the group distributions are identical [55].

The test statistic is based on the ranks of all observations:

$$H = \frac{12}{N(N+1)} \sum_{i=1}^k n_i (\bar{R}_i - \bar{R})^2.$$

Under the null hypothesis, H converges in distribution to χ^2_{k-1} . p -values are computed from the chi-square distribution.

4.4.5 The Kolmogorov–Smirnov test

The Kolmogorov–Smirnov test was developed in the 1930s by Kolmogorov and later extended by Smirnov as a general goodness-of-fit procedure [56, 57]. It compares an empirical distribution to a fully specified theoretical distribution. The parametric analogue is the chi-square goodness-of-fit test, which relies on binning and asymptotic approximations. The Kolmogorov–Smirnov test instead measures the maximum discrepancy between distribution functions.

The test statistic is

$$D = \sup_x |F_n(x) - F_0(x)|.$$

Under the null hypothesis, D has a known distribution independent of F_0 . p -values are computed from this distribution or its asymptotic form.

4.4.6 The Shapiro–Wilk test

The Shapiro–Wilk test was introduced by Shapiro and Wilk in 1965 as a powerful goodness-of-fit test specifically designed to assess normality [58]. It was motivated by the low power of general-purpose tests when applied to normal models. The parametric analogue is not a test of means or variances, but rather the assumption of normality underlying t -tests, F -tests, and ANOVA. The Shapiro–Wilk test directly targets this assumption.

The test statistic is

$$W = \frac{\left(\sum_{i=1}^n a_i x_{(i)}\right)^2}{\sum_{i=1}^n (x_i - \bar{x})^2},$$

where the coefficients a_i depend on normal order statistics. The distribution of W under the null hypothesis is obtained via approximation or simulation, and p -values are computed accordingly.

4.5 Error types in hypothesis testing

Modern hypothesis testing emerged in the early 20th century as an attempt to formalize uncertainty, error, and decision making in empirical science. Three major approaches—Fisherian significance testing, Neyman–Pearson hypothesis testing, and Bayesian inference—address these issues in fundamentally different ways, while later philosophical analyses by Reichenbach and Popper clarified their distinct aims. Subsequent commentators such as Cox, Mayo, and Lehmann have emphasized both the strengths of each framework and the conceptual tensions created by their later amalgamation in textbook practice.

Ronald A. Fisher introduced significance tests in the 1920s as tools for assessing the *strength of evidence* against a null hypothesis [47, 48]. In Fisher’s view, a null hypothesis H_0 is a reference model, and the p -value is defined as the probability, under H_0 , of observing data at least as extreme as those obtained. Small p -values indicate discordance between data and model, but Fisher rejected fixed decision thresholds and did not formalize Type II errors or power. Type I error appears implicitly as the tail probability under H_0 , not as a long-run operating characteristic. Hypothesis testing, for Fisher, is evidential rather than decisional: it informs scientific judgment but does not prescribe action.

Jerzy Neyman and Egon Pearson developed a sharply different framework in the 1930s, motivated by repeated decision making [43]. Here, hypotheses H_0 and H_1 are competing models, and tests are designed to control error rates in the long run. Type I error (α) and Type II error (β) are central primitives, and optimal tests maximize power subject to a fixed α . p -values play no essential role; instead, decisions are based on pre-specified critical regions. This approach interprets hypothesis testing as a rule for action under uncertainty rather than as a measure of evidential support.

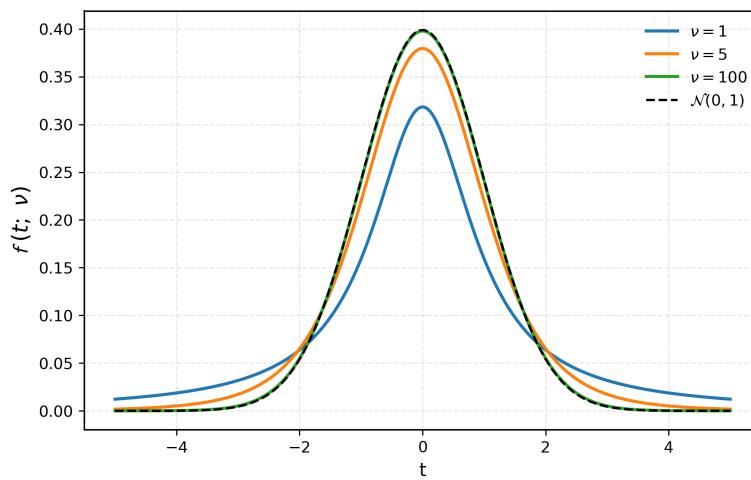
Bayesian inference, originating in Bayes’s posthumous essay [39] and developed by Laplace and later subjectivists such as de Finetti [40], rejects Type I and Type II errors as fundamental concepts. Probability is interpreted as rational degree of belief, and hypotheses themselves are assigned probabilities. Inference proceeds by updating prior beliefs via Bayes’ theorem to obtain posterior probabilities or Bayes factors. Hypothesis testing becomes model comparison, and decisions—if required—are made by minimizing expected loss. The Bayesian framework thus dissolves the classical error dichotomy by reframing uncertainty epistemically rather than behaviorally.

Hans Reichenbach provided the clearest philosophical articulation of the frequentist stance underlying Neyman–Pearson theory [59]. He distinguished *prediction*—statements about long-run frequencies—from *inference*—claims about truth or belief. Statistical tests, on this view, justify actions and predictions through their error properties, not through probabilistic assertions about hypotheses. This position sharply contrasts with Bayesian epistemology and clarifies why frequentist testing can function without assigning probabilities to hypotheses.

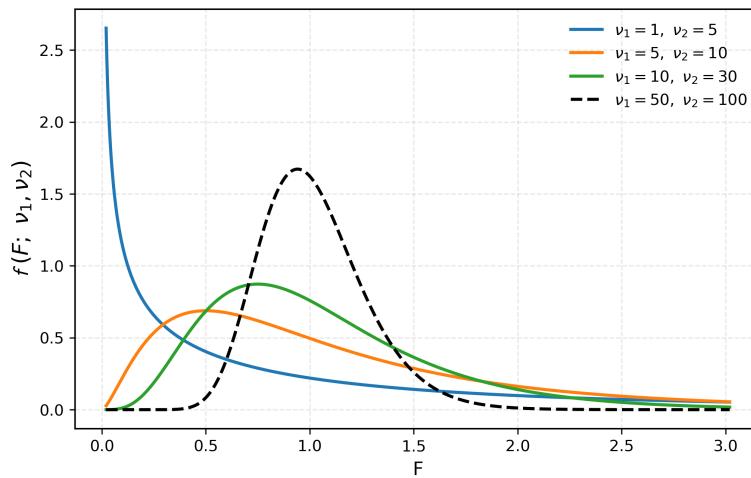
Karl Popper rejected probabilistic confirmation altogether, arguing that science advances through bold conjectures and severe attempts at falsification [60]. Statistical tests, in his view, contribute by formulating risky predictions whose failure can refute theories, not by accumulating evidence or controlling long-run errors. Popper’s philosophy is incompatible with Bayesian confirmation and only partially aligned with frequentist testing, insofar as both emphasize error and refutation rather than belief.

Erich Lehmann, in his definitive treatment of hypothesis testing [61], emphasized the formal coherence and optimality of Neyman–Pearson theory while explicitly distinguishing it from Fisher’s evidential approach. D. R. Cox later argued that the routine combination of p -values with fixed significance thresholds conflates logically distinct inferential goals [62]. Deborah Mayo further developed an error-statistical philosophy in which evidential interpretation is grounded in the severity with which hypotheses are tested [63, 64]. Together, these authors converge on a common diagnosis: the modern textbook procedure of hypothesis testing is a pragmatic but conceptually hybrid construct, blending incompatible foundations.

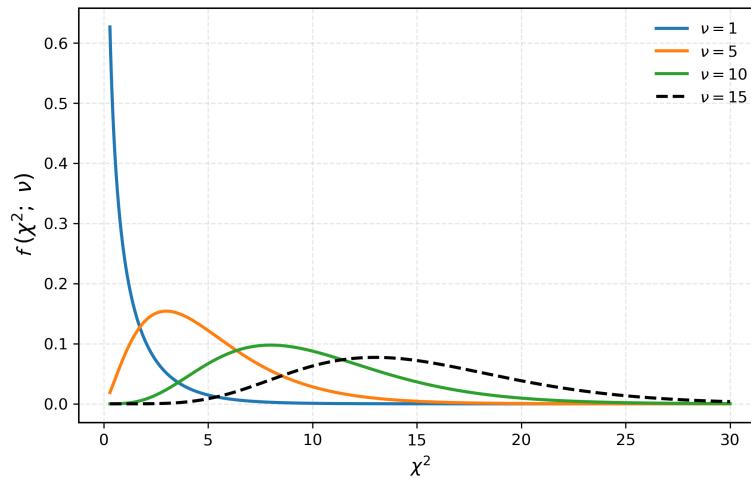
The coexistence of Fisherian evidence, Neyman–Pearson decision rules, Bayesian belief updating, Popperian falsification, and Reichenbach’s predictive frequentism reflects not confusion but plurality. Each framework answers a different question—about evidence, action, belief, or prediction—and Type I and Type II errors acquire meaning only within the Neyman–Pearson decision-theoretic context. Understanding these distinctions is essential for the principled use and interpretation of hypothesis tests in modern statistics.



(a) The Central Limit Theorem 1



(b) The Central Limit Theorem 2



(c) The Central Limit Theorem 3

Figure 4.2: Statistical distributions

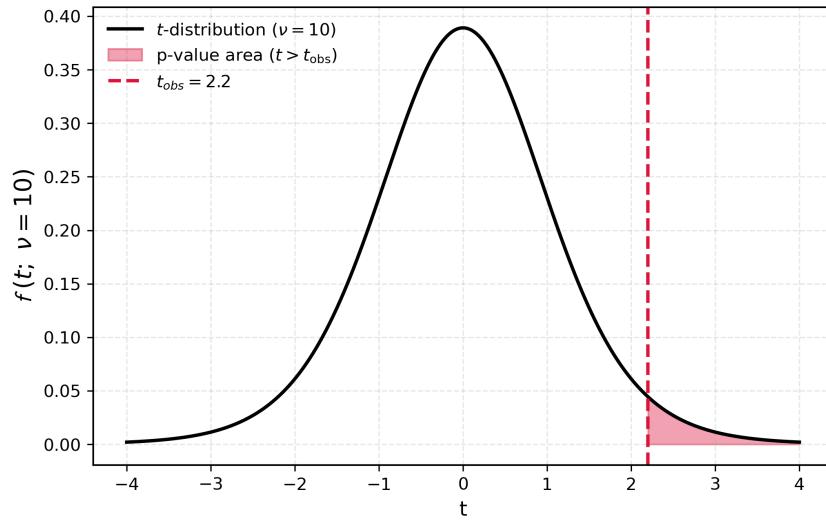
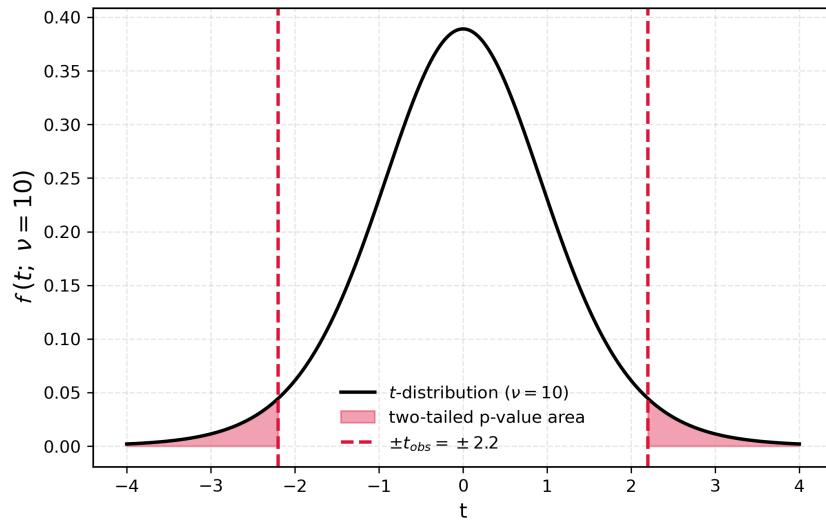
(a) One sided p -value.(b) One sided p -value.

Figure 4.3: Representation of the 1-sided and 2-sided p -value as the cumulative probability—the integral of the tails, the area under the curve —of the Student’s t -distribution.

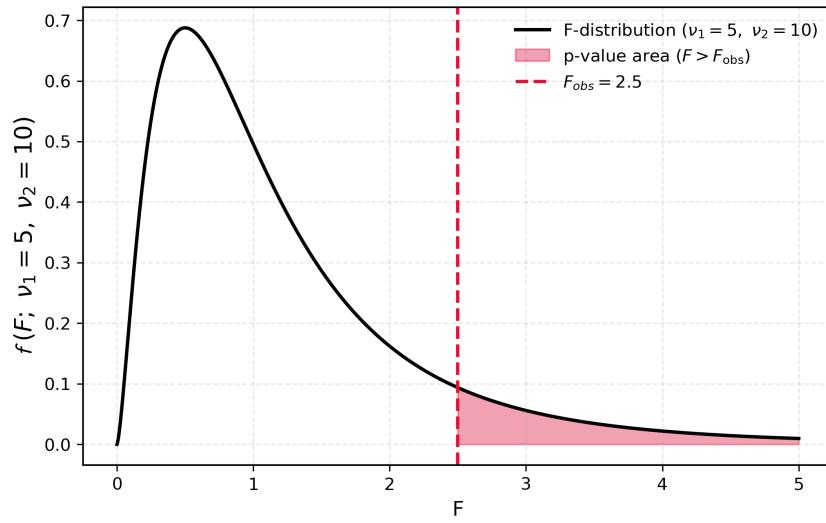
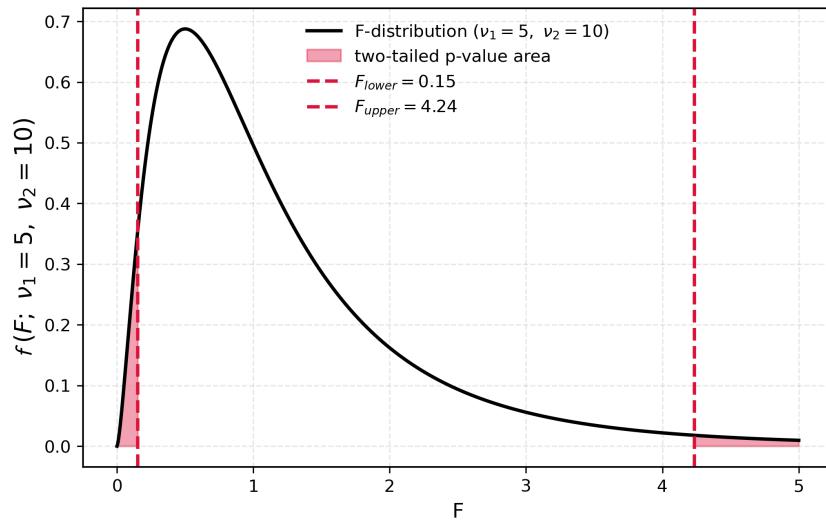
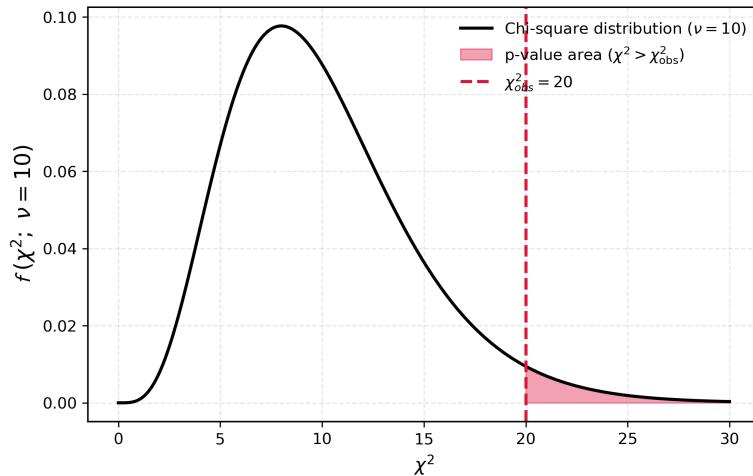
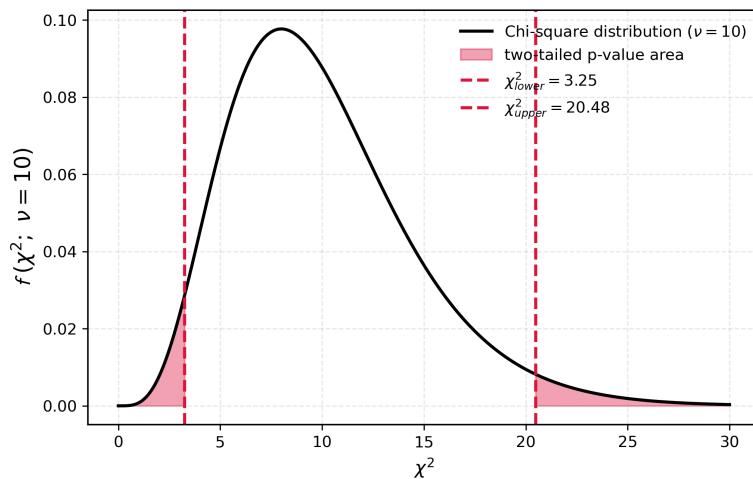
(a) One sided p -value.(b) One sided p -value.

Figure 4.4: Representation of the 1-sided and 2-sided p -value as the cumulative probability—the integral of the tails, the area under the curve —of the Fisher t -distribution.



(a) Representation of the one-sided p -value for the χ^2 -test, computed as the integral of the right tail of the distribution.



(b) Representation of the two-sided p -value for the χ^2 -test, computed as the integral of the right tail of the distribution.

Figure 4.5: Representation of the 1-sided and 2-sided p -value as the cumulative probability—the integral of the tails, the area under the curve —of the Fisher t -distribution.

Chapter 5

Modelling, dependency, and correlation

Chapter 6

Introduction to Bayesian probability

Chapter 7

Stochasticity and Markov Processes

Appendix A

Appendix: A quick review of linear algebra

Linear algebra is one of the central languages of modern mathematics and science. It provides the formal framework for describing linear relations, symmetry, and structure, and it underlies vast areas of analysis, probability, statistics, physics, computer science, and data science. Historically, linear algebra did not arise as a single theory, but rather as a collection of methods developed to solve systems of linear equations, study geometry, and understand transformations of space. Only in the late nineteenth and early twentieth centuries was it unified into the abstract theory now taught under the name *linear algebra*.

From a philosophical perspective, linear algebra marks a transition from concrete computation to structural thinking. Instead of focusing on individual equations or numerical solutions, the subject emphasizes vector spaces, mappings between them, and invariant properties under change of coordinates. This abstraction allows the same mathematical ideas to apply equally to geometry, differential equations, probability models, and statistical inference.

A solid background in linear algebra typically includes the following core topics, which are either required or strongly recommended for further study in probability, statistics, and applied mathematics:

Vectors and vector spaces. Understanding vectors as elements of a vector space over a field, together with the operations of addition and scalar multiplication. This includes linear combinations, span, linear independence, bases, and dimension. These concepts formalize the idea of degrees of freedom and coordinate representations.

Matrices and systems of linear equations. Matrices arise naturally as representations of linear maps. Key topics include matrix operations, matrix inversion, rank, row reduction, and the solution of linear systems. Historically, these ideas trace back to the work of Carl Friedrich Gauss and the development of systematic elimination methods.

Linear transformations. The interpretation of matrices as functions between vector spaces is essential. Topics include kernel and image, injectivity and surjectivity, change of basis, and composition of linear maps. This viewpoint emphasizes structure over computation and clarifies the geometric meaning of matrices.

Inner products and geometry. Inner product spaces introduce notions of length, angle, and orthogonality. Important concepts include norms, orthogonal projections, orthonormal bases, and the Gram–Schmidt process. These ideas are foundational for least squares methods, regression, and statistical estimation.

Eigenvalues and eigenvectors. Eigenvalues describe intrinsic directions and scaling properties of linear transformations. Diagonalization, spectral decomposition, and symmetric matrices

play a central role in applications ranging from differential equations to principal component analysis.

Determinants and volume. Although less central in modern abstract treatments, determinants provide geometric insight into volume, orientation, and invertibility. They also play a role in change-of-variables formulas and multivariate analysis.

Historically, the development of linear algebra is associated with several key figures and works. Gauss laid the foundations for systematic solution of linear systems. Hermann Grassmann introduced abstract vector spaces in his *Ausdehnungslehre* (1844), a work far ahead of its time. Arthur Cayley and James Joseph Sylvester developed matrix theory in the nineteenth century, while David Hilbert and Emmy Noether contributed decisively to the structural and axiomatic understanding of linear spaces and linear operators.

In modern mathematics, linear algebra serves both as a computational toolkit and as a conceptual foundation. Mastery of its basic structures is essential not only for solving concrete problems, but also for understanding more advanced theories where linear spaces provide local or approximate descriptions of complex phenomena. As such, linear algebra is best learned not merely as a collection of techniques, but as a coherent framework for reasoning about structure, symmetry, and linearity.

Appendix B

Appendix: A quick review of functions and derivatives

Calculus begins with the study of how quantities depend on one another and how they change. At its foundation lies the concept of a *function*, which formalizes the idea that one quantity is determined by another. Functions provide the language through which variation, motion, and growth are described in mathematics, physics, and the natural sciences.

Historically, the notion of a function evolved gradually. Early uses appear implicitly in the work of René Descartes, who introduced coordinate geometry and expressed curves through algebraic equations. The explicit concept of a function as a mapping between quantities was later clarified in the eighteenth century by Leonhard Euler, whose writings established much of the notation and terminology still in use today.

A central idea in calculus is that of a *limit*. Limits capture the behavior of a function as its input approaches a given value, even if the function is not defined or not well behaved at that point. Informally, limits allow us to reason about processes that involve approaching, rather than reaching, a value. This concept is essential for making precise sense of continuity, instantaneous change, and accumulation.

The derivative arises from the study of limits and provides a precise definition of instantaneous rate of change. Geometrically, the derivative of a function at a point corresponds to the slope of the tangent line at that point. Physically, it describes quantities such as velocity or growth rate. The basic definition of the derivative is given by a limit of difference quotients, linking algebraic computation with geometric intuition.

The development of differential calculus is closely associated with Isaac Newton and Gottfried Wilhelm Leibniz, who independently formulated its fundamental principles in the late seventeenth century. Newton emphasized motion and physical interpretation, while Leibniz introduced a symbolic notation that proved especially flexible and influential. Their work laid the groundwork for centuries of mathematical and scientific progress.

From a philosophical standpoint, calculus represents an effort to make sense of continuous change using finite reasoning. The introduction of limits resolved long-standing paradoxes about infinity and infinitesimals by replacing informal arguments with precise definitions. Modern calculus, as taught today, builds on this foundation by emphasizing clarity, rigor, and conceptual understanding rather than purely mechanical computation.

Appendix C

Appendix: A quick review of integral calculus

Integral calculus is concerned with accumulation, total change, and the measurement of quantities such as area, volume, and total mass. Whereas differential calculus studies how quantities change at a point, integral calculus focuses on how these changes add up over an interval. Together, the two form a unified framework for analyzing continuous phenomena.

The basic problem of integration can be stated simply: given a varying quantity, how can one compute its total effect? Early examples include determining the area under a curve or the distance traveled by an object with varying speed. These questions were studied in ancient mathematics, notably by Archimedes, who used geometric arguments to compute areas and volumes with remarkable precision.

In modern terms, the integral of a function over an interval is defined as the limit of finite sums, where the interval is subdivided and the contributions of each subinterval are added together. This idea formalizes the intuitive notion of accumulation and provides a bridge between discrete approximation and continuous exactness.

A fundamental result of calculus is the *Fundamental Theorem of Calculus*, which establishes a deep connection between differentiation and integration. It shows that integration can be performed by finding an antiderivative, linking the problem of accumulation directly to the study of rates of change. This theorem unifies the two branches of calculus into a single coherent theory.

As with differential calculus, the systematic development of integral calculus is attributed to Newton and Leibniz. Leibniz's notation for integrals, inspired by the idea of summation, remains standard today. Over time, the theory of integration was refined and extended by mathematicians such as Augustin-Louis Cauchy and Bernhard Riemann, who provided precise definitions suitable for rigorous analysis.

Philosophically, integral calculus addresses the challenge of understanding the whole from infinitely many parts. By replacing informal geometric reasoning with limit processes, it provides a reliable method for reasoning about continuous quantities. At an introductory level, integral calculus offers both practical tools and conceptual insight into how local behavior combines to produce global effects.

Appendix D

Appendix: Some special functions

Linear algebra is one of the central languages of modern mathematics and science. It provides the formal framework for describing linear relations, symmetry, and structure, and it underlies vast areas of analysis, probability, statistics, physics, computer science, and data science. Historically, linear algebra did not arise as a single theory, but rather as a collection of methods developed to solve systems of linear equations, study geometry, and understand transformations of space. Only in the late nineteenth and early twentieth centuries was it unified into the abstract theory now taught under the name *linear algebra*.

From a philosophical perspective, linear algebra marks a transition from concrete computation to structural thinking. Instead of focusing on individual equations or numerical solutions, the subject emphasizes vector spaces, mappings between them, and invariant properties under change of coordinates. This abstraction allows the same mathematical ideas to apply equally to geometry, differential equations, probability models, and statistical inference.

A solid background in linear algebra typically includes the following core topics, which are either required or strongly recommended for further study in probability, statistics, and applied mathematics:

Vectors and vector spaces. Understanding vectors as elements of a vector space over a field, together with the operations of addition and scalar multiplication. This includes linear combinations, span, linear independence, bases, and dimension. These concepts formalize the idea of degrees of freedom and coordinate representations.

Matrices and systems of linear equations. Matrices arise naturally as representations of linear maps. Key topics include matrix operations, matrix inversion, rank, row reduction, and the solution of linear systems. Historically, these ideas trace back to the work of Carl Friedrich Gauss and the development of systematic elimination methods.

Linear transformations. The interpretation of matrices as functions between vector spaces is essential. Topics include kernel and image, injectivity and surjectivity, change of basis, and composition of linear maps. This viewpoint emphasizes structure over computation and clarifies the geometric meaning of matrices.

Inner products and geometry. Inner product spaces introduce notions of length, angle, and orthogonality. Important concepts include norms, orthogonal projections, orthonormal bases, and the Gram–Schmidt process. These ideas are foundational for least squares methods, regression, and statistical estimation.

Eigenvalues and eigenvectors. Eigenvalues describe intrinsic directions and scaling properties of linear transformations. Diagonalization, spectral decomposition, and symmetric matrices play a central role in applications ranging from differential equations to principal component analysis.

Determinants and volume. Although less central in modern abstract treatments, determinants provide geometric insight into volume, orientation, and invertibility. They also play a role in change-of-variables formulas and multivariate analysis.

Historically, the development of linear algebra is associated with several key figures and works. Gauss laid the foundations for systematic solution of linear systems. Hermann Grassmann introduced abstract vector spaces in his *Ausdehnungslehre* (1844), a work far ahead of its time. Arthur Cayley and James Joseph Sylvester developed matrix theory in the nineteenth century, while David Hilbert and Emmy Noether contributed decisively to the structural and axiomatic understanding of linear spaces and linear operators.

In modern mathematics, linear algebra serves both as a computational toolkit and as a conceptual foundation. Mastery of its basic structures is essential not only for solving concrete problems, but also for understanding more advanced theories where linear spaces provide local or approximate descriptions of complex phenomena. As such, linear algebra is best learned not merely as a collection of techniques, but as a coherent framework for reasoning about structure, symmetry, and linearity.

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