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Chapter 12

Bayesian Hypothesis Testing: An Alternative to Null Hypothesis Significance Testing (NHST) in Psychology and Social Sciences

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Abstract

Since the mid-1950s, there has been a clear predominance of the Frequentist approach to hypothesis testing, both in psychology and in social sciences. Despite its popularity in the field of statistics, Bayesian inference is barely known and used in psychology. Frequentist inference, and its null hypothesis significance testing (NHST), has been hegemonic through most of the history of scientific psychology. However, the NHST has not been exempt of criticisms. Therefore, the aim of this chapter is to introduce a Bayesian approach to hypothesis testing that may represent a useful complement, or even an alternative, to the current NHST. The advantages of this Bayesian approach over Frequentist NHST will be presented, providing examples that support its use in psychology and social sciences. Conclusions are outlined.

Keywords: Bayesian inference, Bayes factor, NHST, quantitative research

1. Introduction

“Scientific honesty then requires less than had been thought: it consists in uttering only highly probable theories: or even in merely specifying, for each scientific theory, the evidence, and the probability of the theory in the light of this evidence”. Lakatos [1, p. 208].

The nature and role of experimentation in science found its origins in the rise of natural sciences during the sixteenth and seventeenth centuries [2]. Since then, knowledge meant that theories have to be corroborated either by the power of the intellect or by the evidence of the senses [1]. However, until the mid-late 1800s, “psychological experiments had been performed, but the science was not yet experimental” [3, p. 158]. It was not until 1875 that—either at
Wundt laboratory in Leipzig or at James' laboratory in Harvard—experimental procedures were introduced and contributed to the development of psychology as an independent science [3]. From almost one and a half centuries, scientific research mostly relies on empirical findings to provide support to their hypotheses, models, or theories. From this point of view, psychology and social sciences must take distance from rhetorical speculations, desist from unproven statements and build its knowledge on the basis of empirical evidence [1, 4]. Almost a decade ago, Curran reemphasized that the aim of any empirical science is to pursue the construction of a cumulative base of knowledge [5]. However, it has also been emphasized that such a cumulative knowledge—for a true psychological science—is not possible through the current and widespread paradigm of hypothesis testing [5–9]. Since approximately two decades ago, some explicit claims have appeared in peer review articles, such as "Psychology will be a much better science when we change the way we analyze data" [7], "We need statistical thinking, not statistical rituals" [10], "Why most research findings are false" [11] or "Yes, psychologists must change the way they analyze their data..." [12]. Most critiques have been directed toward the current—and still predominant—approach to hypothesis testing (i.e., NHST) and its overreliance on p-values and significance levels [6, 11, 13], emphasizing its pervasive consequences against the construction of a cumulative base of knowledge in psychological science [8]. Despite all warnings, they seem not to have generated a noteworthy echo in the scientific community, even though "it is evident that the current practice of focusing exclusively on a ... decision strategy of null hypothesis testing can actually impede scientific progress" [14, p. 100]. Therefore, it seems reasonable to suggest that there is a need to make considerable changes to how we usually carry out research, especially if the goal is to ensure research integrity [6]. Regarding this matter, a frequently proposed alternative has been moving from the exclusive focus on p-values to incorporate other existing techniques such as “power analysis” [15] and “meta-analysis” [16], or to report and interpret “effect sizes” and “confidence intervals” [7]. However, in our view, a souner alternative would be to move from a Frequentist paradigm to a Bayesian approach, which allows us not only to provide evidence against the null hypothesis but also in favor of it [17]. Furthermore, Bayesian analysis allows us to compare two (or more) competing models in light of the existent data and not only based in “theoretical probability distributions,” as in the Frequentist approach to hypothesis testing [18].

A Bayesian approach would offer some interesting possibilities for both individual psychology researchers and the research endeavor in general. First, Bayesian analysis allows us to move from a dichotomous way of reasoning about results (e.g., either an effect exists or it does not) to a less artificial view that interprets results in terms of magnitude of evidence (e.g., the data are more likely under $H_0$ than $H_a$), and therefore, allows us to better depict to which extent a phenomenon may occur. Second, a Bayesian approach naturally allows us to directly test the plausibility of both the null and the alternative hypothesis, but the current NHST paradigm does not. In fact, when a researcher does not reach a desired p-value oftentimes it is—falsely—assumed that the effect “does not exist.” As a consequence, the researcher’s chances of getting his or her results published decrease dramatically, which moves us to our third argument. As broadly known, the most scientific peer-reviewed journals do not show much interest in results, which are “non-statistically significant.” This common practice—or scientific standard—sadly reinforces the idea of thinking in terms of relevant or irrelevant findings. In our view,
such standards do not promote scientific advance and quickly lead us to ignore some promising but “non-significant” findings that may be further explored, fed into meta-analysis, or just be considered by other researchers in the field. Of course, systematically ignoring a portion of the research undermines the primary goal of scientific inquiry that is to collect evidence and not only to reject hypothesis. The facts and ideas exposed in this introductory section set forth the necessity to reanalyze the way in which scientific evidence has been conceived during the NHST era.

The following sections will: (a) concisely address the NHST procedure, (b) introduce a Bayesian framework to hypothesis testing, (c) provide an example that highlights the advantages of a Bayesian approach over the current NHST in terms of the way in which scientific evidence is quantified, and (d) briefly summarize and discuss the benefits of a Bayesian approach to hypothesis testing.

2. Null hypothesis significance testing (NHST)

"Never use the unfortunate expression: accept the null hypothesis." Wilkerson and the Task Force on Statistical Inference APA Board of Scientific Affairs [19, p. 602].

The most influential methods to modern null hypothesis significance testing (NHST) were developed by Fisher, and by Neyman and Pearson in the early and mid-1900s [20]. Since then, the NHST has been broadly used to provide an association between empirical evidence and models or theories [21]. In the traditional NHST procedure, two hypotheses are postulated: a null hypothesis (i.e., \( H_0 \)) and a research hypothesis, also called alternative (i.e., \( H_a \)), which describe two contrasting conceptions about some phenomenon [22]. When conducting a NHST, researchers usually pursue to reject the null hypothesis (\( H_0 \)) on the basis of a p-value. When the observed p-value is lower than a predetermined significance level (i.e., alpha, usually corresponding to \( \alpha = 0.05 \)), the conclusion is that such p-value constitutes supporting evidence that favors the plausibility of the alternative hypothesis [23]. However, a more important feature of this procedure that remains unknown for most scientists, including psychology researchers, is that the NHST constitutes an amalgamation of two irreconcilable schools of thought in modern statistics: the Fisher test of significance, and the Neyman and Pearson hypothesis test [24, 25]. To this respect, Goodman stated that “it is not generally appreciated that the p-value, as conceived by Fisher, is not compatible with the Neyman and Pearson hypothesis in which it has become embedded” [25, p. 485]. In this synthesized NHST, the Fisherian approach includes a test of significance of p-values obtained from the data, whereas the Neyman and Pearson method incorporates the notion of error probabilities from the test (i.e., Type I and Type II).

2.1. Origins and rationale of NHST

First, in the early 1900s, Fisher [26, 27] developed a method that tested a single hypothesis (i.e., null or \( H_0 \)), which has been mainly referred to as a hypothesis of “no effect” between variables (e.g., relationship, difference). The null hypothesis, as conceived by Fisher, has a known
distribution of the test statistic $t$. Thus, as the test statistic moves away from its expected value, then the null hypothesis becomes progressively less plausible. In other words, it appears less likely to occur by chance. Then, if $H_0$ achieves a probability of occurrence sufficiently lower than the significance level (i.e., a small $p$-value) then it should be rejected. Otherwise, no conclusion can be reached. Subsequently, the question that logically arises is: what $p$-value is sufficiently small to reject $H_0$? The answer to this question was clearly addressed by Fisher when he stated that this threshold should be determined by the context of the problem, and it was not until the 1950s that Fisher presented the first significance tables to establishing rejection thresholds \[22\]. However, Fisher \[28\] refused the idea of establishing a conventional significance level and, in its place, recommended reporting the exact $p$-value instead of a significance level (e.g., $p = 0.019$, but not $p < 0.05$; see \[10\]). Similarly, May et al. indicated that the choice of a significance level should depend on the consequences of rejecting or failing to reject the null hypothesis \[29\]. Despite these recommendations about threshold determination, most scientists from different research fields adopted standard significance levels (i.e., $\alpha = 0.05$ or $\alpha = 0.01$), which have been used—or misused—regardless of the hypotheses being tested.

Later, in 1933, Neyman and Pearson proposed a procedure in which two explicitly stated rival hypotheses were contrasted, being one of them still considered as the “null” hypothesis, as in the Fisher test \[30\]. Neyman and Pearson rejected Fisher’s idea of only testing the null hypothesis. In this scenario, there are now two hypotheses (i.e., the null and the alternative), and based on the observed $p$-value, the researcher has to decide whether to reject or not to reject the null hypothesis. This decision rule faces the researcher with the probability of committing two kinds of errors: Type I and Type II. As defined by Neyman and Pearson, the Type I error is the probability of falsely rejecting $H_0$ (i.e., null) when $H_0$ is true \[30\]. Conversely, the probability of failing to reject $H_0$ when $H_0$ is false is the Type II error. For the sake of simplicity, an analogy of both kinds of errors can be found in the classic fairy tale “The boy who cried wolf!” When the young shepherd, called Peter, shouted out: “Help! the wolf is coming!” The village’s people believed the young boy warning and quickly came to help him. However, when they found out that all was a joke, they got angry. To believe in the boy’s false, alarm can be considered as a Type I error. Peter repeated the same joke a couple of times and, when the wolf actually appeared, the villagers did not believe the young shepherd’s desperate calls. This situation is analogous to be engaged in a Type II error \[31\].

Within this NHST framework, the Fisher’s $p$-value is then used to dichotomize effects into two categories: significant and non-significant results \[21\]. Consequently, on one hand, obtaining significant results led us to assume that the phenomenon under investigation can be considered as “existing” and, therefore, can be used as supporting evidence for a particular model or theory. On the other hand, non-significant results are usually (and erroneously) considered as “noise,” implicating the nonexistence of an effect \[21\]. In this last case, there are no findings that could be reported. From this view, the evidence in favor of a research finding is then solely judged on the ability to reject $H_0$ when a sufficiently low $p$-value is observed. This simple and appealing decision rule may constitute a very seductive way of thinking about results, that is: A phenomenon either exists or it does not. However, thinking in this fashion is fallacious, led to misinterpretations of results and findings, and more importantly “it can distract us from a higher goal of scientific inquiry. That is, to determine if the results of a test have any practical value or not” \[32, p. 7\].
2.2. NHST: Common misconceptions and criticisms

As previously stated, most problems and criticisms to the current NHST paradigm appear as a result of the mismatch of these essentially incompatible statistical approaches [10, 33, 34]. In this line, Nickerson stated that “A major concern expressed by critics is that such testing is misunderstood by many of those who use it” [35, p. 241]. Some of these misconceptions are common among researchers and are interpretative in nature. As a matter of fact, Badenes-Ribera et al. recently reported the results of a survey conducted to 164 academic psychologists who were questioned about the meaning of p-values [36]. Results confirmed previous findings regarding the occurrence of wrongful interpretations of p-values. For instance, the false belief that the p-value indicates the conditional probability of the null hypothesis given certain data (i.e., $p(H_0|D)$), instead of the probability of witnessing a given result, assuming that the null hypothesis is true [37]. This wrong interpretation of a p-value is known as “the inverse probability” fallacy. Another common misconception regarding p-values is that they provide direct information about the magnitude of an effect, that is, a p-value of 0.00001 represents evidence of a bigger effect than a p-value of 0.01. This conclusion is wrong because the only way to estimate the magnitude of an effect is to calculate the value of the effect size with the appropriate statistic and its confidence interval (e.g., Cohen’s $d$; see [38]). This erroneous interpretation of a p-value is known as “the effect size” fallacy. A comprehensive review of these and other common misconceptions is out of the scope of this chapter, but several resources on these topics are available for the interested readers (see [14, 35, 37–40]).

Likewise, the rationale under the NHST has been largely criticized. Most criticisms against NHST are focused on the way in which data are (unsoundly) analyzed and interpreted, for example:

a. NHST only provides evidence against the plausibility of $H_0$, but does not provide probabilistic evidence in favor of the plausibility of $H_a$.

b. NHST uses inference procedures based on hypothetical data distributions, instead of being based on actual data.

c. NHST does not provide clear rules for stopping data collection; therefore, as long as sample size increases any $H_0$ can be rejected (see [9, 18]).

However, an issue that is of particular interest for this chapter is related to the use of p-values as a way to quantify statistical evidence [13, 41]. As previously stated in this chapter, rejecting $H_0$ does not provide evidence in favor of the plausibility of $H_a$ and all that can be concluded is that $H_0$ is unlikely [9]. Conversely, failing to reject $H_0$ simply allows us to state that—given the evidence at hand—one cannot make an assertion about the existence of some effect or phenomenon [42]. Hence, rejecting $H_0$ is not a valid indicator of the magnitude of evidence of a result [43]. In Schmidt’s words: “… reliance on statistical significance testing in psychology and the other social sciences has led to frequent serious errors in interpreting the meaning of data, errors that have systematically retarded the growth of cumulative knowledge” [16, p. 120].

Despite the existence of scientific literature that highlights the weaknesses of NHST [9, 16, 21, 22, 39, 43–46], it is still considered as the: “sine qua non of the scientific method” [10, p. 199]. Moreover, NHST is arguably the most widely used method of data analysis in psychology since the mid-1950s and still governs the interpretation of quantitative data in social science.
research [35, 47]. In Krueger’s words: “NHST is the researcher’s workhorse for making inductive inferences” [45, p. 16]. An immediate matter of concern is that most of scientific discoveries, in a wide range of research fields, are based on a procedure that still generates controversy (see [12, 48–50]). Since the focus of research should be on what data tell us about the magnitude of effects, it seems necessary to shift from our reliance on NHST to more robust alternatives [14]. Some recommended practices include estimates based on effect sizes, confidence intervals, and meta-analysis [6]. However, a sounder alternative comes from the Bayesian paradigm through the use of a simple estimate of the magnitude of evidence called Bayes factor (BF) [17]. This approach to hypothesis testing has shown several benefits. First, it is not oriented to pursue the rejection of $H_0$; on the contrary, it provides a way to obtain evidence for and against $H_0$. Second, it does not use arbitrary thresholds (i.e., significance levels) to reach dichotomous decisions about the plausibility or implausibility of $H_0$; on the contrary, it directly contrasts the magnitude of evidence for and against both $H_0$ and $H_a$. Third, it permits the continuous update of evidence as long as new data are available, which is in line with the nature of scientific inquiry. Bayesian methods have been largely suggested as a practical alternative to NHST [9, 17, 23, 51], but—until now—they have not received enough attention from researchers in psychology and social sciences.

3. Bayesian hypothesis testing: An alternative to NHST

“(...) prior and posterior are relative terms, referring to the data. Today’s posterior is tomorrow’s prior.” Lindley [52, p. 301].

In the field of statistics, probabilities can be interpreted under two predominant paradigms: Frequentist inference and Bayesian inference. The former makes predictions about experiments whose outcomes depend basically upon random processes [53]. The latter assigns probabilities to any statement, even when a random process is not involved [54]. In a Bayesian framework, a probability is a way to embody an individual’s degree of belief in a statement. Since the mid-1950s, there has been a clear predominance of the Frequentist approach to hypothesis testing, both in psychology and social sciences. The hegemony of Frequentist inference and its null hypothesis significance testing (NHST) might be partially attributed to the massive incorporation of such approaches in psychology undergraduate programs [9] and also to the fact that the Neyman and Pearson approach had the most well-developed computational software to conduct statistical inference [18]. However, the current scenario has drastically changed, and the development of sampling techniques like Markov-Chain Monte Carlo (MCMC; see [55, 56]) along with the availability and improvement of specifically developed software (e.g., WinBUGS, see [57, 58]; JAGS, see [59, 60]; JASP, see [61]) makes exact Bayesian inferences possible even in very complex models. As a result, “Bayesian applications have found their way into most social science fields” [22, p. 665], and psychologists can now easily implement Bayesian analysis for many common experimental situations (see for example JASP Statistics: https://jasp-stats.org/).
3.1. Bayes in a nutshell

In Bayesian inference, our degrees of belief about a set of hypotheses are quantified by probability distributions over those hypotheses [47, 62], which makes the Bayesian approach fundamentally different from the Frequentist approach, which relies on sampling distributions of data [47]. A Bayesian analysis usually implicates the updating of prior knowledge or information in light of newly available experimental data [63]. The latter clearly reflects the aim of any empirical science, which is to strive for the elaboration of a cumulative base of knowledge. Any Bayesian analysis implies the combination of three sources of information as follows:

a. a model that specifies how latent parameters (e.g., $\theta$) generate data (e.g., $D$);

b. prior information about those parameters (i.e., prior distribution); and

c. the observed data (i.e., likelihood).

This prior information, represented by $p(\theta)$, represents our degree of uncertainty about the parameters included in the model. Conversely, this prior distribution may also represent our degree of knowledge about the same parameters. Then, the more informative is our prior distribution, the less will be our degree of uncertainty about the parameters. The likelihood is the conditional probability of observing the data under some latent parameter (i.e., $p(D|\theta)$).

Following the Bayes theorem [64], the combination of these three elements produces an updated knowledge about the model parameters after the data have been observed, which is also known as the posterior distribution. The change from the prior to the posterior distribution reflects what has been learned from the data (see Figure 1). Thus, within a Bayesian framework, a researcher can invest more effort in the specification of prior distributions by translating existing knowledge about the phenomenon under study into prior distributions [65]. As suggested by Lee and Wagenmakers “such knowledge may be obtained by eliciting prior beliefs from experts, or by consulting the literature for earlier work on similar problems” [65, p. 110].

As shown in Figure 1, the strength of each source of information is indicated by the narrowness of its curve. A narrower curve is more informative about the value of parameters, whereas a wider one is less informative.

Bayes’ rule specifies how the prior information $p(\theta)$ and the likelihood $p(D|\theta)$ are combined to arrive at the posterior distribution denoted by $p(\theta|D)$, in Eq. (1):

$$p(\theta|D) = \frac{p(D|\theta)p(\theta)}{p(D)}$$

(1)

Eq. (1) is usually paraphrased as:

$$p(\theta|D) \propto p(D|\theta)p(\theta)$$

(2)

which means, “the posterior is proportional (i.e., $\propto$) to the likelihood times the prior.” In other words, the observed data (i.e., likelihood) increases our previous degree of knowledge (i.e.,
prior) in a proportional way to its informative strength, producing a new state of knowledge about the parameters of the model (i.e., posterior). One of the benefits of the Bayesian approach is that the prior (i.e., \( p(\theta) \); our present knowledge about the model parameters moderates the influence provided by the data (i.e., \( p(D|\theta) \)). This compromise leads to less pessimism when data are unexpectedly bad and less optimism when it is unexpectedly good [66]. Both influences are beneficial and help us to make more realistic inferences and take better decisions. For more detailed information on Bayesian inference, see, for instance, O’Hagan and Forster [54], Kruschke [59], and Jackman [67].

### 3.2. Bayes factor

Bayesian approaches for hypothesis testing are comparative in nature. Different models often represent competing theories or hypotheses, and the focus of interest is on which one is more plausible and better supported by the data [65]. Therefore, the Bayesian approach allows to quantify the plausibility of a given model or hypothesis (i.e., \( H_0 \)) against that of an alternative model (i.e., \( H_a \)). For any comparison of two competing models or hypotheses (e.g., \( H_a \) vs. \( H_0 \)), we can rely on an estimate of evidence known as the Bayes factor [52]. One of the attractive features of the Bayes factor is that it follows the principle of parsimony: When two models fit the data equally well, the Bayes factor prefers the simple model over the more complex one [68]. Nonetheless, in contrast to the NHST approach, “Bayesian statistics assigns no special
status to the null hypothesis, which means that *Bayes factors* can be used to quantify evidence for the null hypothesis just as for any other hypothesis” [65, p. 108].

Before observing the data, the *prior odds* of \( H_a \) over, e.g., \( H_0 \), are \( p(H_a)/p(H_0) \), and after having observed the data we have the *posterior odds* \( p(H_a|D)/p(H_0|D) \). Therefore, the ratio of the posterior odds and the prior odds is defined as the Bayes factor:

\[
BF_{H_aH_0} = \frac{(D|H_a)}{(D|H_0)} = \frac{p(H_a|D)}{p(H_0|D)} = \frac{p(H_a)}{p(H_0)} \frac{p(D|H_a)}{p(D|H_0)}
\]

Eq. (3) shows the Bayes factor for given data \( D \) and two competing hypotheses (i.e., \( H_0 \) vs. \( H_a \)), which is a measure of the evidence for \( H_a \) against \( H_0 \) provided by the data. In other words, the Bayes factor is the probability of the data under one hypothesis relative to the other. For instance, a \( BF_{H_aH_0} = 3 \) indicates that \( H_a \) is three times more plausible relative to \( H_0 \) than it was a priori.

From this view, the Bayes factor may be considered as analogous to the Frequentist likelihood ratio. Nevertheless, in the Bayesian context there is no reference at all to theoretical probability distributions as it is customary in a Frequentist approach. In a Bayesian framework, all inferences are made conditional on the observed data, and therefore, the Bayes factor has to be interpreted as a summary measure of the information provided by the data about the relative plausibility of two models or hypotheses (e.g., \( H_a \) vs. \( H_0 \)). Jeffreys [52] suggests the following scale for interpreting the Bayes factor (Table 1), although some people argue against the use of thresholds, least we fall in a different version of the old \( p < 0.05 \) ritual (see, for instance, [69]).

<table>
<thead>
<tr>
<th>Bayes factor</th>
<th>Interpretation</th>
</tr>
</thead>
<tbody>
<tr>
<td>&gt; 100</td>
<td>Extreme evidence for ( H_a )</td>
</tr>
<tr>
<td>30</td>
<td>Very strong evidence for ( H_a )</td>
</tr>
<tr>
<td>10</td>
<td>Strong evidence for ( H_a )</td>
</tr>
<tr>
<td>3</td>
<td>Moderate evidence for ( H_a )</td>
</tr>
<tr>
<td>1</td>
<td>Anecdotal evidence for ( H_a )</td>
</tr>
<tr>
<td>1/3</td>
<td>No evidence</td>
</tr>
<tr>
<td>1/10</td>
<td>Anecdotal evidence for ( H_0 )</td>
</tr>
<tr>
<td>1/30</td>
<td>Moderate evidence for ( H_0 )</td>
</tr>
<tr>
<td>1/100</td>
<td>Strong evidence for ( H_0 )</td>
</tr>
<tr>
<td>&lt; 1/100</td>
<td>Extreme evidence for ( H_0 )</td>
</tr>
</tbody>
</table>

Adapted from Jeffreys [52, p. 433], and Lee and Wagenmakers [65, p. 105].

Table 1. Evidence categories for the Bayes factor.
4. Bayesian vs. Frequentist approaches to hypothesis testing: An example

Bayes factors to evaluate the amount of evidence in favor or against $H_0$ and $H_a$ are one of the big selling points of the Bayesian framework.\(^1\) As stated in the previous section, the core idea is that the magnitude of evidence in favor of the null hypothesis compared to that of the alternative hypothesis can be estimated (or vice-versa). As we have seen, this approach has multiple advantages, such as departing from a *hit-or-miss* approach to results reporting, or being able to show evidence in favor of the null. The possibility of providing evidence in favor of both the null and the alternative hypotheses has some important advantages. One of them is that it helps to overcome one of the most common issues behind the well-known file-drawer effect, in that results do not suddenly become meaningless when the *p*-value is over certain threshold. Another advantage is that it gives us more freedom when establishing hypothesis, particularly in topics where hypothesizing the absence of differences may be necessary for theoretical advance.

In this section, an example from a field known as Bayesian reasoning will be presented, which deals with how people update their beliefs when new evidence is available (e.g., when receiving a positive result in a medical test, how likely it is that I have a disease?). There is a long standing debate in the field about why people are unable to solve medical screening problems such as the one shown in Table 2 when the information is shown in a standard probability format (i.e., single-event probabilities; for instance, 1% have cancer), but have a comparatively better time when the same information is shown in a standard frequency format (i.e., natural frequencies; for instance, 10 in 1000 have cancer). As it is often the case, the debate about these issues is very complex (for a review, see \cite{71}), and the present example will focus on a single unnuanced aspect with the goal of showing the usefulness of the Bayesian statistics paradigm.

---

**Standard probability format**

The probability of breast cancer is 1% for women at age 40 who participate in routine screening. If a woman has breast cancer, the probability is 80% that she will get a positive mammography. If a woman does not have breast cancer, the probability is 9.6% that she will also get a positive mammography.

A woman in this age group had a positive mammography in a routine screening. What is the probability that she actually has breast cancer? _____%  

**Standard frequency format**

Ten out of every 1000 women at age 40 who participate in routine screening have breast cancer. Eight of every 10 women with breast cancer will get a positive mammography. Ninety-five out of every 990 women without breast cancer will also get a positive mammography.

Here is a new representative sample of women at age 40 who got a positive mammography in routine screening. How many of these women do you expect to actually have breast cancer? ____ out of ____

---

\footnote{However, we recommend the interested reader to revise a recent paper by Lakens \cite{70}, which describes an approach to test for equivalence within a Frequentist framework.}

Table 2. Standard probability and standard frequency format problems, as shown by Gigerenzer and Hoffrage \cite{72}.  

---

\(^1\) However, we recommend the interested reader to revise a recent paper by Lakens \cite{70}, which describes an approach to test for equivalence within a Frequentist framework.
Some authors [73, 74] argue that the crucial factor explaining the differences between the two versions is not the representation format (i.e., probabilities or natural frequencies), but the reference class or more specifically the computational complexity is caused by the reference class of the problems [75]. In brief, as the probability version has a relative reference class, and all the numbers refer to the group above them (e.g., 80% from the 1% who have breast cancer will get a positive mammography). To solve the problem, we need to use the base-rates (in this example, percentage of women with and without breast cancer; 1 and 99%), and the percentage of women who got a positive mammography amongst those two groups (e.g., 80 and 9.6%; see Eq. (4)). In the frequency version, as the reference class is absolute, and all numbers can be seen as referring to the 1000 women, we can ignore the base-rates and directly use the positive mammographies for women with and without cancer (8 and 95; see Eq. (5)). The above-mentioned authors hypothesized that when reference class and computational complexity are taken into account, there is no difference between probabilities and natural frequencies. In other words, they expect the null hypothesis to be true (Figure 2).

\[
p(H|D) = \frac{1\% \times 80\%}{1\% \times 80\% + 99\% \times 9.6\%} = 0.077 \tag{4}
\]

\[
p(H|D) = \frac{8}{8 + 95} = 0.077 \tag{5}
\]

Now, imagine two PhD students, a Frequentist (i.e., Student 1) and a Bayesian (i.e., Student 2). After reading a critical but often ignored Fiedler’s paper [73], they had the idea that computational complexity class (and not representation format) is the key issue when trying to understand how people solve Bayesian reasoning problems. They devise a very simple experiment where two different groups of people will be asked to solve one Bayesian reasoning problem that will be shown either in single-event probabilities or in natural frequencies. In both cases, the arithmetic complexity (i.e., number of arithmetic steps required to solve the problem) will be exactly 2. That is, to solve the problems, participants would need to do two arithmetic operations, a sum and a division. They used a test with a 100% sensitivity and 0% specificity, which could not have any clinical application, but it is useful to get a few arithmetic steps out of the probability format and check if computational complexity underlies Bayesian reasoning. With this manipulation, the algorithms to solve the probability and frequency versions become

Figure 2. Relative and absolute reference classes represented by the reference of the last row (test results). In the Relative reference class, the information about the test, for example, 80% positive (+) and 20% negative results (−) refers to the 1% women with BC, but not to the 100% of the women (it is not an 80% of the 100%). However, in the absolute reference class, the same information, 8+ and 2−, refers to the women with BC, but also to the 1000 women directly. This translates in the need to use Eq. (4) for relative probabilities and Eq. (5) for absolute frequencies.
Eqs. (6) and (7), respectively. It is easy to see how both have become roughly equivalent now in terms of arithmetic complexity.

\[
p(H|D) = \frac{10\% \times 100\%}{10\% \times 100\% + 90\% \times 100\%} = \frac{10\%}{10\% + 90\%} = 0.1 \quad (6)
\]

\[
p(H|D) = \frac{10}{10 + 90} = 0.1 \quad (7)
\]

As it can be deduced, Student 1 would have a Fisherian approach to statistics and Student 2 a Bayesian approach. Both run an experiment with a total of 62 participants (31 per group),\(^2\) and have the following results:

<table>
<thead>
<tr>
<th>Contingency tables</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Representation format</strong></td>
</tr>
<tr>
<td><strong>Accuracy</strong></td>
</tr>
<tr>
<td>0</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td><strong>Total</strong></td>
</tr>
</tbody>
</table>

### 4.1. PhD Student 1—Frequentist

Student 1, as the most good NHST practitioners would do, conducts a Chi-square test and reports that he did not obtain a significant effect of representation format when arithmetic steps were equal ($\chi^2 = 0.088$, $p = 0.767$). He is happy, because this is congruent with his hypothesis. He then writes a brief report detailing his idea and experimental results and sends the manuscript draft to his advisor. A few days later, he receives his advisor feedback, telling him that his non-significant results could be caused by a number of reasons, and as a consequence, the non-significant results are hard to interpret.

<table>
<thead>
<tr>
<th>Chi-square tests</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Value</strong></td>
</tr>
<tr>
<td>$\chi^2$</td>
</tr>
<tr>
<td><strong>N</strong></td>
</tr>
</tbody>
</table>

\(^2\)Of course, the sample size and manipulation for this experiment is more congruent with a pilot experiment than a real one that could be sent to a journal on its own. As a side note, take into account that one of the advantages of the Bayesian framework some authors propose is a sequential sampling rule, where sampling stops when the evidence (BF) is over a predetermined threshold (e.g., $\text{BF}_{10} > 10$ or $< 0.1$), see Lindley [76].
His advisor suggests carrying out a few more experiments using variations of the task and decent sample-sizes, to be able to perform a meta-analysis that could convince the editorial board of a journal that their endeavor is noteworthy, as they would probably have a hard time publishing those non-significant results by themselves.

4.2. PhD Student 2—Bayesian

Student 2, instead of performing a Chi-square test, prefers to use a well-known analysis among Bayesian statisticians called Bayes factor (BF; see [17, 65]). He uses a very simple to use software called JASP [61], that incorporates Bayesian contingency tables, and outputs BF results in ready to use APA formatted tables. He finds that when arithmetic steps are equal, there is a BF of 4.656, that is, there is 4.6 times more evidence in favor of the null-hypothesis than the alternative-hypothesis. Along his advisor, they send the manuscript to a journal, pushing for the relative importance of arithmetic complexity over representation format. In practical terms, it is more likely that the editor will be willing to publish this interesting result, although the amount of evidence in favor of the null would be considered moderate by some standards (see [53]).

<table>
<thead>
<tr>
<th>Bayesian contingency tables tests</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>BF$_{0+}$, independent multinomial</td>
<td>4.656</td>
</tr>
<tr>
<td>$N$</td>
<td>62</td>
</tr>
</tbody>
</table>

Note: For all tests, the alternative hypothesis specifies that group Natural-Frequencies is greater than group Probabilities.

As the evidence for the null effect is not very strong, they would need to run a few more studies with variations to replicate the finding and show, using BF, how much more evidence there is for the null hypothesis compared to the alternative hypothesis. Alternatively, they could increase the sample size in their experiment until the stopping rule threshold (e.g., BF$_{10} < 0.1$) is reached.

This example was aimed to describe (in a very simplified manner) one of the practical advantages of the Bayesian framework, that is, being able to present the amount of evidence for and against both the null and alternative-hypotheses. This, combined with the incremental nature of the Bayesian inference process, allows us to move further from the hit-or-miss approach generally reinforced by the NHST framework, in which significant results are seen as more valuable than non-significant ones.

5. Conclusion

During the past 70 years, the NHST has dominated the way in which knowledge is produced and interpreted and still governs the way in which researchers analyze their data, reach
conclusions, and report results [10, 45]. This approach has been largely criticized [9, 16, 21, 22, 39, 43–46], and “a major concern expressed by critics is that such testing is misunderstood by many of those who use it” [35, p. 241]. Some authors [9, 13] emphasized that one of the most pervasive influences of the NHST approach has been its over reliance on p-values, and in particular, in the way that p-values have been interpreted (see, for instance [35, 36, 77]). One of the most common misinterpretations of p-values it has been to consider a p-value as a valid indicator of the magnitude of evidence of a result (i.e., effect size fallacy). Regarding this point, Cohen emphasized that the only way to estimate the magnitude of an effect is to calculate the value of the effect size with the appropriate statistic and its confidence interval [38]. The correct way to interpret p-values is two-fold. On one hand, to reject $H_0$ only allows us to conclude that $H_0$ is unlikely. On the other hand, failing to reject $H_0$ simply allows us to state that—given the evidence at hand—one cannot make an assertion about the existence of some effect or phenomenon [42]. An immediate consequence of the wrong way in which a big number of researchers interpret p-values is that null results have been usually considered as the absence of evidence of the existence of an effect. This perspective regarding the decisions made when a given p-value threshold is not reached (i.e., $p < 0.05$) do not promote scientific advance and quickly leads us to a systematic bias toward ignoring promising but “non-significant” findings that may be further explored, fed into meta-analysis, of just be considered by other researchers in the field. This fact is against the pursue of any empirical science and may be harmful to the construction of a cumulative base of knowledge [5].

As a way to provide a complementary (or alternative) method to deal with the current NHST practice, we described here a Bayesian approach to hypothesis testing. A Bayesian approach allows us to think about phenomena in terms of the magnitude of evidence that supports the existence of an effect, instead of a dichotomous and artificial way of thinking in which an effect either exists or does not exist [21]. As described in previous sections, a Bayesian approach provides us a measure of evidence for and against both the null and the alternative hypotheses (i.e., Bayes factor, BF; see [17]). The use of Bayes factors helps to overcome one of the most common issues behind the well-known file-drawer effect, reducing the existing bias through which results suddenly become meaningless when the p-value is over certain threshold (e.g., $p > 0.05$). A straightforward feature of this approach is that “Bayesian statistics assigns no special status to the null hypothesis, which means that Bayes factors can be used to quantify evidence for the null hypothesis just as for any other hypothesis” [65, p. 108]. Therefore, a Bayesian approach gives us more freedom when establishing hypothesis, for example in topics where hypothesizing the absence of differences may be necessary for theoretical advance.

However, a major problem with Bayesian statistics has historically been that they require complex and intricate mathematical calculations that were analytically intractable, at least without the required techniques and specialized software. However, this scenario changed dramatically during the 1990s with the development of sampling techniques like Markov-Chain Monte Carlo (MCMC; see [55]) along with the availability and improvement of specifically developed software (e.g., WinBUGS, see [57, 58]; JAGS, see [59, 60]) that makes exact Bayesian inferences possible even in very complex models. Nowadays, the relatively recent implementation and availability of Bayesian analysis in “easy-to-use” and open software such as JASP [61], R toolboxes such as Bayes factor [78], or more specialized ones like WinBUGS,
JAGS, or Stan (http://mc-stan.org/) makes Bayesian statistics more accessible to all researchers, academics and students. This widespread availability, paired with the advantages of the Bayesian approach described in this chapter, and several times elsewhere [79–82], should help establish the Bayesian paradigm as a viable and popular alternative to NHST.

Despite all the important Bayesian paradigm advantages, as always, there is potential for misuse. As pointed out by Morey, Bayes factor interpretation is very natural (i.e., as the amount of evidence in favor of one hypothesis in comparison to another), and does not need specific decision thresholds, as it is the case of p-values [83]. However, some standards that could help to communicate BF results have been proposed (see [53]) and may be helpful to people that are not familiar with them. Nonetheless, the introduction of these labels also creates an opportunity for misuse, as they could be misinterpreted as decision boundaries. It is very important to be aware of this fact, and be careful when using them, to avoid making “BF > 3” the new “p < 0.05.”

To sum up, the main goal of this chapter has been to increase the degree of awareness regarding the limitations of the NHST approach and highlight the advantages of the Bayesian approach. We expect that the inclusion of an easy-to-understand example of a specific case where a Bayesian paradigm shows its practical utility may offer the newborn readers on this matter a glimpse to the usefulness of this alternative to the way in which they can analyze and interpret their data. As a final remark, we would like to point an often-heard recommendation for people interested in starting to use BF, which is to introduce them alongside p-values and effect size measures, to ease the transition to the new paradigm, and make them comprehensible to people not yet familiarized with them.

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