# Replication and *p* Intervals

## *p* Values Predict the Future Only Vaguely, but Confidence Intervals Do Much Better

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ABSTRACT—*Replication is fundamental to science, so statistical analysis should give information about replication. Because* p *values dominate statistical analysis in psychology, it is important to ask what* p *says about replication. The answer to this question is "Surprisingly little." In one simulation of 25 repetitions of a typical experiment,* p *varied from <.001 to .76, thus illustrating that* p *is a very unreliable measure. This article shows that, if an initial experiment results in two-tailed* $p = .05$, *there is an 80% chance the one-tailed* p *value from a replication will fall in the interval (.00008, .44), a 10% chance that* $p < .00008$, *and fully a 10% chance that* $p > .44$. *Remarkably, the interval—termed a* p interval*—is this wide however large the sample size.* p *is so unreliable and gives such dramatically vague information that it is a poor basis for inference. Confidence intervals, however, give much better information about replication. Researchers should minimize the role of* p *by using confidence intervals and model-fitting techniques and by adopting meta-analytic thinking.*

> *[*p *values] can be highly misleading measures of the evidence . . . against the null hypothesis.*
>
> —Berger & Sellke, 1987, p. 112

> *We must finally rely, as have the older sciences, on replication.*
>
> —Cohen, 1994, p. 1002

If my experiment results in $p = .05$, for example, what $p$ is an exact replication—with a new sample of participants—likely to give? Surprisingly, the answer is "Pretty much anything."

Replication is at the heart of science. If you repeat an experiment and obtain a similar result, your fear that the initial result was merely a sampling fluctuation is allayed, and your confidence in the result increases. We might therefore expect statistical procedures to give information about what a replication of an experiment is likely to show. Null hypothesis significance testing (NHST) based on $p$ values is still the primary technique used to draw conclusions from data in psychology (Cumming et al., 2007) and in many other disciplines. It is therefore pertinent to ask my opening question.

In this article, I investigate $p$ values in relation to replication. My conclusion is that, if you repeat an experiment, you are likely to obtain a $p$ value quite different from the $p$ in your original experiment. The $p$ value is actually a very unreliable measure, and it varies dramatically over replications, even with large sample sizes. Therefore, any $p$ value gives only very vague information about what is likely to happen on replication, and any single $p$ value could easily have been quite different, simply because of sampling variability. In many situations, obtaining a very small $p$ value is like winning a prize in a lottery. Put differently, even if we consider a very wide range of initial $p$ values, those values account for only about 12% of the variance of $p$ obtained on replication. These severe deficiencies of $p$ values suggest that it is unwise to rely on them for research decision making.

Confidence intervals (CIs), by contrast, give useful information about replication. There is an 83% chance that a replication gives a mean that falls within the 95% CI from the initial experiment (Cumming, Williams, & Fidler, 2004). Any 95% CI can thus be regarded as an 83% prediction interval for a replication mean. The superior information that CIs give about replication is a good reason for researchers to use CIs rather than $p$ values wherever possible.

## OVERVIEW

The first main section of this article presents an example experiment to illustrate how $p$ varies over replications. The experiment compares two independent groups ($N$s = 32) and is typical of many in psychology. A simulation of results, assuming a given fixed size for the true effect in the population, shows that

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$p$ varies remarkably over repetitions of the experiment. I introduce the idea of a *p interval*, or prediction interval for $p$, which is an interval with a specified chance of including the $p$ value given by a replication. Unless stated otherwise, the $p$ intervals I discuss are 80% $p$ intervals. The very wide dispersion of $p$ values observed in the example illustrates that $p$ intervals are usually surprisingly wide. I then describe the distribution of $p$ and calculate $p$ intervals when it is assumed that the size of the true effect in the population is known.

I go on to investigate the distribution of $p$ values expected on replication of an experiment when the population effect size is not known and when only $p_{\mathrm{obt}}$, the $p$ value obtained in the original experiment, is known. This allows calculation of $p$ intervals without needing to assume a particular value for the population effect size. These $p$ intervals are also remarkably wide.

I then consider studies that include multiple independent effects rather than a single effect. Replications of such studies show very large instability in $p$ values: Repeat an experiment, and you are highly likely to obtain a different pattern of effects. The best approach is to combine evidence over studies by using meta-analysis. I close by considering practical implications and make four proposals for improved statistical practice in psychology.

Selected steps in the argument are explained further in Appendix A, and equations and technical details appear in Appendix B. I start now by briefly discussing $p$ values, the statistical reform debate, and replication.

## *p* Values, Statistical Reform, and Replication

A $p$ value is the probability of obtaining the observed result, or a more extreme result, if the null hypothesis is true. A typical null hypothesis states that the effect size in the population is zero, so $p = .05$ means there is only a 5% chance of obtaining the effect we observed in our sample, or a larger effect, if there is actually no effect in the population. Psychologists overwhelmingly rely on $p$ values to guide inference from data, but there are at least three major problems. First, inference as practiced in psychology is an incoherent hybrid of the ideas of Fisher and of Neyman and Pearson (Gigerenzer, 2004; Hubbard, 2004). Second, the $p$ value is widely misunderstood in a range of ways, and, third, it leads to inefficient and seriously misleading research decision making. Chapter 3 of Kline's (2004) excellent book describes 13 pervasive erroneous beliefs about $p$ values and their use and also explains why NHST causes so much damage. For decades, distinguished scholars have made cogent arguments that psychology should greatly diminish its reliance on $p$ values and instead adopt better techniques, including effect sizes, CIs, and meta-analysis.

Kline's (2004, p. 65) Fallacy 5 is the *replication fallacy*: the belief that $1 - p$ is the probability a result will replicate or that a repetition of the experiment will give a statistically significant result. These beliefs are badly wrong: Finding that $p = .03$, for example, does not imply anything like a 97% chance that the result will replicate or that a repetition of the experiment will be statistically significant. After obtaining $p = .03$, there is actually only a 56.1% chance that a replication will be statistically significant with two-tailed $p < .05$, as Appendix B explains. Misconceptions about $p$ and replication are, however, widely held: Oakes (1986) found that 60% of his sample of researchers in psychology endorsed a statement of the replication fallacy, and Haller and Krause (2002) reported that 49% of academic psychologists and fully 37% of teachers of statistics in psychology in their samples endorsed the fallacy.

Given the crucial role of replication in science and the ubiquity of NHST and $p$ values, it is curious that there has been almost no investigation of what $p$ does indicate about replication. (I mention in Appendix A some articles that have touched on this question.) This omission is all the more serious because of the widespread misconceptions, and because $p$ gives only extremely vague information about replication—meaning that $p$ intervals are extremely wide. The uninformativeness of $p$ is another reason for psychology to cease its reliance on $p$ and pursue statistical reform with vigor.

Note also that psychology rightly pays great attention to the reliability and validity of its measures. The validity of $p$ as a measure that can inform inference from data continues to be debated—as I note in Appendix A. Reliability must, however, be considered prior to validity, and my discussion demonstrates that the test–retest reliability of $p$ is extremely low.

## Replication: Exact Or Broad

*Exact replication* refers to a repeat experiment in which everything is exactly the same, except that a new, independent sample of the same size is taken from the same population. It is the *mere replication* referred to by Mulkay and Gilbert (1986). Conducting exact replications and combining the results reduces the influence of sampling variability and gives much more precise estimates of parameters.

Considered more broadly, replication includes repetitions by different researchers in different places, with incidental or deliberate changes to the experiment. Such broad replication also reduces the influence of sampling variability and, in addition, tests the generality of results.

Of course, exact replication is an abstraction because, in practice, even the most careful attempt at exact repetition will differ in some tiny details from the original experiment. The results of an attempted exact repetition are therefore likely to differ even more from the original than are the results of the ideal exact replications I will discuss, and $p$ values are likely to vary even more dramatically than my analysis indicates. Throughout this article, the replication I consider is exact replication, and I am assuming that sampling is from normally distributed populations. First, consider a fictitious example and a picture (Fig. 1).

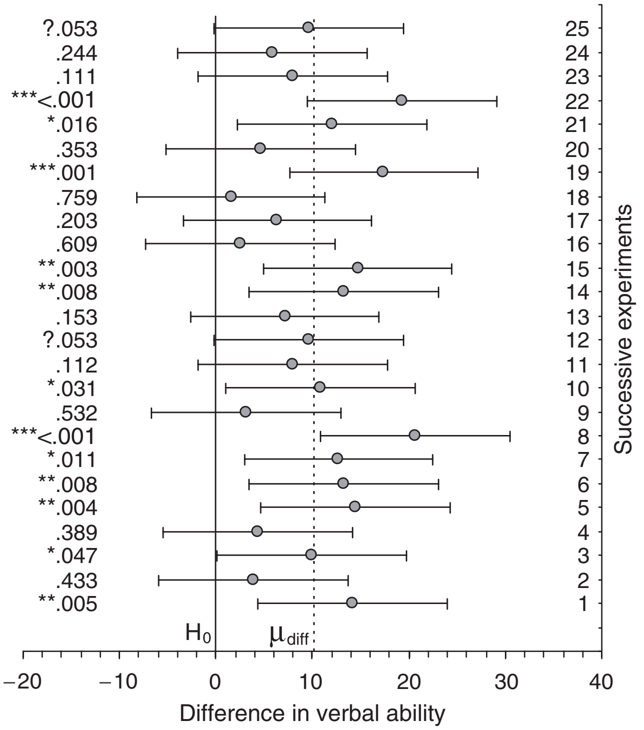


**Fig. 1.** Simulation of 25 independent experiments, each with two groups (*N*s = 32) from normally distributed populations of verbal ability scores. Both the difference between population means $\mu_{\text{diff}} = 10$ (dotted vertical line) and the population *SD* $\sigma = 20$ are assumed to be known. For each experiment, the sample mean difference $M_{\text{diff}}$ (grey dot) and its 95% confidence interval (CI) is shown. At left is the two-tailed $p$ for a test of the null hypothesis $H_0$: $\mu_{\text{diff}} = 0$ (solid vertical line). ? = $.05 < p < .10$, * = $p < .05$, ** = $p < .01$, and *** = $p < .001$. Note the extremely large variation in $p$, from <.001 to .759.

## REPLICATION: AN EXAMPLE WITH KNOWN POPULATION EFFECT SIZE

Suppose a test of children's verbal ability has been well-standardized to have normally distributed scores in the reference population, with a SD of $\sigma = 20$. We wish to compare the scores of children in two school districts, and we are willing to assume $\sigma = 20$ in both districts. We obtain test scores for a random sample of children from each district (*N*s = 32). Suppose we find that $M_{\text{diff}}$, the difference between the two sample means, is 14.15. This $M_{\text{diff}}$ value is plotted as the large dot for Experiment 1, near the bottom of Figure 1.

There are two common ways to analyze data from this experiment. Taking an NHST approach, we test the null hypothesis that there is no difference between the population means for the two districts ($H_0$:$\mu_{\text{diff}} = 0$). This hypothesis is marked by the solid vertical line in Figure 1. We calculate the familiar $z$ test statistic for the difference and then use tables or software to determine the two-tailed $p$ value corresponding to that $z$ value. For Experiment 1, $z = 2.83$ and $p = .005$, as reported in Figure 1.

The second approach is to calculate the 95% CI for the difference, which is an interval centered on $M_{\text{diff}}$. For Experiment 1 it is 14.15 ± 9.80, or [4.35, 23.95], and is shown as the error bars on the large dot that is the bottom $M_{\text{diff}}$ value in Figure 1. We interpret $M_{\text{diff}}$ as our point estimate of the unknown $\mu_{\text{diff}}$, which is the difference between the mean verbal ability in the two districts. The CI is the interval estimate, which indicates a range of plausible values for $\mu_{\text{diff}}$.

Suppose the true difference between the population means of the two districts is $\mu_{\text{diff}} = 10$, as marked by the vertical dotted line in Figure 1. This difference is the population effect size, which can be expressed in units of $\sigma$ to give Cohen's $\delta$, so $\delta = \mu_{\text{diff}}/\sigma = 10/20 = 0.5$ is the standardized population effect size. For each experiment in the computer simulation,[1] I drew a random sample ($N = 32$) from each of two normal distributions, which represented the population scores in the two school districts. Each distribution had $\sigma = 20$ as we earlier assumed, and the difference between their means was $\mu_{\text{diff}} = 10$.

Figure 1 illustrates 25 replications of our experiment. For each experiment, $M_{\text{diff}}$ is plotted as the large dot, the 95% CI is shown as the error bars on this dot, and the two-tailed $p$ for testing $H_0$:$\mu_{\text{diff}} = 0$ is reported. The $p$ values less than .05 are marked with conventional asterisks, and those between .05 and .10 are labeled with a question mark.

The most striking aspect of Figure 1 is the extreme variation in $p$, from <.001 to .76. It seems $p$ for a replication of our experiment could take almost any value!

The statistical power for this situation is .52. (I use two-tailed $\alpha = .05$ to calculate power.) Therefore, in the long run, 52% of experiments will give $p < .05$, and in Figure 1 just 12 out of 25 do so. This experiment is typical of a range of fields in psychology, in which studies of published research have found that median estimated power to find a medium-sized effect (i.e., $\delta = 0.5$ in the population) is around .5 (Maxwell, 2004, p. 148). Therefore the dramatic variation in $p$ illustrated in Figure 1 cannot be dismissed as merely arising from unusually small samples or unusually low power. Also, variation in $p$ is similarly dramatic if $\sigma$ is not assumed known and our test statistic is $t$ rather than $z$.

Carrying out such an experiment—as much of psychology spends its time doing—is equivalent to closing your eyes and randomly choosing 1 of the 25 experiments (or any of the infinite number of others that could have been illustrated) in Figure 1. A *** result ($p < .001$) is first prize in this $p$ value lottery, and you need almost the luck of a lottery winner to obtain it. Given the extreme variation in $p$, you may wonder whether it is worth carrying out such experiments. That is an excellent question!

## DISTRIBUTION OF $p$ WHEN POPULATION EFFECT SIZE $\delta$ IS KNOWN

Imagine running the simulation of Figure 1 numerous times and collecting all the $p$ values. They would form the histogram in

[1] Figures 1, A1, and A3 are from a component of ESCI ("ess-key"; Exploratory Software for Confidence Intervals), which runs under Microsoft Excel. This component of ESCI may be downloaded from www.latrobe.edu.au/psy/esci.

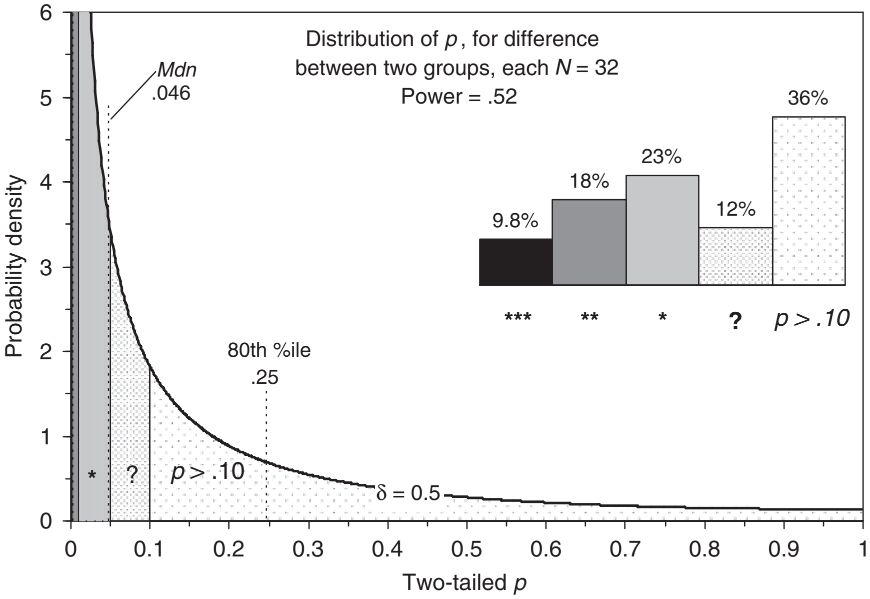


**Fig. 2.** The probability distribution of two-tailed *p*, when population effect size $\delta = 0.5$ and $N = 32$ for each of two groups. The area under the curve gives the probability that *p* falls in any chosen interval on the horizontal (*p*) axis. The median of the distribution is marked (*Mdn* = .046), meaning that 50% of *p* values will be less than .046. The 80th percentile is also marked (80th %ile; dotted line at .25), meaning that 80% of the area under the curve lies to the left of .25, that 80% of *p* values will be less than .25, and that .25 is the upper limit of the 80% *p* interval that has a lower limit of 0. The lightly dotted area under the curve to the right of $p = .10$ is .36, the closely dotted area between .05 and .10 labeled "?" is .12, the light grey area between .01 and .05 labeled "*" is .23, and the areas between .001 and .01 (**) and to the left of .001 (***) are too narrow and tall to be seen clearly in the figure—their areas are .18 and .098 respectively. Probabilities corresponding to these conventional intervals of *p* are illustrated as percentages in the histogram. The area to the left of .05 is the power (.52) for two-tailed $\alpha = .05$.

Figure 2. This histogram summarizes the curve in Figure 2, which is the probability distribution of *p* for two independent samples (*N*s = 32) when $\delta = 0.5$. It is based on Equation B1 in Appendix B, which can be used to plot the distribution of the two-tailed *p* value whenever δ and *N* are known.

The curve in Figure 2 has large variance and is highly skewed. Areas under the curve give the probability that *p* lies in any chosen interval on the horizontal (*p*) axis. For example, the lightly dotted area is .36, which is the probability that $p > .10$; correspondingly, the histogram shows that 36% of *p* values will be greater than .10. The "?" region under the curve corresponds to $.05 < p < .10$ and has an area of .12, so 12% of *p* values will fall in that range. The proportions of replications that give * ($p < .05$), ** ($p < .01$), and *** results are shown as bars in the histogram and as shaded areas under the curve, although the two leftmost areas, for ** and ***, are too tall and narrow to be easily visible.

The power is .52, meaning 52% of the area under the curve lies to the left of .05 (because we use $\alpha = .05$ for power), and this is the sum of the *, **, and *** areas. The median (.046) is marked, meaning 50% of *p* values are less than .046.

The 80th percentile (.25) is also marked, which means that $p < .25$ for 80% of replications and that $p > .25$ for fully 20% of replications, so an interval that includes 80% of two-tailed *p* values is (0, .25). If 95% is preferred, the interval is (0, .67), which is also remarkably wide; there is a 5% chance that $p > .67$! It is a recurring theme that such intervals are very wide, implying that a replication is likely to give a *p* value quite different from the original $p_{\text{obt}}$. The choice of interval percentage is arbitrary, but I choose 80%, by distant analogy with psychology's custom of seeking power of .80 and to reduce the risk that my analysis is dismissed as extreme and produces very wide intervals only because it uses 95% or some other very high percentage. As noted earlier, I refer to these intervals for replication *p* as *p* intervals and, unless otherwise mentioned, I use 80% *p* intervals.

Figure 3 shows further examples of the probability distribution of *p*. The curves apply when $N = 32$ for each of two samples, and $\delta = 0$, 0.2, 0.5, and 0.8. The $\delta = 0.5$ curve is the same as in Figure 2, and the $\delta = 0$ line corresponds to $H_0$ true (i.e., zero difference between the two district means). The horizontal line for $\delta = 0$ arises because, when $H_0$ is true, every possible *p* value is equally likely. This may seem surprising, but it follows directly from the definition of *p*.

Figure 3 also shows the power for the four curves, the medians, the 80th percentiles, and the four histograms. Only at very high power are *p* values heavily concentrated at very low values. If in

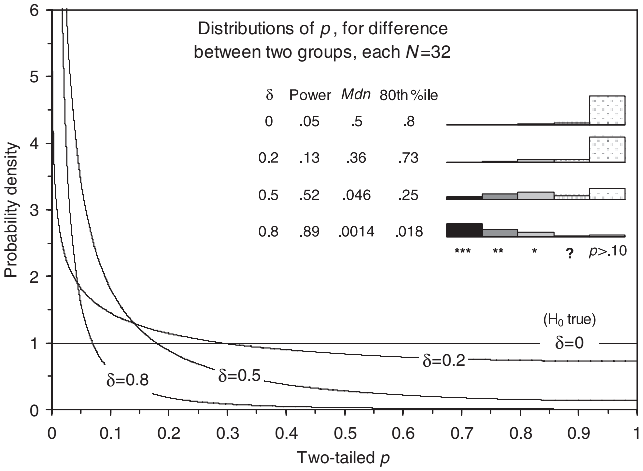


**Fig. 3.** Probability distributions of $p$ for two groups ($N$s = 32) when $\delta = 0$ (i.e., $H_0$ true) and $\delta = 0.2$, 0.5, and 0.8, which can be regarded as small, medium and large effects, respectively. The $\delta = 0.5$ curve is the same as that in Figure 2. For each value of $\delta$, the power, median (*Mdn*), and 80th percentile (80th %ile) are tabulated and the histogram of $p$ values is shown; the 80th percentile is the upper limit of the $p$ interval with a lower limit of 0. ? = $.05 < p < .10$, * = $p < .05$, ** = $p < .01$, and *** = $p < .001$.

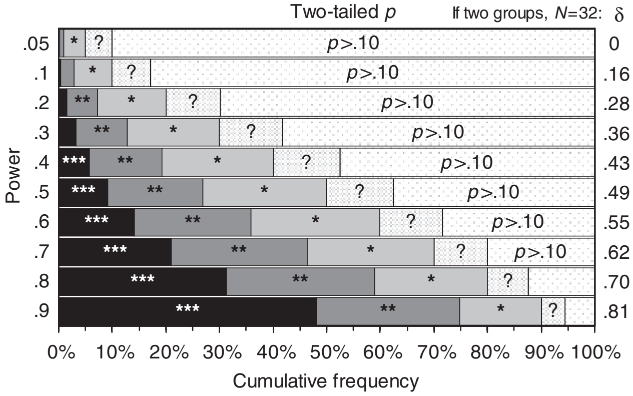


**Fig. 4.** Cumulative frequencies for $p$, for different values of power. When $H_0$ is true (the top bar), the power is .05 and the shaded bars show a cumulated 5% chance of $p$ in the three ranges marked by asterisks (<.001; .001–.01; .01–.05, respectively) and a further 5% chance that $.05 < p < .10$. The percentages for .5 power are very similar to those in the histogram in Figure 2, in which the power is .52. For a given power, the percentages are independent of $N$. If $N = 32$ for each of two groups, the corresponding $\delta$ values are shown at right.

our example $\mu_{\text{diff}} = 16$ and thus $\delta = 0.8$—conventionally regarded as a large effect—then power is .89, which is a very high value for psychology. Even then the $p$ interval is (0, .018), so fully 20% of $p$ values will be greater than .018.

### Distribution of *p* Depends Only on Power

Power determines the distribution of $p$, as Appendix B explains. Power varies with $N$ and population effect size $\delta$, and a particular value of power can reflect a number of pairs of $N$ and $\delta$ values. Any pair that gives that value of power will give the same distribution of $p$. Thus, in the example, power is .52 for two samples of $N = 32$ when $\delta = 0.5$. Power would also be .52 for various other combinations of sample size and population effect size: for example, $N = 8$ and $\delta = 1.0$, or $N = 200$ and $\delta = 0.2$, or even $N = 800$ and $\delta = 0.1$. The distribution and histogram in Figure 2 applies in all of those cases, because power is .52 for each. Even for a very large $N$, if power is .52, the $p$ interval will still be (0, .25).

A curve and histogram like those in Figures 2 and 3 can be calculated for any given power. Figure 4 shows in cumulative form the percentages of the different ranges of $p$ for a selection of power values from .05 (i.e., $\delta = 0$, or $H_0$ true) to .9. The values for the bar representing a power of .5 are very similar to the percentages shown in Figure 2, in which power is .52. To help link the distributions in Figure 4 back to my example, the corresponding effect sizes ($\delta$ values) when $N = 32$ for each group are shown at the right.

### *p* Is a Poor Basis for Inference

Consider how uninformative $p$ is for the true value of $\delta$. Noting where $p$, calculated from data, falls along the horizontal axis in Figure 3 does not give a clear indication as to which of the infinite family of curves—which of the possible $\delta$ values—is likely to be correct. Figure 4 also shows only a gradual change in distributions with changes in power or effect size, again suggesting $p$ is very uninformative about $\delta$. Obtaining $p = .05$, for example, gives very little hint as to which of the curves in Figure 3 or which of the $\delta$ values in Figure 4 is the best bet to be the cause of that particular $p$ value.

Alternatively, we could focus not on estimating $\delta$, but only on judging whether $H_0$ is true; that is, whether $\delta$ equals zero or not. Figure 3 suggests that most $p$ values do not provide a good basis for choosing between the $\delta = 0$ horizontal line and any other curve. Figure 4 shows that $p$ values greater than .01 or even .05 are quite common for medium to high power (the lower bars in the figure), and that a minority of $p$ values less than .01 do occur for low to medium power (the upper bars). In other words, most $p$ values provide very poor guidance as to whether or not $H_0$ is true. This conclusion throws doubt on conventional practice in which a $p$ value is used to make sharp discriminations between situations allowing rejection of $H_0$ and those that do not. Only ***, and to a lesser extent **, $p$ values have much diagnostic value about whether $H_0$ is true. However, a result of *** is often sufficiently clear cut to hit you between the eyes, and so it is hardly a triumph for $p$ that it rejects a hypothesis of zero effect in such cases!

In summary, the distribution of two-tailed $p$ when the power is known or when $\delta$ and $N$ are known is illustrated in Figures 2 and 3. The distribution is highly skewed (unless $\delta = 0$) and is independent of $N$ for a given power. It generally has large variance, and the $p$ intervals are very wide. Figures 3 and 4 suggest only very small $p$ values have much diagnostic value as to whether or not the true effect size is zero.

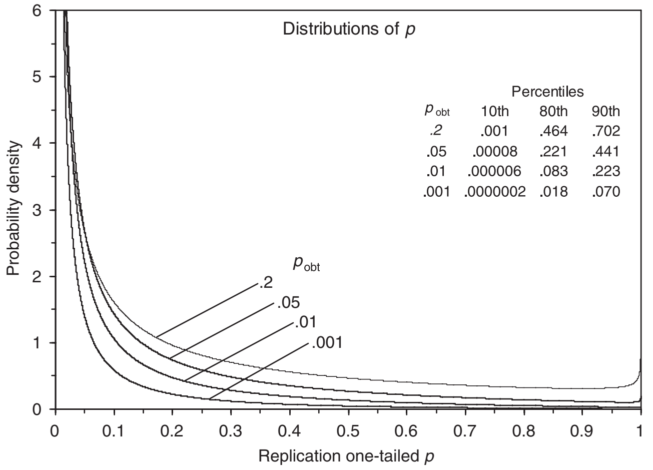
## DISTRIBUTION OF $p$ GIVEN ONLY AN INITIAL $p_{\text{obt}}$

The initial example above was based on the unrealistic assumption that we know δ, the size of the effect in the population, and the distributions in Figures 2–4 relied on knowing δ and $N$, or power. I now assume that δ is not known and consider the distribution of the $p$ value after an initial experiment has yielded $M_{\text{diff}}$, from which the $p_{\text{obt}}$ is calculated. The appendices explain how the probability distribution of $p$ can be derived without knowing or assuming a value for δ (or power). The basic idea is that our initial $M_{\text{diff}}$ is assumed to come from populations with some unknown effect size δ. Our $M_{\text{diff}}$ does not give a precise value for δ, but does give sufficient information about it for us to find a distribution for replication $p$ values, given only $p_{\text{obt}}$ from the initial experiment. We do not assume any prior knowledge about δ, and we use only the information $M_{\text{diff}}$ gives about δ as the basis for the calculation for a given $p_{\text{obt}}$ of the distribution of $p$ and of $p$ intervals.

I have set my whole argument, including the derivation of $p$ intervals without assuming a value for δ, in a conventional frequentist framework because that is most familiar to most psychologists. However, an alternative approach within a Bayesian framework is appealing, although it is important to recognize that the two conceptual frameworks are quite different and license different interpretive wording of conclusions. Even so, they sometimes give the same numerical results. For example in some simple situations, using reasonable assumptions, the 95% CI is numerically the same as the Bayesian 95% credible interval. A researcher can regard the interval as a pragmatically useful indication of uncertainty, without necessarily being concerned with the niceties of the interpretation permitted by either framework. Similarly, when finding $p$ intervals without assuming a value for δ, a Bayesian analysis would start with a prior probability distribution that expresses our ignorance of δ. Then, as an anonymous reviewer pointed out, it could give formulas for $p$ intervals that are the same as mine, but with different underlying conceptualizations. Therefore, $p$ intervals indicate the vagueness of the information given by $p$, no matter which conceptual framework is preferred.

So far all $p$ values have been two-tailed. I based the first discussion on two-tailed $p$ because of its familiarity. However, even using two-tailed $p_{\text{obt}}$, it is more natural to consider one-tailed $p$ values given by replications (replication one-tailed $p$), because the initial experiment indicates a direction for the effect—although of course this could be wrong. From here on I will, unless otherwise stated, use two-tailed $p_{\text{obt}}$ and replication one-tailed $p$.

The probability distribution of replication $p$, for any chosen value of $p_{\text{obt}}$, can be plotted by use of Equation B3 in Appendix B. Four examples of this distribution are shown in Figure 5. These distributions depend only on $p_{\text{obt}}$, and do not require knowledge of $N$ or δ. Again, the distributions of $p$ have a large variance and are highly skewed. Replication $p$ values are only heavily concentrated at very low values when $p_{\text{obt}}$ is very small. The percentiles reported in Figure 5 specify the $p$ intervals for the listed $p_{\text{obt}}$ values. For example, if $p_{\text{obt}} = .05$, then the one-sided $p$ interval, which extends from 0 to the 80th percentile, is (0, .22). This means that, following an initial experiment resulting in a $p$ value of .05, there is an 80% chance that a replication will result in a $p$ value less than .22 and a 20% chance that the replication one-tailed $p$ is greater than .22. A two-sided $p$ interval extending from the 10th to the 90th percentile is (.00008, .44), which means there is an 80% chance that the $p$ value of a replication falls within that interval, a 10% chance that the $p$ value is less than .00008, and a 10% chance that the $p$ value is greater than .44. These are very wide intervals, indicating great uncertainty about replication $p$!



| | Percentiles | | |
|---|---|---|---|
| $p_{\text{obt}}$ | 10th | 80th | 90th |
| .2 | .001 | .464 | .702 |
| .05 | .00008 | .221 | .441 |
| .01 | .000006 | .083 | .223 |
| .001 | .0000002 | .018 | .070 |

**Fig. 5.** Probability distributions of replication one-tailed $p$ for selected values of the two-tailed $p$ value obtained in an original experiment ($p_{\text{obt}}$). No value is assumed for δ. For each $p_{\text{obt}}$, three percentiles are shown, and these define one-sided and two-sided $p$ intervals. For example, if $p_{\text{obt}}$ = .05, the $p$ intervals are (0, .22) and (.00008, .44).

Figure 6 shows those three percentiles and the median—the 50th percentile—as functions of $p_{\text{obt}}$, and thus allows one- or two-sided $p$ intervals to be determined for any $p_{\text{obt}}$. Note the very large vertical separation between 0 and the 80th percentile and between the 10th and 90th percentiles for all but extremely small $p_{\text{obt}}$ values. In other words, $p$ intervals are very wide for all but extremely small $p_{\text{obt}}$ values. Example $p$ intervals are given in Table 1.

My conclusion is that $p_{\text{obt}}$ gives only very vague, inaccurate information about the outcome of replications. Correspondingly, any $p_{\text{obt}}$ could easily have been very different had we taken a different sample, simply because of sampling variability. The $p$ value is a sadly unreliable measure.

## MULTIPLE EFFECTS

I have been discussing a single result in isolation, but most studies in psychology examine more than one effect and/or use more than one measure. Consider for example a study with six effects (or measures), all independent, with a true population

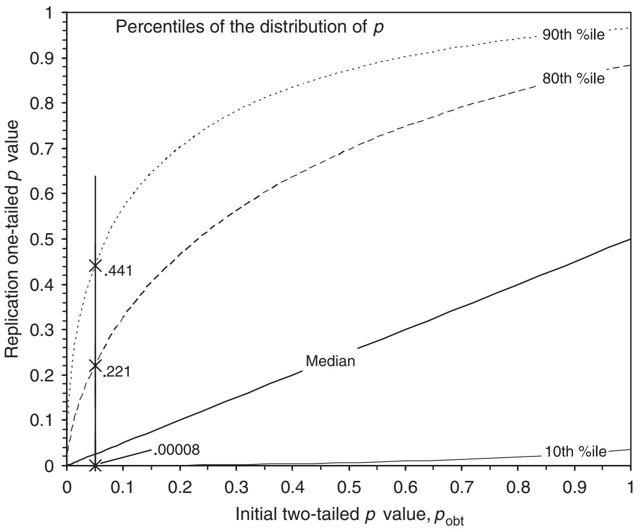


**Fig. 6.** Percentiles of the distribution of one-tailed $p$ expected on replication, as a function of the initial two-tailed $p_{obt}$. No value is assumed for $\delta$. The unbroken line is the median (the 50th percentile), and the dashed line is the 80th percentile, which is the upper limit of the one-sided $p$ interval with a lower limit of 0. The interval between the 10th and 90th percentiles (dotted lines) is a two-sided $p$ interval. All these curves apply for any $N$, provided that $\sigma$ is known. Intersections of the curves with the vertical line at $p_{obt} = .05$ show the one-sided $p$ interval is (0, .22) and a two-sided $p$ interval is (.00008, .44).

effect of $\delta = .5$ in every case and power of .52 to find each effect. These values match those in my initial example, so the study would yield six two-tailed $p$ values from the distribution (and histogram) in Figure 2 or from the left column in Figure 1. It might give the results shown for Study 1 in the top row of Table 2. The authors would interpret at least any ** and *** results as real effects—and the $p$ values give some grounds for that. However, they almost certainly would seek causes for the difference between the effects identified as real and those for which $p$ is greater than .05 or greater than .10, thus implicitly accepting the null hypotheses for the latter effects—although the $p$ values give no grounds whatever for that. Given only the $p$ values, such interpretation—especially the search for causes of apparent differences—is unjustified because the pattern of diverse $p$ values is perfectly consistent with sampling variation for medium power and medium-sized true effects.

**TABLE 1**

p *Intervals for Replication One-Tailed* p *for Selected Values of* p *obt*

| $p_{obt}$[a] | One-sided $p$ interval[b] | Two-sided $p$ interval[c] |
|---|---|---|
| .001 | (0, .018) | (.0000002, .070) |
| .01 | (0, .083) | (.000006, .22) |
| .02 | (0, .13) | (.00002, .30) |
| .05 | (0, .22) | (.00008, .44) |
| .1 | (0, .32) | (.00027, .57) |
| .2 | (0, .46) | (.00099, .70) |
| .4 | (0, .64) | (.0040, .83) |
| .6 | (0, .75) | (.0098, .90) |

**Note.** $p_{obt}$ is the initial two-tailed $p$ value obtained from an experiment. The $p$ intervals are 80% $p$ intervals for replication one-tailed $p$, based on Equation B3.

[a] All $p_{obt}$ values are two-tailed.

[b] One-sided $p$ intervals extend from 0 to the 80th percentile.

[c] Two-sided $p$ intervals extend from the 10th to the 90th percentile.

Suppose we find reports of three other identical studies and again assume that $\delta = .5$ for every effect. Each study would report a further random sample of six $p$ values from Figure 2 and again a likely spread from ** or *** to $p > .10$, perhaps as shown for Studies 2–4 in Table 2. (The results in Table 2 are the first 24 results shown in Figure 1.) Considering the simulated results in Table 2 from four separate studies—or, equivalently, from an initial study and three replications—it is hard to resist interpreting lumps in the randomness (Abelson, 1995, p. 20). Surely Effect 1 is fairly firmly established, whereas Effect 5 shows repeated failure to replicate an initial clear finding? Results from such a set of studies need to be combined by meta-analysis, and the bottom two rows in Table 2 show that doing so fairly clearly establishes the existence of each effect and gives 95% CIs half the width of those shown in Figure 1.

Recall that the effect size and power of my initial example and of each effect in Table 2 are typical for psychology. We should therefore expect to observe in psychology the striking variation in results over studies—or with replication—that Table 2 and Figure 1 illustrate. Such variation is caused simply by sampling variability (Maxwell, 2004), even if there are no true differences in population effects. Table 2 must surely reinforce the conclusion that using $p$ values for dichotomous decision making (reject or do not reject $H_0$), even if supplemented by counting asterisks, is a dreadful way to interpret data.

## DISCUSSION AND CONCLUSION

Clearly, $p$ gives dramatically uncertain information about replication: $p$ is an unreliable indicator and $p$ intervals are very wide. Some authors, Thompson (1996) and Sohn (1998) for example, have gone further and argued that $p$ values do not inform us about replication at all. A tight definition of replication can justify that position: Sohn, for example, regarded a replication as being a study that "may be counted on to produce the essentially same outcome as that of the original study" (p. 292). However, I have asked the broader question of whether $p$ gives any information at all about what $p$ value a replication of an experiment is likely to give. My answer is that it gives very imprecise information.

Figure 6 shows that median replication $p$ does increase with $p_{obt}$, so $p$ gives a modicum of information about replication, and this observation gives a modicum of support for the widespread interpretation of $p$ as an indicator of strength of evidence. However, it is an extremely poor indicator, as Figure 6 also shows: The 10th and 90th percentiles are spaced very far apart, meaning that knowing a $p_{obt}$ value—on the horizontal axis—

**TABLE 2**

*Simulated Results and the Meta-analytic Combination of Four Studies, Each Examining Six Effects That Are Assumed to be Independent*

| | Effect | | | | | |
|---|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 | 6 |
| Study 1 | **<br>.005 | $p > .10$<br>.433 | *<br>.047 | $p > .10$<br>.389 | **<br>.004 | **<br>.008 |
| Study 2 | *<br>.011 | ***<br><.001 | $p > .10$<br>.532 | *<br>.031 | $p > .10$<br>.112 | ?<br>.053 |
| Study 3 | $p > .10$<br>.153 | **<br>.008 | **<br>.003 | $p > .10$<br>.609 | $p > .10$<br>.203 | $p > .10$<br>.759 |
| Study 4 | ***<br>.001 | $p > .10$<br>.353 | *<br>.016 | ***<br><.001 | $p > .10$<br>.111 | $p > .10$<br>.244 |
| Meta-analysis of Studies 1–4 | ***<br><.000001 | ***<br>.00002 | ***<br>.00007 | ***<br>.0002 | ***<br>.0002 | **<br>.002 |
| 95% CI[a] | [7.9, 17.7] | [5.7, 15.5] | [5.0, 14.8] | [4.4, 14.2] | [4.3, 14.1] | [2.7, 12.5] |

**Note.** The lower value in each cell is the two-tailed $p$ value. Each study is assumed to examine six independent effects, each of which has true effect size $\delta = .5$, and each study is assumed to have power of .52 to detect each effect. The results match the first 24 in Figure 1.
?= $.05 < p <.10$, *01 $< p < .05$, **001 $< p < .01$, and ***$p < .001$.
[a]The 95% confidence interval (CI) for the mean difference estimated by meta-analysis of the four studies.

gives only the most hazy notion of what value—on the vertical axis—the next replication $p$ will take.

Another way to assess what $p_{\text{obt}}$ tells us about replication is in terms of variance accounted for. In Appendix A, I consider a set of $p_{\text{obt}}$ values ranging from .01 to .99 and find that, even with such a widely diverse set, $p_{\text{obt}}$ accounts for only about 12% of the variance in replication $p$. So the information a $p$ value gives about replication is extremely imprecise, and $p$ is a very unreliable indicator of strength of evidence. Any $p$ could easily have been very different, simply because of sampling variability. Repeat the experiment, and you are likely to get a quite different $p$. Remarkably, this is true (assuming $\sigma$ is known) whatever the sample size: For any $p_{\text{obt}}$, the $p$ intervals are just as wide whether $N$ is 20 or 2,000. (If this statement seems unbelievable, bear in mind that, to give the same $p_{\text{obt}}$, the observed effect size needs to be much larger when $N = 20$ than when $N = 2{,}000$.)

My conclusions hold whether we assume $\delta$ is known, as illustrated by Figures 1–4, or do not make this assumption and assume we know only the result of an initial experiment, as seen in Figures 5 and 6. My conclusions hold whether one- or two-tailed $p$s are considered: $p$ intervals for two-tailed replication $p$ are even wider than those for one-tailed. In addition, Appendix B reports that the results are broadly similar even if $\sigma$ is not assumed known, at least down to $N = 10$ for a single group experiment.

## Practical Implications

What is to be done? I have four proposals.

### *Calculate* p *Intervals, to Acknowledge the Vagueness of* p

First, we should recognize how unreliable $p$ is, how little information $p$ values give, and how misleading they can be if used to sort results dichotomously. Fisher was correct to regard $p < .05$ primarily as a suggestion for further research. Further, he stated, "A phenomenon is experimentally demonstrable when we know how to conduct an experiment which will rarely fail to give us a statistically significant result" (Fisher, 1966, p. 14). He was acknowledging the importance of replication and requiring that a replication have a very low chance of giving $p > .05$. However, he does not seem to have realized how tiny a single $p$ must be for a result to satisfy his stringent requirement. To achieve a $p$ interval of (0, .05), it is necessary to have two-tailed $p_{\text{obt}} = .0046$, and even then there is a 20% chance of $p > .05$ and the replication failing to give a statistically significant result. For the 90% $p$ interval to be (0, .05), $p_{\text{obt}}$ must equal .00054. An even smaller $p_{\text{obt}}$ value is needed for a replication to "rarely fail" to give $p < .05$. If just a single experiment is carried out, only the very tiniest initial $p$ would satisfy Fisher's standard for a result to be experimentally demonstrable.

To appreciate the vagueness of what $p$ tells us, consider the values in Table 1. For $p_{\text{obt}} = .01$, a one-sided $p$ interval is (0, .08). For a larger $p_{\text{obt}}$, we may prefer the two-sided $p$ interval: If $p_{\text{obt}} = .10$, the two-sided $p$ interval is (.0003, .57), which for practical purposes means any value at all.

Keep in mind those values of Table 1, the vast spreads between the percentiles pictured in Figure 6, and the patterns of Table 2. It is the norm, in situations typical of psychology and many other disciplines, that results do not replicate, patterns do not repeat, and much of what we see in tables of asterisks may be attributable to sampling variability. Anything other than very small $p$ values give close to no information at all. Whenever you see a $p$ value reported, mentally replace it with an interval of potential alternative values from Table 1.

Rosenthal and Gaito (1963, 1964) presented evidence that psychologists show a cliff effect, meaning that small differences in $p$ near .05 give fairly sharp differences in confidence that an effect exists. My analyses give further reasons why such beliefs are unjustified. Rosnow and Rosenthal (1989) famously stated "Surely, God loves the .06 nearly as much as the .05" (p. 1277), to which we can now reply "Yes, but God doesn't love either of them very much at all, because they convey so little!" The seductive certainty touted by $p$ values may be one of the more dramatic and pernicious manifestations of the ironically named Law of Small Numbers (Tversky & Kahneman, 1971), which is the misconception that even small samples give accurate information about their parent populations.

Psychologists have expended vast effort to develop sophisticated statistical methods to minutely adjust $p$ value calculations to avoid various biases in particular situations, while remaining largely blind to the fact that the $p$ value being precisely tweaked could easily have been very different. You are unlikely to be anxious to calculate $p = .050$ so exactly if you know the $p$ interval is (.00008, .44)!

In many disciplines it is customary to report a measurement as, for example, 17.43 ± .02 to indicate precision. By analogy, if a $p$ value is to be reported, journals should also require reporting of the $p$ interval to indicate the level of vagueness or unreliability. Having to report a test of statistical significance as "$z = 2.05, p = .04, p$ interval (0, .19)" may be the strongest motivator for psychologists to find better ways to draw inferences from data.

### *Use CIs*

The American Psychological Association (APA) *Publication Manual* (APA, 2001, p. 22) strongly recommends the use of CIs. Many advocates of statistical reform, including Kline (2004, Chapter 3) and Cumming and Finch (2005), have presented reasons why psychologists should use CIs wherever possible. My discussion of replication identifies a further advantage of CIs. Consider Figure 1 again. Following a single experiment, would you prefer to be told only the $p$ value (and perhaps $M_{\mathrm{diff}}$) or would you prefer to see the CI? Is a single $p$ value representative of the infinite set of possible results? Is it a reasonable exemplar of the whole set? Hardly! I suggest a single CI is more representative, a better exemplar, and can give a better sense of the whole set, including the inherent uncertainty. A $p$ value gives only vague information about what is likely to happen next time, but doesn't a CI give more insight?

In other words, CIs give useful information about replication. More specifically, any CI is also a prediction interval: The probability is .83 that the mean of a replication will fall within a 95% CI (Cumming & Maillardet, 2006; Cumming et al., 2004), so CIs give direct information about replication. In Figure 1, in 17 of 24 cases, the pictured 95% CI includes the mean of the next experiment; in the long run, 83% of the CIs will include the next mean. A 95% CI is not only an interval estimate for $\mu_{\mathrm{diff}}$, it is also an 83% prediction interval for where the next $M_{\mathrm{diff}}$ will fall.

### *Think Meta-Analytically*

A possible response to my findings is to continue using NHST but acknowledge the message of Figure 4—which is that only *** (and perhaps **) results are very clearly diagnostic of an effect—and by adopting a small $\alpha$ and, for example, rejecting the null hypothesis only when $p$ is less than .01 or even less than .001. The problem, however, is that even with the dreamworld power of .9 there is a 25% chance of not obtaining $p < .01$. Therefore, at the less-than-ideal power psychologists typically achieve, obtaining ** or *** results requires luck, which implies there is much unlucky research effort that is wasted. It is worse than wasted because, as meta-analysts make clear (Schmidt, 1996), if asterisks influence publication, then estimates of effect sizes based on published evidence are inflated.

It is a worthy goal to conduct high-powered studies. Investigate large effects if you can, raise large grants so you can afford to use large samples, and use every other strategy to increase power (Maxwell, 2004). Finding effects that pass the interocular trauma test—that hit you between the eyes—largely sidesteps the problems of statistical inference.

However, as we have seen, not even high power guarantees that a single experiment will give a definitive result. In the words of the APA Task Force on Statistical Inference: "The results in a single study are important primarily as one contribution to a mosaic of study effects" (Wilkinson & Task Force on Statistical Inference, 1999, p. 602). There is usually more error variability inherent in any single result than we realize. A CI makes that uncertainty salient—that is why CIs in psychology are often depressingly wide. By contrast, a $p$ value papers over the inherent uncertainty by tempting us to make a binary decision, which can easily mislead us to believe that little doubt remains.

The uncertainty in single results implies that evidence needs to be combined over experiments. Recognizing the central role of replication for scientific progress also emphasizes the need to combine evidence over experiments, and meta-analysis is the way to do this quantitatively. Meta-analysis applied to the four experiments in Table 2 establishes each effect virtually conclusively and gives reasonably precise estimates of each. On this large scale of combining evidence from different studies, meta-analysis provides the best foundation for progress, even for messy applied questions. When high power is not feasible, meta-analysis of a number of studies is especially necessary.

Reports surface from time to time, from any of a range of disciplines, of difficulty in replicating published findings. In medicine, for example, recent discussion (Ioannidis, 2005) has identified many cases of apparently clear results being questioned after attempts at replication. Selective and biased reporting of single results may play a role, but the surprising extent of sampling variability, as illustrated in Table 2, may be a primary contributor to any surprising disagreement between similar studies. Any cases of failure to replicate need to be examined by meta-analysis to determine the extent that mere sampling variability might explain the observed pattern of results.

Meta-analysis can also be used to combine evidence within a single study. The astute experimenter recognizes the uncertainty of any individual result and seeks converging results relevant to the issue of interest—perhaps different manipulations or measures in a single study, perhaps different studies. Then, a meta-analytic combination of comparable results will increase the precision of estimates, and *p* values for individual results will be proven irrelevant. Such local meta-analysis is valuable even—or especially—for research in a new area, thus illustrating that meta-analysis can contribute not only when there is a large body of previous research. The argument has been made many times (Hunter & Schmidt, 2004, Chapter 1), but the large variance of *p* provides one more reason why meta-analysis is so important and why it is the best route to truth in a world of error variability.

Cumming and Finch (2001) described *meta-analytic thinking*, which is based on recognition that meta-analysis gives the best appreciation of one's own study in relation to other studies—past and future—and to the whole research literature. Meta-analytic thinking was discussed with approval by Kline (2004, p. 12) and Thompson (2006, Chapters 7 & 9). Meta-analytic thinking should influence all consideration of data and drawing of conclusions. It should encourage researchers to seek converging evidence and thus avoid the *p* temptation to base a conclusion on a single result.

### *Find Better Techniques*

My final proposal is that psychology should speed its investigation of alternative approaches to data analysis and inference (Fidler & Cumming, 2007). The unreliability of *p* reinforces the case for major statistical reform. Kline (2004) and Thompson (2006) provided extensive practical guidance for how psychology can do better. Goodman (2001) proposed using minimum Bayes factors as an easy stepping stone from *p* value practices to the Bayesian world. Other disciplines such as conservation biology (Fidler, Burgman, Cumming, Buttrose, & Thomason, 2006; Fidler, Cumming, Burgman, & Thomason, 2004) make wider use of model-fitting and model-selection techniques including information theoretic and Bayesian approaches. Wagenmakers (2007) gave a cogent and withering critique of *p* values and recommended Bayesian methods that can be based on output from SPSS or other widely used software.

In this article, my analysis of replication has emphasized the problems of *p* values and thus is largely negative. By contrast, Killeen (2005, 2006, 2007) proposed $p_{\text{rep}}$ as the probability a replication gives a result in the same direction, and thus $p_{\text{rep}}$ makes positive use of information about replication. It is not yet clear whether $p_{\text{rep}}$ can support improved practical ways to draw conclusions from data, but the approach deserves further investigation (Cumming, 2005).

## The Bottom Line for the Busy Researcher

First, be skeptical about any conclusion based on *p* values. Any experiment could easily have given very different *p* values and, most likely, a different pattern of effects—especially in terms of statistical significance—simply because of sampling variability. With the exception of a $p < .001$ result (or, possibly, a $p < .01$ result), a *p* value gives virtually no information about what is true in the world. It is better to think in terms of converging lines of evidence, replication, meta-analysis, and cumulation of evidence over studies.

Second, I encourage others to join in and support the reform of statistical practices, as explained for example by Kline (2004, Chapter 3). As a first step, use CIs wherever possible. CIs give readily interpretable information about replication and make adoption of meta-analytic thinking more natural, both within a research program and across a whole field of research. CIs can help us to think about point and interval estimates of an effect and not focus only on whether or not an effect exists. As Meehl (1978) argued so cogently, moving beyond the dichotomous thinking of *p* values to estimation—and, we can add, modeling techniques—can encourage psychology to develop a more quantitative and theoretically rich understanding of the world. Acknowledging the dramatic vagueness of *p* values in relation to replication—and replication is all that really matters—should energize psychology to reform its statistical practices and thus improve the way it does science.

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## REFERENCES

Abelson, R.P. (1995). *Statistics as principled argument*. Hillsdale, NJ: Erlbaum.

American Psychological Association. (2001). *Publication manual of the American Psychological Association* (5th ed.). Washington, DC: Author.

Berger, J.O., & Sellke, T. (1987). Testing a point null hypothesis: The irreconcilability of *p* values and evidence. *Journal of the American Statistical Association*, *82*, 112–122.

Cohen, J. (1994). The earth is round ($p < .05$). *American Psychologist*, *49*, 997–1003.

Cumming, G. (2005). Understanding the average probability of replication: Comment on Killeen (2005). *Psychological Science*, *16*, 1002–1004.

Cumming, G. (2007). Inference by eye: Pictures of confidence intervals and thinking about levels of confidence. *Teaching Statistics*, *29*, 89–93.

Cumming, G., Fidler, F., Leonard, M., Kalinowski, P., Christiansen, A., Kleinig, A., et al. (2007). Statistical reform in psychology: Is anything changing? *Psychological Science*, *18*, 230–232.

Cumming, G., & Finch, S. (2001). A primer on the understanding, use, and calculation of confidence intervals that are based on central and noncentral distributions. *Educational and Psychological Measurement*, *61*, 530–572.

Cumming, G., & Finch, S. (2005). Inference by eye: Confidence intervals and how to read pictures of data. *American Psychologist*, *60*, 170–180.

Cumming, G., & Maillardet, R. (2006). Confidence intervals and replication: Where will the next mean fall? *Psychological Methods*, *11*, 217–227.

Cumming, G., Williams, J., & Fidler, F. (2004). Replication, and researchers' understanding of confidence intervals and standard error bars. *Understanding Statistics*, *3*, 299–311.

Dixon, P. (1998). Why scientists value *p* values. *Psychonomic Bulletin & Review*, *5*, 390–396.

Estes, W.K. (1997). On the communication of information by displays of standard errors and confidence intervals. *Psychonomic Bulletin & Review*, *4*, 330–341.

Fidler, F., Burgman, M., Cumming, G., Buttrose, R., & Thomason, N. (2006). Impact of criticisms of null-hypothesis significance testing on statistical reporting practices in conservation biology. *Conservation Biology*, *20*, 1539–1544.

Fidler, F., & Cumming, G. (2007). The new stats: Attitudes for the twenty-first century. In J.W. Osborne (Ed.), *Best practices in quantitative methods* (pp. 1–12). Thousand Oaks, CA: Sage.

Fidler, F., Cumming, G., Burgman, M., & Thomason, N. (2004). Statistical reform in medicine, psychology and ecology. *Journal of Socio-Economics*, *33*, 615–630.

Fisher, R.A. (1959). *Statistical methods and scientific inference* (2nd ed.). Edinburgh, United Kingdom: Oliver and Boyd.

Fisher, R.A. (1966). *The design of experiments* (8th ed.). Edinburgh, United Kingdom: Oliver & Boyd.

Gigerenzer, G. (2004). Mindless statistics. *Journal of Socio-Economics*, *33*, 587–606.

Goodman, S.N. (1992). A comment on replication, *p*-values and evidence. *Statistics in Medicine*, *11*, 875–879.

Goodman, S.N. (2001). Of *p*-values and Bayes: A modest proposal. *Epidemiology*, *12*, 295–297.

Goodman, S.N., & Royall, R. (1988). Evidence and scientific research. *American Journal of Public Health*, *78*, 1568–1574.

Greenwald, A.G., Gonzalez, R., Harris, R.J., & Guthrie, D. (1996). Effect sizes and *p* values: What should be reported and what should be replicated? *Psychophysiology*, *33*, 175–183.

Haller, H., & Krauss, S. (2002). Misinterpretations of significance: A problem students share with their teachers? *Methods of Psychological Research*, *7*, 1–20.

Hubbard, R. (2004). Alphabet soup. Blurring the distinction between *p*s and αs in psychological research. *Theory & Psychology*, *14*, 295–327.

Hung, H.M.J., O'Neill, R.T., Bauer, P., & Köhne, K. (1997). The behaviour of the *p*-value when the alternative hypothesis is true. *Biometrics*, *53*, 11–22.

Hunter, J.E., & Schmidt, F.L. (2004). *Methods of meta-analysis. Correcting error and bias in research findings* (2nd ed.). Thousand Oaks, CA: Sage.

Ioannidis, J. (2005). Contradicted and initially stronger effects in highly cited clinical research. *Journal of the American Medical Association*, *294*, 218–228.

Kahrimanis, G., & Berleant, D. (2007). *Direct pivotal predictive inference: I. The case of additive noise*. Unpublished manuscript.

Killeen, P.R. (2005). An alternative to null hypothesis significance tests. *Psychological Science*, *16*, 345–353.

Killeen, P.R. (2006). Beyond statistical inference: A decision theory for science. *Psychonomic Bulletin & Review*, *13*, 549–562.

Killeen, P.R. (2007). Replication statistics. In J.W. Osborne (Ed.), *Best practices in quantitative methods* (pp. 103–124). Thousand Oaks, CA: Sage.

Kline, R.B. (2004). *Beyond significance testing: Reforming data analysis methods in behavioral research*. Washington, DC: American Psychological Association.

Maxwell, S.E. (2004). The persistence of underpowered studies in psychological research: Causes, consequences, and remedies. *Psychological Methods*, *9*, 147–163.

Meehl, P.E. (1978). Theoretical risks and tabular asterisks: Sir Karl, Sir Ronald, and the slow progress of soft psychology. *Journal of Consulting and Clinical Psychology*, *46*, 806–834.

Morgenthaler, S., & Staudte, R.G. (2007). *Interpreting significant* p-*values*. Manuscript submitted for publication.

Mulkay, M., & Gilbert, G.N. (1986). Replication and mere replication. *Philosophy of the Social Sciences*, *16*, 21–37.

Oakes, M. (1986). *Statistical inference: A commentary for the social and behavioural sciences*. Chichester, United Kingdom: Wiley.

Posavac, E.J. (2002). Using *p* values to estimate the probability of a statistically significant replication. *Understanding Statistics*, *1*, 101–112.

Rosenthal, R., & Gaito, J. (1963). The interpretation of levels of significance by psychological researchers. *Journal of Psychology*, *55*, 33–38.

Rosenthal, R., & Gaito, J. (1964). Further evidence for the cliff effect in the interpretation of levels of significance. *Psychological Reports*, *15*, 570.

Rosnow, R.L., & Rosenthal, R. (1989). Statistical procedures and the justification of knowledge in psychological science. *American Psychologist*, *44*, 1276–1284.

Sackrowitz, H., & Samuel-Cahn, E. (1999). *p* values as random variables—expected *p* values. *American Statistician*, *53*, 326–331.

Schmidt, F.L. (1996). Statistical significance testing and cumulative knowledge in psychology: Implications for training of researchers. *Psychological Methods*, *1*, 115–129.

Sohn, D. (1998). Statistical significance and replicability: Why the former does not presage the latter. *Theory & Psychology*, *8*, 291–311.

Thompson, B. (1996). AERA editorial policies regarding statistical significance testing: Three suggested reforms. *Educational Researcher*, *25*, 26–30.

Thompson, B. (2006). *Foundations of behavioral statistics: An insight-based approach*. New York: Guilford.

Tversky, A., & Kahneman, D. (1971). Belief in the law of small numbers. *Psychological Bulletin*, *92*, 105–110.

Wagenmakers, E.-J. (2007). A practical solution to the pervasive problems of *p*-values. *Psychonomic Bulletin & Review*, *14*, 779–804.

Wilkinson, L. & Task Force on Statistical Inference. (1999). Statistical methods in psychology journals: Guidelines and explanations. *American Psychologist*, *54*, 594–604.

## APPENDIX A

### Replication: An Example With Known Population Effect Size

For each experiment, the 95% CI for the difference is $[M_{\text{diff}} \pm 1.96\sigma\sqrt{(2/N)}]$ or $[M_{\text{diff}} \pm 9.80]$. The intervals all have the same width because we are assuming $\sigma$ is known. The test statistic for the difference is $z = M_{\text{diff}}/(\sigma\sqrt{(2/N)}) = M_{\text{diff}}/5$.

There are several further aspects of Figure 1 worth noting.

1. It pictures a simulation. In real life, we have only a single experiment and don't know $\mu_{\text{diff}}$ or $\delta$.
2. Sample mean differences—the large grey dots—are normally distributed around $\mu_{\text{diff}} = 10$, are equally likely to fall above or below 10, and will be most tightly bunched near 10; the means in Figure 1 fit these expectations.
3. There is a precise relation between the *p* value and the position of a CI in relation to the $H_0$ line at 0 (Cumming, 2007). If the CI has its lower limit at 0, then $p = .05$; Experiments 25, 12, and 3 come close. If a CI falls in such a way that 0 is further within the interval, then *p* is progressively larger (see Experiments 17, 16, 18, in that order), and if the CI does not include 0, *p* is less than .05 and is progressively smaller for intervals further from 0 (see Experiments 21, 15, 22, in that order).
4. The samples all come from populations with $\mu_{\text{diff}} = 10$, so, in the long run, 95% of the CIs will include 10 and 5% will not. In the figure, only Experiment 8 has a 95% CI that does not include 10.

### Distribution of *p* When Population Effect Size δ Is Known

Figure A1 shows distributions of the test statistic $z = M_{\text{diff}}/(\sigma(2/N))$ for samples from two normal populations (*N*s = 32) with $\sigma = 20$. If $H_0$ is true, $\delta = 0$ and the left curve applies. The right curve applies if the effect size $\delta = 0.5$, as in the example. The horizontal axis is marked with both the verbal ability difference scale, showing a $\mu_{\text{diff}}$ of 0 for the left curve and 10 for the right, and the *z* scale, whose units are $SE = \sigma\sqrt{(2/N)} = 5$.

The heavy vertical line marks the mean $M_{\text{diff}}$ and *z* for an experiment. The sum of the two areas filled with vertical lines is the two-tailed *p* for this experiment. For $H_0$ true, $\delta = 0$, the left curve applies, and the probability that future replications will result in a *p* value this small or smaller is just *p*. That's the definition of *p*: the probability of getting the same or a more extreme result if $H_0$ is true. If, however, $\delta = 0.5$ and the right curve applies, the probability (*P*) of getting a *p* value this small or smaller is the large horizontally striped area $P_R$ plus the minuscule left tail area $P_L$. In the case illustrated, $z = 1.60$, $p = .11$, and $P = .656$. The accompanying simulation allows the heavy line to be moved, so the way *P* changes with *p* can be observed. Finding *P* as a function of *p* gives the cumulative distribution function of the *p* value for $\delta = 0.5$ and $N = 32$.

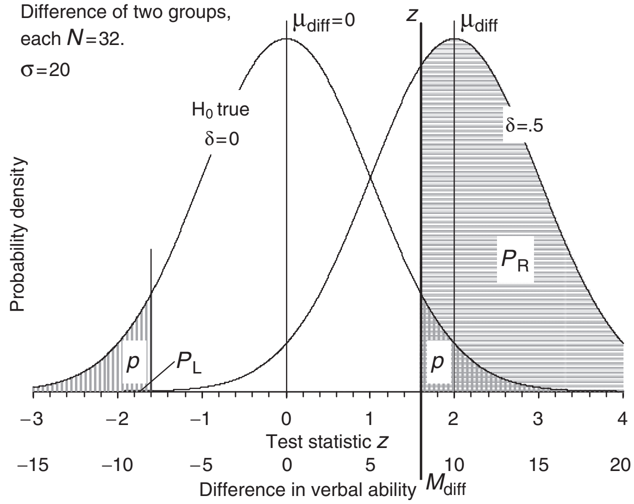

**Fig. A1.** Sampling distributions of the test statistic $z = M_{\text{diff}}/(\sigma\sqrt{(2/N)})$. The populations are assumed normal, with $\sigma = 20$, and two groups have 32 participants each. Under $H_0$, $\mu_{\text{diff}} = 0$ and the left curve applies, and under the alternative, $\mu_{\text{diff}} = 10$, the right curve applies. The population effect size is the separation of the two curves and is Cohen's $\delta = \mu_{\text{diff}}/\sigma = 10/20 = 0.5$. The horizontal axis is marked in units of *z* (i.e., units of $SE = \sigma\sqrt{(2/N)} = 5$) and also in the original units of verbal ability difference. Two-tailed *p* is the sum of the two areas under the $H_0$ curve marked with vertical lines. If the alternative hypothesis is true, the probability of obtaining on replication a two-tailed *p* value less than *p* is the sum of the two areas under the right curve marked with horizontal lines, labeled $P_L$ (area too small to be visible) and $P_R$. In the case illustrated, $M_{\text{diff}} = 8.0$, $z = 1.60$, $p = .11$, and $P = P_L + P_R = .656$. Equation B1 expresses *P* as a function of *p*, and this functional relationship is illustrated by the way *p* and *P* change as the heavy vertical line is moved, thus changing *z* (and $M_{\text{diff}}$). The accompanying simulation allows the line to be moved and the resulting changes to *p* and *P* observed.

If Figure A1 looks familiar, you are correct—it is simply the power diagram, in which *P* is the statistical power for $\alpha = p$. Asking how *P* varies with *p* is the same as asking how power varies with $\alpha$. In Appendix B, Figure A1 is used to derive Equation B1, which gives the distributions of *p* in Figures 2 and 3.

Both likelihood (Goodman & Royall, 1988) and Bayesian approaches (Goodman, 2001) confirm that *p* is usually only weakly diagnostic between the null and alternative hypotheses, as Figures 3 and 4 illustrate. In many situations, $p = .05$ is not notably less likely under $H_0$ than it is under the alternative hypothesis. Berger and Sellke (1987) discussed several assessments of what *p* values tell us and concluded, "[they] can be highly misleading measures of the evidence . . . against the null hypothesis" (p. 112). Indeed, *p* is very often interpreted as an indicator of strength of evidence (Dixon, 1998; Morgenthaler &

Staudte, 2007), but the theoretical basis for this interpretation can be convincingly challenged (Goodman & Royall, 1988; Wagenmakers, 2007). These discussions question the validity of $p$ as a basis for inference, whereas my analysis in this article primarily concerns its reliability.

In the main text and in Figures 2 and 3, I refer to 80% $p$ intervals that extend from 0 to the 80th percentile of the distribution of two-tailed $p$; when power is .52, this $p$ interval is (0, .25). Such intervals are *low one-sided* p *intervals*, because their lower limit is zero. The corresponding *high one-sided* p *interval* (.005, 1) extends from the 20th percentile to 1. A *two-sided* p *interval* extends from the 10th to the 90th percentile—or perhaps between other percentiles that differ by 80%. I chose the 10th and 90th percentiles, however, because they give two-sided $p$ intervals with equal chances that $p$ falls above and below the interval. In the example, this two-sided $p$ interval is (.001, .46).

### Distribution of $p$ Given Only an Initial $p_{\mathrm{obt}}$

The problem is that Equation B1 needs a value of $\delta$. One possibility is to make the implausible assumption that our experiment estimates the population effect size precisely, so $\delta = d$ where $d = M_{\mathrm{diff}}/\sigma$ is the obtained effect size. Using this assumption, the distribution of $p$ was discussed by Hung, O'Neill, Bauer, and Köhne (1997), Morgenthaler and Staudte (2007), and Sackrowitz and Samuel-Cahn (1999). In psychology, discussions of the probability of obtaining statistical significance ($p < .05$) on replication, including those published by Greenwald, Gonzalez, Harris, and Guthrie (1996), Oakes (1986, p. 18), and Posavac (2002), were similarly based on this assumption.

Suppose our initial experiment results in $p_{\mathrm{obt}} = .046$, which implies $z_{\mathrm{obt}} = 2.00$ and (if $N = 32$) that $M_{\mathrm{diff}} = 10$. If we assume $\delta = d$, the right curve in Figure A1 applies, the distribution of $p$ is as in Figure 2, and the $p$ interval for two-tailed replication $p$ is (0, .25).

Appendix B explains that the distribution of replication $p$ depends only on $p_{\mathrm{obt}}$, regardless of $N$ and $\delta$. Assuming that $\delta = d$, Equation B1 can be used to find the percentiles and $p$ intervals for replication two-tailed $p$ for any $p_{\mathrm{obt}}$.

#### *Distribution of* p *Without Assuming* $\delta = d$

The assumption $\delta = d$ is unrealistic, as the substantial deviations of $M_{\mathrm{diff}}$ from $\mu_{\mathrm{diff}}$ in Figure 1 illustrate. Consider Figure A2: The lower panel shows the estimation errors ($M_{\mathrm{diff}} - \mu_{\mathrm{diff}}$) for the first 11 experiments of Figure 1. The distribution of those errors for all experiments is the distribution of $M_{\mathrm{diff}}$ relative to $\mu_{\mathrm{diff}}$, which is the right curve in Figure A1. Its standard deviation is $\sigma\sqrt{(2/N)}$. However, drawing that curve requires knowledge of $\delta$.

Now consider the upper panel in Figure A2, which shows differences between successive results ($M_{\mathrm{diff(i+1)}} - M_{\mathrm{diff(i)}}$). The distribution of $M_{\mathrm{diff}}$ has a standard deviation of $\sigma\sqrt{(2/N)}$ and, therefore, a variance of $2\sigma^2/N$. Because successive experiments are independent and the variance of the difference of two independent variables is the sum of the variances of the two variables, the variance of ($M_{\mathrm{diff(i+1)}} - M_{\mathrm{diff(i)}}$) is $4\sigma^2/N$. The $SD$ of ($M_{\mathrm{diff(i+1)}} - M_{\mathrm{diff(i)}}$) is thus $\sqrt{2}(\sigma\sqrt{(2/N)})$, and plotting these differences relative to an initial $M_{\mathrm{diff}}$ gives the right curve in Figure A3, which has an $SD$ of $\sqrt{2}$ (about 1.4) times that of the right curve in Figure A1. The right curve in Figure A3 is the distribution of where a replication $M_{\mathrm{diff}}$ (or replication $z$) will fall, without assuming that $\delta = d$. Its greater standard deviation is consistent with the appearance of the ($M_{\mathrm{diff(i+1)}} - M_{\mathrm{diff(i)}}$) differences in Figure A2 being longer, on average, than the ($M_{\mathrm{diff}} - \mu_{\mathrm{diff}}$) errors in the lower panel.

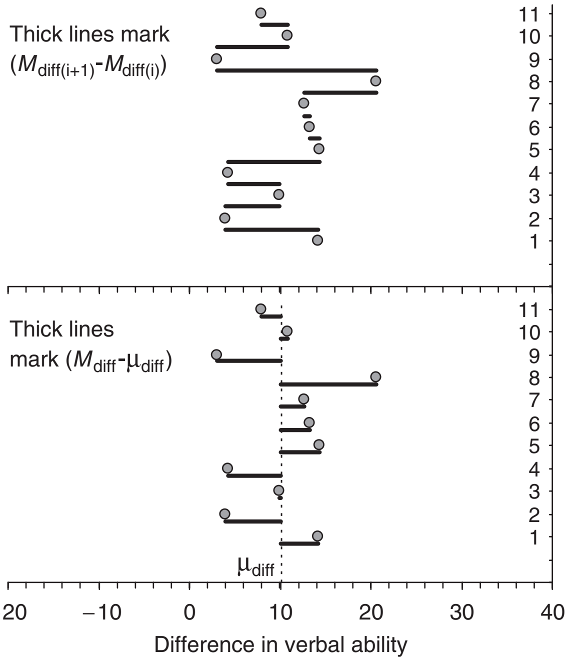

**Fig. A2.** Two views of obtained mean differences 1–11 (the grey dots) from the simulation shown in Figure 1. In the lower panel, $\mu_{\mathrm{diff}}$ is indicated by the vertical dotted line, and the thick lines denote ($M_{\mathrm{diff}} - \mu_{\mathrm{diff}}$) the error of estimation for each experiment. The distribution of these errors around $\mu_{\mathrm{diff}} = 10$ is the right curve in Figure A1. In the upper panel, the thick lines denote the differences between successive means $M_{\mathrm{diff(i)}}$ and $M_{\mathrm{diff(i+1)}}$ and no value is assumed for $\delta$. These line lengths have a distribution with a standard deviation that equals that of the right curve in Figure A3.

Appendix B uses Figure A3 to derive Equation B3, which gives the distribution of replication one-tailed $p$, given only $p_{\mathrm{obt}}$ and without assuming a value for $\delta$. The central step is the elimination of the parameter $\delta$ to find the right curve in Figure A3. Fisher (1959, p. 114) introduced the method used above, Estes (1997) used it to calculate the probability a replication mean would fall within an initial CI, and we used it to discuss further the capture of replication means by a CI (Cumming & Maillardet, 2006; Cumming et al., 2004). It also underlies Killeen's (2005) $p_{\mathrm{rep}}$, the probability a replication will give a result in the same direction as the initial experiment, without assuming

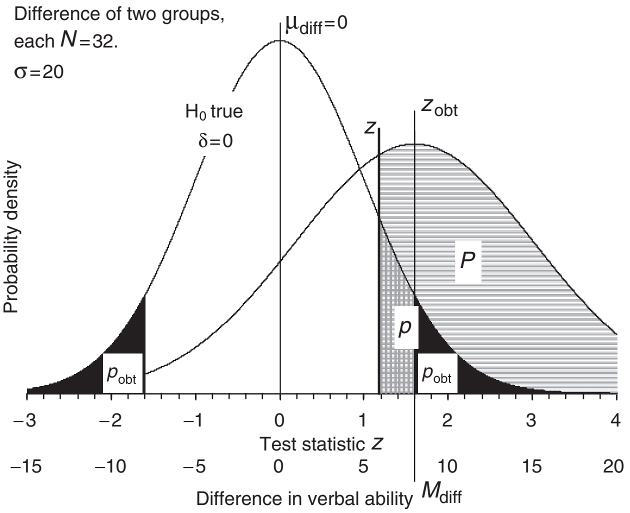

**Fig. A3.** The left curve is the sampling distribution of test statistic $z$ under $H_0$, as in Figure A1. The right curve is the sampling distribution of $z$ for replication experiments, given that $z_{\text{obt}} = 1.60$ (and, therefore, that $p_{\text{obt}} = .11$) for an initial experiment. Equivalently, it is the sampling distribution of replication mean differences $M_{\text{diff}}$, given an initial $M_{\text{diff}} =$ 8.0. No value is assumed (or known) for δ. The vertically striped area is replication one-tailed $p$, and $P$ is the probability that replication $p$ will be less than $p$.

a value for δ. The method was examined in detail by Kahrimanis and Berleant (2007). Applying this method to $p$ values is the novel step in the present article.

If $p_{\text{obt}} = .05$, it is correct to say our $p$ interval is (0, .22) and there is an 80% probability that a single replication will give a one-tailed $p$ in that interval. However it is not justified to say that repeating our experiment, with our unknown but fixed δ, 100 times will necessarily give approximately 80 $p$ values in that interval. Numerous replications with a single δ would be described by a curve from Figure 3 or a similar curve and not by a curve from Figure 5. The best way to think about the curves in Figures 5 and 6, and about $p$ intervals given only an initial $p_{\text{obt}}$, is in terms of the probability of the $p$ value a single replication will give.

Further discussion of these tricky issues within a frequentist framework, and of figures and simulations[2] intended to illuminate them, were provided by Cumming et al. (2004) and Cumming and Maillardet (2006) in the context of CIs and replication and by Cumming (2005) in relation to Killeen's $p_{\text{rep}}$.

### *Comparison of* p *Intervals When δ Is or Is Not Assumed Known*

Figures 1–3 and Table 2 refer to the probability distribution of $p$ when δ is assumed to be known. Taking this approach, if we are to calculate $p$ intervals for any chosen two-tailed $p_{\text{obt}}$, we need to make the assumption that $\delta = d$. Then, Equation B2 gives $p$ intervals for one-tailed $p$. Alternatively, we can use Equation B3 to calculate $p$ intervals for replication one-tailed $p$ for any given $p_{\text{obt}}$ without assuming a value for δ. Table 1 reports examples of such intervals.

The $p$ intervals based on the unrealistic assumption that $\delta = d$ are generally shorter, especially for small $p_{\text{obt}}$. For example, for $p_{\text{obt}} = .05$, one- and two-sided $p$ intervals for replication one-tailed $p$ based on $\delta = d$ using Equation B2 are, respectively, (0, .13) and (.0006, .25). The corresponding intervals in Table 1, based on Equation B3, are (0, .22) and (.00008, .44). For $p_{\text{obt}} =$ .2, $p$ intervals based on $\delta = d$ are (0, .33) and (.005, .50); the intervals in Table 1 are (0, .46) and (.00099, .70). The analyses mentioned earlier by Hung et al. (1997) and others relied on the $\delta = d$ assumption and therefore generally understated the amount of uncertainty in replication $p$.

### Proportion of Variance Accounted For

Another way to assess the paucity of information $p_{\text{obt}}$ gives is to consider proportion of variance accounted for. At each value of two-tailed $p_{\text{obt}}$ from .01 to .99, in steps of .01, I randomly generated 100 values of replication one-tailed $p$, without assuming a value for δ. For example, for $p_{\text{obt}} = .05$, the 100 values would fall on the vertical line marked in Figure 6, with approximately half of them above the median and half below and with about 20 falling above the 80th percentile. Using mean replication $p$ as the value predicted, $p_{\text{obt}}$ accounts for only 11.9% of the variance of replication $p$ in the whole set of 9,900 values. If, given the large skew, the median is preferred as the value predicted, $p_{\text{obt}}$ accounts for only 13.7% of the sum of squares of replication $p$ about its overall median. These percentages depend on the set of $p_{\text{obt}}$ values chosen, but my set ranging from .01 to .99 gives $p_{\text{obt}}$ large variance and thus every chance to predict—so the above percentages are high estimates and are further indicators of how poor the information that $p$ gives is. If $p_{\text{obt}}$ values just from .01 to .2 are considered, $p_{\text{obt}}$ accounts for only 4.6% of the variance of replication $p$.

## APPENDIX B

### Distribution of $p$ When δ Is Known

Let $\Phi(z)$ be the cumulative distribution function of the standard normal distribution. Considering the vertically striped areas in Figure A1, $p = 2(1-\Phi(z))$. Expressed in Microsoft Excel functions, $p$ = 2*(1 − NORMSDIST($z$)) and $z$ = NORMSINV (1 − $p$/2).

Let $z_\mu$ be the $z$ value at $\mu_{\text{diff}}$, so $z_\mu = \mu_{\text{diff}}/(\sigma\sqrt{(2/N)})$. The population effect size is $\delta = \mu_{\text{diff}}/\sigma$. By substitution, $z_\mu = \delta(N/2)$.

When the population effect size is δ and the right curve applies, $P$ is the probability of obtaining, on replication, a $p$ value less than or equal to the $p$ value illustrated as the vertically striped areas, and $P$ is the sum of the tiny area labeled $P_L$ and the

[2] The simulations are, respectively, ESCI Ustanding Stats, ESCI CInext PM, and ESCI APR Simulation. They may be downloaded from www.latrobe.edu.au/psy/esci.

horizontally striped area $P_R$ at right. Therefore $P = 1 - \Phi(z_\mu + z) + \Phi(z_\mu - z)$. Alternatively,

$$P = 1 - \text{NORMSDIST}(z_\mu + \text{NORMSINV}(1 - p/2)) \\ + \text{NORMSDIST}(z_\mu - \text{NORMSINV}(1 - p/2)). \tag{B1}$$

Equation B1 can be used to plot the cumulative distribution function of the two-tailed $p$ value or the probability density function, which is shown in Figure 2 for $\delta = 0.5$ ($N = 32$). In this case, $z_\mu = \delta\sqrt{}(N/2) = 2$, as in Figure A1 and the example in Figure 1. Enter those values and $p = \alpha = .05$ in Equation B1 to confirm the power is .52.

Equation B1 depends on $z_\mu = \delta\sqrt{}(N/2)$, which is the separation between the two curves in Figure A1. As $\delta$ increases from 0, power increases monotonically. Therefore, assuming that $\delta \geq 0$, a given power determines $\delta\sqrt{}(N/2)$, which in turn determines via Equation B1 the distribution of $p$, which is thus independent of $N$ and dependent only on power. Figure 4 can therefore show the percentages of $p$ for particular values of power with no mention of $\delta$ or $N$.

For completeness, I note the relationship for $\delta$ known for one-tailed $p$ is as follows:

$$P = \text{NORMSDIST}(z_\mu - \text{NORMSINV}(1 - p)). \tag{B2}$$

### Distribution of $p$ Given Only an Initial $p_{\text{obt}}$

First, assume $\delta = d$, or equivalently that $z_\mu = z_{\text{obt}}$. Note that $z_{\text{obt}} = d\sqrt{}(N/2)$, where $d$ is the effect size in the initial experiment. Then Equations B1 and B2 give, respectively, the distributions of two-tailed and one-tailed $p$. Note that $z_{\text{obt}} = \text{NORMSINV}(1 - p_{\text{obt}}/2)$, with $z_{\text{obt}} \geq 0$, so the distributions of $p$ are dependent only on $p_{\text{obt}}$ and not on $N$.

Now drop the $\delta = d$ assumption. Considering Figure A3, the relation for replication one-tailed $p$ is as follows:

$$P = \text{NORMSDIST}((z_{\text{obt}} - \text{NORMSINV} \\ (1 - p))/\text{SQRT}(2)). \tag{B3}$$

For completeness, I note the relation for replication two-tailed $p$ is as follows:

$$P = 1 - \text{NORMSDIST}((z_{\text{obt}} + \text{NORMSINV}(1 - p/2))/ \\ \text{SQRT}(2)) + \text{NORMSDIST}((\text{z}_{\text{obt}} \\ - \text{NORMSINV}(1 - p/2))/\text{SQRT}(2)). \tag{B4}$$

Substitute $z_{\text{obt}} = \text{NORMSINV}(1 - p_{\text{obt}}/2)$ in Equations B3 and B4 to confirm that, when we do not assume $\delta = d$, $P$ depends only on $p_{\text{obt}}$ and not on $N$. Also, use Equation B4 to calculate that, when $p_{\text{obt}} = .03$, the probability is .561 that the replication two-tailed $p$ is less than .05, as mentioned in the section $p$ Values, Statistical Reform, and Replication.

### Dropping the Assumption That $\sigma$ Is Known

For a known $\sigma$, two groups with 32 participants each is equivalent to a single group of 16. Figures 1–3, A1–A3, and all $p$ intervals are the same for a single group experiment (with $N = 16$) as they would be for a two group experiment with $N = 32$ for each group. To investigate the simplest case of $\sigma$ not being known, I considered a single group experiment for various values of $N$.

If we drop the assumption that $\sigma$ is known, the sample standard deviation ($s$) is used to estimate $\sigma$. The left curve in Figure A1 becomes the central $t$ distribution, with $df = N - 1$, where $N$ is the size of the single group, and the right curve becomes the noncentral $t$ distribution, with $df = N - 1$ and noncentrality parameter $\Delta = \delta\sqrt{N}$. Cumming and Finch (2001) described noncentral $t$ and its uses. Equations analogous to B1 and B2 allow calculation of the distribution of $p$, for a known $\delta$ or if it is assumed that $\delta = d$. For $N = 10$, $p$ intervals are somewhat narrower than they are for the known $\sigma$ analysis, especially for small $p_{\text{obt}}$. Overall, however, the results are similar, and broad conclusions from my main discussion assuming $\sigma$ known very largely apply also for an unknown $\sigma$, at least for single groups down to $N = 10$.

### Verification of Numerical Results

Equations B1 and B2 give results that agree with replication one-tailed $p$ and mean $p$ values for a range of percentiles and values of power reported by Hung et al. (1997, Tables 1, 2, and 3), post hoc power for one-tailed $\alpha = .025$ (although mislabeled as .05) for a range of $p_{\text{obt}}$ values reported by Posavac (2002, Table 2), two-tailed post hoc power reported by Goodman (1992, Table 1, column 2), and quartiles for $p$ reported by Morgenthaler and Staudte (2007, p. 9).

In addition, I tested my results by simulation. For each of a selection of $p_{\text{obt}}$ values, I generated data from 100,000 experiments and found percentiles for the empirical distribution of 100,000 $p$ values. The results agreed with my calculated values, for both one- and two-tailed $p$, for $\delta$ known, and for $\delta$ not known without assuming $\delta = d$. I similarly confirmed by simulation my calculations when $\sigma$ is not assumed known and $N = 10$.