How to Tell When a Result Will Replicate: Significance and Replication in Distributional Null Hypothesis Tests

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Abstract

There is a well-known problem in Null Hypothesis Significance Testing: many statistically significant results fail to replicate in subsequent experiments. We show that this problem arises because standard ‘point-form null’ significance tests consider only within-experiment but ignore between-experiment variation, and so systematically underestimate the degree of random variation in results. We give an extension to standard significance testing that addresses this problem by analysing both within- and between-experiment variation. This ‘distributional null’ approach does not underestimate experimental variability and so is not overconfident in identifying significance; because this approach addresses between-experiment variation, it gives mathematically coherent estimates for the probability of replication of significant results. Using a large-scale replication dataset (the first ‘Many Labs’ project), we show that many experimental results that appear statistically significant in standard tests are in fact consistent with random variation when both within- and between-experiment variation are taken into account in this approach. Further, grouping experiments in this dataset into ‘predictor-target’ pairs we show that the predicted replication probabilities for target experiments produced in this approach (given predictor experiment results and the sample sizes of the two experiments) are strongly correlated with observed replication rates. Distributional null hypothesis testing thus gives researchers a statistical tool for identifying statistically significant and reliably replicable results.

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Confronted with a surprising experimental result and wondering whether it may represent a meaningful discovery, a researcher must ask: could this result simply be a consequence of random variation and no real effect? Such questions are especially important for discovery in domains of high variability (psychology, neuroscience, medicine, genetics, and so on), where random variation can easily produce apparently surprising results. Since by definition a surprising result has not been hypothesised \textit{a priori}, such questions cannot be answered by hypothesis-comparison approaches (Neyman-Pearson hypothesis testing or Bayesian model comparison) which require prior statement of the hypotheses being compared (Christensen 2005; Berger and Pericchi 1996; Morey and Rouder 2011). The standard way to answer such questions is via Fisher's evidential significance test, which assesses the degree to which a result is unexpected under the null statistical model of random variation but no real effect (and so gives evidence against that model) operationalised as the probability $p$ of a result as or more extreme arising under that model.

While the logic of evidential significance testing is compelling (a result is surprising when it is extreme, relative to our expectations; a low $p$-value tells us that our result is extreme, relative to the null model) it has become increasingly clear that significance testing, at least as it is typically used, is fundamentally flawed. Perhaps the most important problem with standard significance testing involves replication and the reliability of results, with standard significance testing being overconfident in identifying apparently nonsensical effects, such as telepathy or precognition, as real (parapsychology ‘offers a truly alarming massive case study of how statistics can mislead and be misused’: Diaconis \textit{et al.} 1991), and more generally, with systematic research showing that many statistically significant
experimental results in psychology and related fields do not occur reliably in replications (e.g. Camerer et al., 2018; Open Science Collaboration et al., 2015; Klein et al., 2018, 2014), results seen as ‘reflecting an unprecedented level of doubt among practitioners about the reliability of research findings in the field’ (Pashler and Wagenmakers, 2012). These flaws are also evident in well-known effects of sample size on significance (the observation that the probability of getting a statistically significant result in the standard approach increases with sample size, irrespective of the presence or absence of a true effect; to quote Thompson (1998): ‘Statistical testing becomes a tautological search for enough participants to achieve statistical significance. If we fail to reject, it is only because we’ve been too lazy to drag in enough participants’) and in the fact that in standard significance tests, null hypotheses are always false (and to quote Cohen, 2016: ‘if the null hypothesis is always false, what’s the big deal about rejecting it?’). Faced with these systematic problems there have been increasingly widespread calls for the wholesale abandonment of the significance testing approach (e.g. McShane et al., 2019; Amrhein and Greenland, 2018; Hunter, 1997; Carver, 1978).

Our aim in this paper is to show that these problems all arise from a basic gap in the standard approach to significance testing: the fact that it considers only within-experiment random variation in estimation, while ignoring between-experiment random variation. In the language of measurement analysis in physics, the standard approach considers the precision of the experiment as a measurement tool (the degree of random variation in measurements within this experiment, a factor which depends on sample size) but ignores the accuracy of the experiment as a measurement tool (the degree to which measurements
in this experiment agree with those obtained from other experiments measuring the same effect; e.g. Mandel, 2012). This gap means that the standard approach systematically underestimates the degree of random variation or error affecting experimental results, and so is overconfident in identifying results as significant. Here we describe a model of significance testing that addresses these problems by analysing both within- and between-experiment random variation. The chance of statistical significance in this ‘distributional’ model does not rise with sample size irrespective of any real effect; this approach does not overestimate the random variation affecting experimental results and so is not overconfident in identifying significance; importantly, this model gives mathematically coherent estimates for the probability of replication of significant results in future experiments.

The paper is organised as follows: In the first section we derive basic expressions for significance, statistical power and probability of replication in this model in the context of a t-test, assuming known between-experiment variation. In the second section we derive unbiased sample estimators for between-experiment variance, give expressions for significance and replication in terms of those sample estimates, and extend these to give simple and practical expressions for significance and replication in terms of the standard T distribution. We also extend this approach to tests of correlation and linear regression, and tests of contingency, and briefly compare this model to a well-known point-form approach to replication (Killeen, 2005a, 2007). In the third section we test this model against the first ‘Many Labs’ replication dataset (Klein et al., 2014), showing that this model’s assumption of between-experiment variation holds, that its judgements of statistical significance are many orders of magnitude more conservative than those obtained in the standard ap-
proach, and that its replication probabilities reliably and accurately predict observed rates of successful replication of individual results. In the fourth section we compare this model to Bayesian approaches to hypothesis testing via the Bayesian $t$-test (e.g., [Rouder et al., 2009]), showing that this Bayesian approach is almost exactly equivalent to point-form test of significance, and outlining the differences and similarities between the general Bayesian approach and our distributional model. In the final section we address some possible criticisms of this model of significance and replication, and argue that this distributional approach to evidential significance testing will help researchers identify experimental results which are both surprising (statistically significant) and amenable to further investigation (replicable). Rather than abandoning significance testing as a way of identifying surprising and interesting results, researchers should consider using significance testing in its more general distributional form.

1 Theoretical Model of Significance and Replication

We consider an experiment involving $N$ measurements which we assume follow a Normal distribution

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

with unknown mean $\mu$ and unknown variance $\sigma^2$ (the standard assumption of normally distributed error), so that the sample mean $\bar{X}$ follows the distribution $\mathcal{N}(\mu, \sigma^2/N)$. Given sample variance $S^2$ and degrees of freedom $\nu$, the variance in $\bar{X}$ is estimated by $S^2/N$ (the sample variance of the mean) and the standard approach assesses significance against the point-form null hypothesis $\mu = 0$ via a $t$-test.
Letting $T_\nu$ represent the cumulative $t$ distribution with degrees of freedom $\nu$, $d = \bar{X}/S$ the normalised sample mean and $t = d\sqrt{N}$ the test statistic, in this approach the point-form significance of a result $t$ in a two-sided test is $p = 2T_\nu(-|t|)$. Since $d$ estimates the true normalised mean $\mu/\sigma$ (a constant), the expected value of $|t|$ rises with $N$ when $\mu \neq 0$, and so the expected value of $p$ falls with $N$ to a limit of 0. Since $\mu = 0$ can never hold exactly, in the standard approach to significance testing every experiment is expected to achieve significance for large enough $N$.

The sample variance of the mean in a given experiment is a function of the degree of random variation within that experiment. This within-experiment variation arises as a consequence of random factors affecting individual measurements in that experiment, with each factor moving individual responses randomly one way or another. If the number of such random confounding factors is large we can, via the central limit theorem, assume that the combined effect of all these factors will follow a Normal distribution (irrespective of the statistical distribution of the individual factors themselves), so that the overall within-experiment variation is approximately Normal.

This within-experiment variation is, however, not the only form of variation in experimental means: means are also affected by between-experiment variation (random variation in experimental means from one experiment to another). This between-experiment variation arises as a consequence of factors that have a fixed or systematic effect within a given experiment, but vary randomly across different experiments with each factor moving the mean $\mu$ in a given experiment randomly one way or another. Assuming that the number of such random between-experiment factors is also large, the overall between-experiment
variation is, again, approximately Normal. Between-experiment variation is very familiar to researchers: a core aim in experimental design is to control for factors or confounds that may influence results. Such factors, however, can never be fully controlled (no experiment is perfect) and so necessarily cause some degree of random variation in experimental results: variation which should be taken into account when assessing significance.

Since the standard approach to significance testing only considers within-experiment variation (sample variance of the mean) it systematically underestimates the degree of random variation in results, and so will identify results as ‘statistically significant’ when in fact they arise as a consequence of random between-experiment variation. To address this, we extend the standard approach by assuming that \( \mu \) itself varies randomly across experiments following

\[
\mu \sim \mathcal{N}(\mu_0, \sigma_0^2)
\]

with unknown variance \( \sigma_0^2 \), with the null hypothesis being \( \mu_0 = 0 \). The variation of \( \bar{X} \) around the overall mean \( \mu_0 \) now has two components: within-experiment variance \( \sigma^2/N \) and between-experiment variance \( \sigma_0^2 \). As \( N \) increases the within-experiment variance of the mean, \( \sigma^2/N \), falls and between-experiment variance comes to be the dominant cause of random variation in means.

### 1.1 Significance for a given variance ratio

We characterise the degree of between-experiment variance \( \sigma_0^2 \) via the variance ratio \( b = \sigma_0^2/\sigma^2 \). For a given value of \( b \) we have

\[
p(\bar{X}|N, \sigma, b) = \int_{-\infty}^{\infty} \mathcal{N}(\bar{X}|\mu, \sigma^2/N) \mathcal{N}(\mu|\mu_0 = 0, b\sigma^2) \, d\mu = \mathcal{N}(\bar{X}|0, (\sigma^2/N)(1 + bN))
\]
and so
\[
\frac{\bar{X}}{(\sigma/\sqrt{N})\sqrt{1 + bN}}
\]
is normally distributed with mean 0 and variance 1. Letting
\[
t = \frac{\bar{X}}{\sqrt{S^2}}\sqrt{\frac{1}{N}}
\]
as before, we thus see that
\[
\frac{\bar{X}}{(\sigma/\sqrt{N})\sqrt{1 + bN}} = \frac{t}{\sqrt{1 + bN}}
\]
follows a t-distribution with \( \nu \) degrees of freedom, and so the statistical significance of a result \( t \) in a two-sided test relative to the variance ratio \( b \) is
\[
p_{\text{sig}}(t|b) = 2T_{\nu} \left( -|t|/\sqrt{1 + bN} \right)
\]
Letting \( t_{\text{crit}} = T_{\nu}^{-1}(1 - \alpha/2) \) be the critical value for significance in a two-sided test, a result \( t \) will be significant at level \( \alpha \) when \( t < -t_{\text{crit}}\sqrt{1 + bN} \) or \( t > t_{\text{crit}}\sqrt{1 + bN} \).

1.2 Significance, \( \alpha \) and type 1 error rate

The \( p \) (in a point-form analysis) or \( p_{\text{sig}} \) (in a distributional analysis) value of a given experimental result tells us the probability of a result as or more extreme arising under our (point-form or distributional) null hypothesis. Given this probability a researcher must decide whether to treat this result as significant. In Fisher’s test for significance this decision is made by comparing the obtained probability against some subjective criterion \( \alpha \), such that a probability less than \( \alpha \) is counted as significant. This criterion \( \alpha \) represents
the type 1 error rate of the test; that is, the probability of incorrectly rejecting the null hypothesis when that hypothesis is true.

Note that this link between $\alpha$ and error rate holds independently of the form of the hypothesis: a point-form test $p < \alpha$ will incorrectly reject the point-form null hypothesis at rate $\alpha$, while a distributional test $p_{\text{sig}} < \alpha$ will incorrectly reject the distributional null hypothesis at rate $\alpha$. This does not, however, mean that point-form and distributional tests at some level $\alpha$ are in any way equivalent. On the contrary, the fact that the distributional approach takes between-experiment variation into account while the point-form approach does not means that many results for which point-form $p < \alpha$ (suggesting a significant result) will simultaneously have $p_{\text{sig}} > \alpha$ (the result is not significant). Indeed, the difference between point-form and distributional significance can be extremely large: in our analysis of experiments in the Many Labs 1 dataset (below), we found that around 10% of experimental results with point-form $p < 0.00001$ (highly significant relative to the point-form null) had $p_{\text{sig}} > 0.05$ (not significant relative to the distributional null).

1.3 Significance and effect size

The size of an effect in a $t$-test is typically estimated in units of sample standard deviation, giving an effect-size estimate of $d = \frac{X}{S}$ (an estimate of the true effect $\delta = \frac{\mu}{\sigma}$). Since in the point-form approach every experiment is expected to achieve significance for large enough $N$, effect size is necessarily independent of significance in this approach: the point-form significance of a result tells us nothing about its effect size. Effect size is thus considered separately from significance, with researchers proposing various criteria to dis-
tistinguish between strong, weak, and negligible effects (Cohen, 1992; Fritz et al., 2012; Kelley and Preacher, 2012; Cohen, 2013) alongside various lower bounds on acceptable effect sizes in terms of, for example, experimental ‘crud’ (Meehl, 1990b,a; Orben and Lakens, 2020).

In the distributional approach, by contrast, significance and effect size are no longer independent. Instead we have

\[ p_{\text{sig}}(t|b) = 2T_\nu \left(-\frac{|t|}{\sqrt{1 + bN}}\right) = 2T_\nu \left(-\frac{|d|}{\sqrt{b + 1/N}}\right) \approx 2T_\nu \left(-\frac{|d|}{\sqrt{b}}\right) \]

and significance and effect size are directly related: if \( p_{\text{sig}}(t|b) \) is low then the observed effect \( d \) is large relative to the variance ratio \( b \), while if \( p_{\text{sig}} \) is high then the effect \( d \) is small.

A common recommendation in effect size analyses is to select effect size criteria based on distributions of effect sizes for comparable outcome measures (Lipsey et al., 2012). This is just what distributional significance provides: given an estimate of the between-experiment variance ratio \( b \) (equivalent to a distribution of effect sizes), in the distributional approach a significance level \( \alpha \) places a bound on detectable effects.

### 1.4 Power, \( \beta \) and type 2 error rate

Where \( \alpha \) by construction estimates the type 1 error rate of an hypothesis test (the probability of incorrectly rejecting the null hypothesis when that hypothesis is true), the related measure \( \beta \) estimates the type 2 error rate of that test (the probability of failing to reject the null hypothesis when it is in fact false), with \( 1 - \beta \) being the statistical power of the experiment (the probability of correctly rejecting the null hypothesis when it is false). Estimates of \( \beta \) are made assuming that some true effect \( \delta = \mu/\sigma > 0 \) holds; here we compare expressions for \( \beta \) in point-form and distributional null approaches.
To estimate $\beta$ for tests relative to a point-form null hypothesis, we let $T_{\nu}(x; \theta)$ represent the cumulative probability from $-\infty$ to $x$ of the non-central $T$ distribution with degrees of freedom $\nu$ and non-centrality parameter $\theta$, and assume that $X \sim \mathcal{N}(\delta \sigma, \sigma^2)$ for some effect size $\delta \neq 0$ (so the null is false). In this situation the variable $t = (X/S)\sqrt{N}$ follows a non-central $t$-distribution with non-centrality parameter $\delta \sqrt{N}$. The probability, in the point-form approach, of getting a non-significant result in a two-sided test with critical value $t_{\text{crit}}$, given that effect $\delta$, is then

$$\beta = T_{\nu}\left(t_{\text{crit}}; |\delta|\sqrt{N}\right) - T_{\nu}\left(-t_{\text{crit}}; |\delta|\sqrt{N}\right)$$

and for an experiment to detect an effect of size $\delta$ with significance $\alpha$ and power $1 - \beta$ we must have a sample size $N$ such that

$$T_{\nu}\left(t_{\text{crit}}; |\delta|\sqrt{N}\right) - T_{\nu}\left(-t_{\text{crit}}; |\delta|\sqrt{N}\right) \leq \beta$$

Since

$$\lim_{N \to \infty} T_{\nu}\left(t; |\delta|\sqrt{N}\right) = 0$$

for all $t$ (as the non-centrality parameter approaches infinity, the area under the non-central $t$ distribution less than any fixed value $t$ necessarily approaches 0) and since

$$\lim_{N \to 0} \left[ T_{\nu}\left(t_{\text{crit}}; |\delta|\sqrt{N}\right) - T_{\nu}\left(-t_{\text{crit}}; |\delta|\sqrt{N}\right) \right] = T_{\nu}\left(t_{\text{crit}}\right) - T_{\nu}\left(-t_{\text{crit}}\right) = 1 - \alpha$$

(the non-central distribution approaching the central distribution in this situation) we see that in the point-form approach $\beta$ has an upper limit of $1 - \alpha$ and falls with increasing $N$ towards a lower limit of 0. The power of a given experiment $(1 - \beta)$ thus has a minimum of
α and rises to a limit of 1 with increasing \( N \) (for any effect \( \delta > 0 \) there is a corresponding sample size \( N \) which can detect that effect with any required power).

In the distributional situation we can do a similar analysis in terms of the overall null hypothesis by assuming some true effect \( \delta = \mu_0/\sigma_0 > 0 \), giving

\[
\bar{X} \sim \mathcal{N}(\delta\sigma_0, (\sigma^2/N)(1+bN))
\]

and so

\[
\frac{X}{(\sigma/\sqrt{N})\sqrt{1+bN}}
\]

is normally distributed with mean \( \delta\sigma_0 \) and variance 1, and defining \( t \) as before we see that

\[
\frac{t}{\sqrt{1+bN}} = \frac{\bar{X} - \delta\sigma_0}{(\sigma/\sqrt{N})\sqrt{1+bN}} + \frac{\delta\sigma_0}{(\sigma/\sqrt{N})\sqrt{1+bN}} \sqrt{\frac{\nu}{\nu \sigma^2 / \nu}}
\]

follows a non-central \( t \)-distribution with \( \nu \) degrees of freedom and non-centrality parameter

\[
\frac{\delta\sigma_0}{(\sigma/\sqrt{N})\sqrt{1+bN}} = \frac{\delta}{\sqrt{1+1/bN}}
\]

For a two-sided test we thus have a type 2 error rate of

\[
\beta = T_\nu \left( t_{\text{crit}}; \frac{|\delta|}{\sqrt{1+1/bN}} \right) - T_\nu \left( -t_{\text{crit}}; \frac{|\delta|}{\sqrt{1+1/bN}} \right)
\]

Here the non-centrality parameter falls towards 0 with declining \( bN \) and so the error rate \( \beta \) rises, approaching an upper limit of \( 1 - \alpha \) as before. As \( bN \) rises, \( \beta \) falls to a lower limit of

\[
\lim_{bN \to \infty} \left[ T_\nu \left( t_{\text{crit}}; \frac{|\delta|}{\sqrt{1+1/bN}} \right) - T_\nu \left( -t_{\text{crit}}; \frac{|\delta|}{\sqrt{1+1/bN}} \right) \right] = T_\nu \left( t_{\text{crit}}; |\delta| \right) - T_\nu \left( -t_{\text{crit}}; |\delta| \right)
\]
We thus see that the power of an experiment rises with \( bN \) from a minimum of \( \alpha \) towards a maximum of

\[
1 - T_\nu(t_{\text{crit}}; |\delta|) + T_\nu(-t_{\text{crit}}; |\delta|) \approx 1 - T_\nu(t_{\text{crit}}; |\delta|)
\]

(since the last term is negligible) and no experiment can detect an effect \( \delta \) with a power greater than this value, irrespective of its sample size \( N \) or the variance ratio \( b \). Since \( T_\nu(t_{\text{crit}}; |\delta|) > 0.5 \) when \( |\delta| < t_{\text{crit}} \) this means that statistical power above 0.5 can only be achieved for effects \( |\delta| > t_{\text{crit}} \), and that power approaches 1 only for very large effect size \( |\delta| \).

Where in the point-form approach we can design an experiment to detect any effect size at any required level of statistical power (by selecting a large enough \( N \)) in the distributional approach this is not possible, because the power of an experiment to detect an effect is a function of effect size rather than \( N \).

### 1.5 Estimating the probability of replication

Because this distributional approach explicitly represents the variation in results across experiments (via the distributional null hypothesis), it allows us to express the probability of obtaining a statistically significant result at level \( \alpha \) in a replication of our original experiment. In this section we give estimates for the replication probability, \( p_{\text{rep}} \), for a given result based first on a fixed value \( b \), and then based on a sample estimate \( \hat{b} \). In subsequent sections we give simple ‘closed form’ approximations to \( p_{\text{sig}} \) and \( p_{\text{rep}} \) in terms of the \( T \) distribution (for significance) and the Normal and inverse \( \chi^2 \) distributions (for replication).

We also give generic bounds on \( p_{\text{sig}} \) and \( p_{\text{rep}} \) that can be used when no estimate for the variance ratio \( \hat{b} \) is available.
For some value of $b$ we assume a replication experiment measuring the same $X$ as the original, with sample mean $X_r \sim N(\mu_r, \sigma_r^2/N_r)$, where $\mu_r$ and $\sigma_r^2$ are the unknown mean and unknown variance of $X$ in the replication, and $N_r$ and $\nu_r$ the number of measurements and the degrees of freedom. We take $S_r^2$ to represent the sample variance of $X$ in the replication, and relate within-experiment variance in the original and replication via the ratio $c = \sigma_r^2/\sigma^2$.

Letting $t_{\text{crit},r} = T_{\nu_r}^{-1}(1 - \alpha/2)$ be the critical $t$ value at level $\alpha$ in this replication experiment and

$$t_r = \frac{X_r}{\sqrt{S_r^2/N_r}}$$

be the test statistic, a result $t_r$ will count as a replication of our original result $t$ if it is significant at the same level $\alpha$, and in the same direction, as $t$. In other words, if our original result $t$ was significant in a left-tailed test ($t < -t_{\text{crit},r}\sqrt{1 + bN}$) then it is replicated if $t_r < -t_{\text{crit},r}\sqrt{1 + bN}$, while if our original result was significant in a right-tailed test ($t > t_{\text{crit},r}\sqrt{1 + bN}$) then it is replicated if $t_r > t_{\text{crit},r}\sqrt{1 + bN}$.

To estimate the probability of replication we must derive a distribution for $t_r$. We update our initial null hypothesis distribution $\mu \sim N(0, \sigma_0^2)$ using the observed value of the sample mean in the original experiment, $\overline{X}$, getting the posterior distribution for $\mu$ of

$$\mu \sim N(\mu_N, \sigma_N^2)$$

where

$$\sigma_N^2 = \frac{\sigma_0^2 \sigma^2}{N \sigma_0^2 + \sigma^2} = \frac{bN}{(1 + bN)}(\sigma^2/N)$$

$$\mu_N = \frac{\sigma_N^2}{(\sigma^2/N)} \overline{X} = \frac{bN}{(1 + bN)} \overline{X}$$
(a property of the Normal distribution; see e.g. Bishop 2006; Murphy 2007). Note that this distribution does not represent an unconditional inference about the probability distribution for \( \mu \): our experimental result does not tell us that \( \mu \) in fact has this distribution (because a distribution for \( \mu \) cannot be inferred from a single mean). Instead this is the inferred distribution for \( \mu \) conditional on the initial null hypothesis; that is, conditional on the initial assumption that \( \mu \sim \mathcal{N}(0, \sigma_0^2) \).

Given this updated distribution for \( \mu \), the probability density of the sample mean \( \bar{X}_r \) in our second experiment is

\[
p(\bar{X}_r|X, b) = \int \mathcal{N}(\bar{X}_r| \mu, c\sigma^2/N_r)\mathcal{N}(\mu|\mu_N, \sigma_N^2) d\mu
\]

and so

\[
\bar{X}_r \sim \mathcal{N}(\mu_N, c\sigma^2/N_r + \sigma_N^2) \sim \mathcal{N}\left(\frac{bN}{1 + bN} \bar{X}, \frac{(\sigma^2/N)}{1 + bN + cN/N_r}\right)
\]

and the variable

\[
\frac{\bar{X}_r - \frac{bN}{1 + bN} \bar{X}}{\frac{\sigma}{\sqrt{N}}\sqrt{\frac{bN}{1 + bN} + \frac{cN}{N_r}}}
\]

is normally distributed with mean 0 and variance 1. This means that the variable

\[
\frac{\bar{X}_r - \frac{bN}{1 + bN} \bar{X}}{\sqrt{\left(\frac{\nu_r S^2_r}{\sigma^2}\right)/\nu_r}\left(\frac{\sigma}{\sqrt{N}}\sqrt{\frac{bN}{1 + bN} + \frac{cN}{N_r}}\right)} = t_r\sqrt{\frac{cN}{N_r} - \frac{bN}{1 + bN} \frac{\bar{X}}{\sqrt{S^2_r/N}}\sqrt{c}/(1 + bN + cN/N_r)}
\]

has a \( t \)-distribution with \( \nu_r \) degrees of freedom.

Since the variance in the replication experiment is \( c \) times that of the original experiment, the variable \( S^2_r/c \) follows approximately the same distribution as the variable \( S^2 \) (a
scaled $\chi^2$ distribution) when $N$ and $N_r$ are similar (with both variables following exactly the same distribution when $N = N_r$), or when both are large. In this situation the variable

$$t_r \sqrt{\frac{cN}{N_r} - \frac{bN}{1+bN} \frac{\overline{S/N}}{\sqrt{S/N}} \sqrt{\frac{bN}{1+bN} + cN}} = t_r \sqrt{\frac{cN}{N_r} - \frac{bN}{1+bN} t} = \frac{t_r \sqrt{c} - t \sqrt{bN}}{\sqrt{c + bN_r/\sqrt{(1 + bN)}}}$$

will follow a $t$-distribution with $\nu_r$ degrees of freedom.

Given this distribution the probability of obtaining a result less than $-t_{crit,r} \sqrt{1 + bN_r}$ in our replication experiment is

$$T_{\nu_r} \left( -t_{crit,r} \sqrt{c(1 + bN_r) - t \frac{bN_N}{1+bN}} \right) \tag{3}$$

and the probability of obtaining a result greater than $t_{crit,r} \sqrt{1 + bN_r}$ is

$$1 - T_{\nu_r} \left( \frac{t_{crit,r} \sqrt{c(1 + bN_r)} - t \frac{bN_N}{1+bN}}{\sqrt{c + bN_r/\sqrt{(1 + bN)}}} \right) = T_{\nu_r} \left( \frac{t \frac{bN_N}{1+bN} - t_{crit,r} \sqrt{c(1 + bN_r)}}{\sqrt{c + bN_r/\sqrt{(1 + bN)}}} \right) \tag{4}$$

If our original result $t$ was negative, then the probability of replication is given by Equation 3 while if positive it is given by Equation 4 and so substituting for $t_{crit,r}$ we see that the probability of replication of any result $t$ (given variance ratios $b$ and $c$) is

$$T_{\nu_r} \left( \frac{|t| \frac{bN_N}{1+bN} - T_{\nu_r}^{-1} (1 - \alpha/2) \sqrt{c(1 + bN_r)}}{\sqrt{c + bN_r/\sqrt{(1 + bN)}}} \right) \tag{5}$$

Since our second experiment is a replication of the first, we can generally assume that the within-experiment variance $\sigma^2$ in both experiments will be approximately the same (so $c = 1$) and, simplifying, we have an expression for the probability of replication of

$$p_{rep}(t|b) = T_{\nu_r} \left( \frac{|t| bN_N - T_{\nu_r}^{-1} (1 - \alpha/2) (1 + bN) \sqrt{1 + bN_r}}{\sqrt{(1 + bN + bN_r)(1 + bN)}} \right) \tag{5}$$
1.6 Bounds on significance and replication

These expressions impose useful bounds on significance and replication probabilities for a range of between-experiment variance values $b$. From Equation 2 we see that the distributional significance of a given result $p_{\text{sig}}(t|b)$ falls with falling $b$, so that if a result is significant at level $\alpha$ for some variance ratio $B$, it is significant at the same level for all $b < B$. A similar result holds for $p_{\text{rep}}(t|b)$: it can be shown that the probability of replication of a given result $p_{\text{rep}}(t|b)$ rises with falling $b$ to a maximum at some value $b_{\text{max}} \approx |d|/\sqrt{N}$, so that $p_{\text{rep}}(t|b) \geq p_{\text{rep}}(t,B)$ for almost all $b \leq B$ (see Appendix 1 for proof). If we have some reasonable upper limit $B$ on the variance ratio for experiments (such that the actual unknown variance ratio for any given experiment is a priori expected to be less than this maximum), then we can define ‘generic’ estimates for distributional significance and replication as

$$\hat{p}_{\text{sig}} = 2T_{\nu} \left(-|t|/\sqrt{1+BN} \right)$$

and

$$\hat{p}_{\text{rep}} = T_{\nu} \left(|t|B\sqrt{NN_r} - T^{-1}_{\nu} (1 - \alpha/2) (1 + BN)\sqrt{1+BN_r} \right) \sqrt{(1+BN+BN_r)(1+BN)}$$

and if for a given result $t$ we have $\hat{p}_{\text{sig}} \leq \alpha$ and $\hat{p}_{\text{rep}} = \rho$, then our result $t$ is significant at level $\alpha$, and has a probability of replication greater than $\rho$, conditional on the assumption that between-experiment variance is less than $B$ times within-experiment variance.

What value should be chosen for this bound $B$? Differences in means across experiments can arise as a consequence of within experiment variance and as a consequence of differential factors affecting experimental means (if the means in one experiment is af-
fected by some confounding factor not present in the other, we expect their means to differ systematically as a function of that confound). Since replication experiments are necessarily designed to be as similar as possible to each other, we expect the effect of these between-experiment confounds to be weaker than the effect of within-experiment variance (if between-experiment confounds have a strong influence on experimental means, then the experiments are not, in fact, replications: they differ in some important aspect). Given that the variance ratio $b$ represents the ratio of between-experiment to within-experiment variance, we thus expect that $b < 1$ will hold for replications and set a maximum bound of $B = 1$.

Note, however, that the lower the value of $B$, the lower the value of $\hat{p}_{\text{sig}}$ and the higher the value of $\hat{p}_{\text{rep}}$ (and so the more likely we are to judge a result as significant and replicable). This means that lower values of $B$ (those that underestimate the true level of between-experiment variance) have a higher type 1 error rate but a lower type 2 rate, while higher values of $B$ (that overestimate the true level of between-experiment variance) have a lower type 1 error rate and a higher type 2 rate. For conservative rejection of the null (only rejecting the null when the evidence is very strong), we should therefore test against a bound of $B$ close to 1; for more liberal rejection of the null (being willing to reject the null even when the evidence is weak), we should test against a bound of $B$ close to 0.

2 Estimating significance and replication

The previous section derived distributional null expressions for significance, power and replication assuming known variance ratio $b$ or bounds on that ratio. These expressions
are both computationally complex, and depend on this unknown value. In this section we derive sample estimators for $b$, and give simple and easily used closed-form estimates for significance and replication in terms of the standard $T$ distribution. We also describe extensions of this approach to different forms of $t$-test and to tests of regression, linear correlation, and contingency.

2.1 Sample Estimators for $b$

Our estimates $\hat{p}_{\text{sig}}$ and $\hat{p}_{\text{rep}}$ are in terms of generic bounds on $b$. Given replication data, however, we can estimate $b$ in terms of its component variances, producing more specific expressions for $p_{\text{sig}}$ and $p_{\text{rep}}$. Estimating $\sigma^2$ is straightforward: given some experiment measuring a normally distributed variable $X \sim N(\mu, \sigma^2)$ with unknown within-experiment variance $\sigma^2$ and degrees of freedom $\nu$, the unbiased estimator for $\sigma^2$ is

$$S^2 = \frac{1}{\nu} \sum_{i=1}^{N} (X_i - \bar{X})^2$$

the sample variance of $X$. We wish to produce an analogous unbiased estimator for $\sigma_0^2$, which we write as $S_0^2$. We obtain this estimator by considering the variance of the means in some set of replications of an experiment similar to ours, and subject to the same broad set of random confounding factors, both within and between experiments. Since in psychology many such factors are related to differences between individual participants (for within experiment variance) and to systematic differences between groups of participants (for between experiment variance), such estimates of the between-experiment variance of means can potentially be applied widely.
Suppose we have $K$ experiments all measuring the same variable $X$. In each experiment $i$ we assume that $X \sim \mathcal{N}(\mu_i, \sigma_i^2)$ for different values of $\mu_i$ and $\sigma_i^2$, where $\mu_i \sim \mathcal{N}(\mu_0, \sigma_0^2)$ ($\sigma_0^2$ representing the between-experiment variance of the mean). We assume that each experiment $i$ has $N_i$ measurements of $X$ with sample mean $\bar{X}_i$ and within-experiment sample variance $S_i^2$, and take $\bar{X}_0$ to be the mean of these sample means $\bar{X}_i$ and

$$S_m^2 = \frac{1}{K-1} \sum_{i=1}^{K} (X_i - X_0)^2$$

to be the sample variance of these sample means. Then $S_0^2$, the unbiased estimator for $\sigma_0^2$, is given by

$$S_0^2 = \frac{1}{K-1} \sum_{i=1}^{K} (\mu_i - \bar{\mu})^2$$

for the unknown values $\mu_i$, and the variable

$$t_i = \frac{\bar{X}_i - \mu_i}{S_i/\sqrt{N_i}}$$

follows a $t$-distribution with $\nu_i$ degrees of freedom. Treating $\mu_i$ as a random variable we define

$$\bar{\mu} = \frac{1}{K} \sum_{i=1}^{K} \mu_i$$

and the expectation value of this expression is

$$\frac{1}{K} \sum_{i=1}^{K} \bar{X}_i = \bar{X}_0$$

Given this the expectation value of $S_0^2$ is

$$\langle S_0^2 \rangle = \frac{1}{K-1} \sum_{i=1}^{K} (X_i - X_0)^2 + \frac{1}{K} \sum_{i=1}^{K} \frac{\nu_i S_i^2}{N_i(\nu_i - 2)} = S_m^2 + \frac{1}{K} \sum_{i=1}^{K} \frac{\nu_i S_i^2}{N_i(\nu_i - 2)}.$$
and $S_0^2$ is an unbiased estimator for $\sigma_0^2$. Since the within-experiment sample variance of the mean $S_i^2/N_i$ declines to 0 with increasing $N_i$, this means that the expression $(K-1)S_0^2/\sigma_0^2$ approximately follows a $\chi^2$ distribution with degrees of freedom $\nu_0 = K-1$ (with the error of the approximation falling with increasing $N_i$).

Note that in the case where we have only seen 1 experiment with mean $\bar{X}$ and sample variance $S^2$ and no data on the variation of sample means across experiments, the above expression for $S_m^2$ is undefined and so an unbiased estimator for $S_0^2$ cannot be given.

Given these unbiased estimators $S^2$ and $S_0^2$ we take $\hat{b} = S_0^2/S^2$ as our estimate for the ratio $b = \sigma_0^2/\sigma^2$, and because both $S^2$ and $S_0^2$ approximately follow $\chi^2$ distributions, we see that $b$ approximately follows an $F_{\nu,\nu_0}$ distribution scaled by this estimate $\hat{b}$ (with the error in the approximation falling with $\nu_0$). The variable $p_{sig}$ is then distributed as a function of the distribution of $b$, and the expected value of that distribution given $\hat{b}$ is

$$p_{sig}(t|\hat{b}) = \int_0^\infty 2T_\nu \left(\frac{-|t|}{\sqrt{1+bN}}\right) f_{\nu,\nu_0}(b)db$$

where $f_{\nu,\nu_0}$ is the probability density of that $F$ distribution. This is our theoretical model for distributional significance, and when $p_{sig}(t|\hat{b}) < \alpha$ we can say that our result $t$ gives statistically significant evidence against the null hypothesis, given the estimated within-experiment and between-experiment variances.

Assuming that sample variances $S^2$ and $S_r^2$ in the two experiments are both estimates of the same underlying within-experiment variance $\sigma^2$, then since these two sample variances both follow a $\chi^2$ distribution with the same mean and with degrees of freedom $\nu$ and $\nu_r$, their ratio $c$ follows an $F$ distribution $F_{\nu,\nu_r}$. Similarly taking $\hat{b} = S_0^2/S^2$ as our estimate for the ratio $b$ we see that the variable $p_{rep}$ is distributed as function of the joint distribution of
Significance and Replication

$b$ and $c$. Since we don’t know the sample variance $S^2_r$ (our replication experiment has not yet been carried out) we simply set $\hat{c} = 1$ and the expected value for $p_{rep}$ given estimate $\hat{b}$ is

$$p_{rep}(t|\hat{b}) = \int_0^\infty \int_0^\infty T_{\nu_r} \left( \frac{|t|\sqrt{N_r N} - T_{\nu_r}^{-1}(1-\alpha/2)(1+bbN)\sqrt{1+bbN}}{\sqrt{(1+bbN+b\hat{b}N_r)(1+b\hat{b}N)}} \right) f_{\nu_r,\nu_0}(b) f_{\nu_r,\nu_0}(c) \, db \, dc \tag{6}$$

This is our theoretical model of the probability of result $t$ being replicated in an experiment with $N_r$ measurements, given an estimate of between-experiment variance in the means of a set of similar experiments and assuming the sample variance in that replication is close to $S^2_r$. Note that this estimate for replication is conditional on evidence against that null hypothesis from the experimental result $t$. This means that if result $t$ does not give evidence against the null hypothesis (that is, if $p_{sig}$ is high) then we are not justified in ‘updating away’ from that hypothesis, and our estimate of $p_{rep}$ does not apply. In other words, we only have evidence for replication when we have evidence against the null.

These integral and double-integral estimates for $p_{sig}$ and $p_{rep}$ are, however, somewhat computationally expensive to calculate in practice; and further, these calculations can be ‘fragile’: dependent in opaque ways on the numerical integration algorithm used, especially for values of $\hat{b}$ close to 0. In the next section we give more practically useful estimates for $p_{sig}$ and $p_{rep}$, expressed in a closed, non-integral form in terms of the standard $T$ distribution.

### 2.2 Closed-form significance and replication estimates

The difference between classical and distributional significance testing is most important for large sample size $N$, because in that situation between-experiment variance $\sigma^2_0$ domi-
nates the sample variance of the mean \( \sigma^2/N \). Here we derive approximate estimates for significance and replication for large values of \( N \): specifically, values such that \( S^2 \) is approximately equal to \( \sigma^2 \) and such that \( \sigma/\sqrt{N} \) is much smaller than \( \sigma_0 \), which means that

\[
\frac{bN}{1 + bN} \approx 1
\]

Then we have

\[
p_{\text{sig}}(t|b) = 2T_\nu \left( \frac{-|t|}{\sqrt{1 + bN}} \right) \approx 2\Phi \left( \frac{-|X|}{\sqrt{\nu_0 S^2_0/\sigma^2_0}} \right) = 2\Phi \left( \frac{-|X|}{\sqrt{\sigma^2_0}} \right)
\]

Since by assumption \( \sigma/\sqrt{N} \) is much smaller than \( \sigma_0 \), we see that \( X \) approximately follows the distribution \( N(0, \sigma^2_0) \). Since \( S^2_0 \) is an unbiased sample estimator for \( \sigma^2_0 \) such that \( \nu_0 S^2_0/\sigma^2_0 \) approximately follows the distribution \( \chi^2_{\nu_0} \), this means that

\[
\Phi \left( \frac{-|X|}{\sqrt{\sigma^2_0}} \right) \approx T_{\nu_0} \left( \frac{-|X|}{\sqrt{S^2_0}} \right)
\]

(Note the change in degrees of freedom for the \( T \) distribution, from \( \nu \) to \( \nu_0 \)). This expression is independent of \( \sigma_0 \), and represents the significance of a distributional \( t \)-statistic

\[
t_0 = \frac{\bar{X}}{\sqrt{S^2_0}} = \frac{t}{\sqrt{bN}}
\]

(the observed mean divided by the sample deviation of means across experiments, rather than the sample deviation of a given experimental mean). Given this we define our general expression for distributional significance as

\[
p_{\text{sig}} = 2T_{\nu_0} \left( \frac{-|t|}{\sqrt{bN}} \right)
\]
For replication we have

\[ p_{rep}(t|b) = T_{\nu_r} \left( \frac{|t|b\sqrt{NN_r}}{\sqrt{(1 + bN)(1 + b(N + N_r))}} - \frac{T_{\nu_r}^{-1} (1 - \alpha/2) \sqrt{(1 + bN)(1 + bN_r)}}{\sqrt{1 + b(N + N_r)}} \right) \]

and since by assumption \( \sqrt{1 + bN} \approx \sqrt{bN} \), we have the approximation

\[ p_{rep}(t|b) \approx T_{\nu_r} \left( \frac{N_r}{N + N_r} |t| - T_{\nu_r}^{-1} (1 - \alpha/2) \sqrt{1 + bN} \right) \]

By assumption we also have \( S^2 \approx \sigma^2 \) so that \( b = \sigma_0^2/\sigma^2 \approx \sigma_0^2/S^2 \) and so we can rearrange to get

\[ p_{rep}(t|b) \approx T_{\nu_r} \left( \sqrt{\frac{bNN_r}{N + N_r}} \left[ \frac{|t|}{\sqrt{bN}} - T_{\nu_r}^{-1} (1 - \alpha/2) \sqrt{\frac{1}{\frac{bN}{S_0^2} + \nu_0}} \right] \right) \]

Since \( \frac{\sigma_0^2}{(\nu_0 S_0^2)} \) approximately follows the inverse distribution \( \chi_{\nu_0}^2 \), and this distribution has a mean of \( 1/(\nu_0 - 2) \) for \( \nu_0 > 2 \), this gives an expected replication probability of

\[ p_{rep} = T_{\nu_r} \left( \sqrt{\frac{bNN_r}{N + N_r}} \left[ \frac{|t|}{\sqrt{bN}} - T_{\nu_r}^{-1} (1 - \alpha/2) \sqrt{\frac{1}{\frac{bN}{S_0^2} + \frac{\nu_0}{\nu_0 - 2}}} \right] \right) \]

which defines our general expression for replication.

These \( p_{sig} \) and \( p_{rep} \) expressions are closed-form estimates for distributional significance and replication, analogous to the classical \( t \) test for significance in that they use the \( \chi^2 \) distribution to replace the unknown variance \( \sigma_0^2 \) with its estimate \( S_0^2 \). We expect these expressions to be less accurate in terms of estimating significance and replication probabilities than the full integral expression given in Equation 6 (with the difference falling as sample size \( N \) rises) but these closed-form estimates have the advantages of simplicity, computational speed, and robustness.
These expressions also clarify the general relationship between distributional significance and replication: given the distributional test statistic $t_0$, a result which is statistically significant in a two-sided test ($p_{sig} < \alpha/2$) necessarily has $|t_0| > T_{\nu_0}^{-1}(1 - \alpha/2)$, which for large $N$ implies $p_{rep} > 0.5$: and so in this approach the more statistically significant a result is, the more likely that result is replicate.

2.3 Extension to related statistical tests

We’ve presented distributional significance testing here in terms of a generalised $t$-test, and so this approach applies to each distinct form of that test. To apply this model to a one-sample $t$-test on a variable $X$ with sample size $N$, we set $\nu = N - 1$ and take $S^2$ to be the sample variance of that variable. To apply to a paired $t$-test on two variables (assuming $N$ pairs) we take the $X$ to represent the difference in pairs and $\bar{X}$ and $S^2$ to be the average difference between pairs and the variance of that difference, and $\nu = N - 1$. To apply to an unpaired or independent $t$-test on two variables (with $N$ measurements in total), we take $\bar{X}$ to be the difference between the means of each variable, $N$ to be the sample size, and $S^2$ to be the pooled sample variance with degrees of freedom $\nu = N - 2$. (Note that we implicitly assume an equal number of samples for the two variables in an unpaired test. This is because the probability of replication of a given result in a future experiment on two unpaired variables will depend on the sample sizes for those two variables in that experiment, which we cannot know. Assuming that these sample sizes vary randomly the expected sample size for each variable will be $N/2$; and so we use the calculated replication probability assuming equal sample sizes as our estimate of the probability of replication.)
The approach also applies to tests of linear regression, correlation and contingency, which can all be related to the $t$-test. Applying the distributional approach to tests of independence for correlation and linear regression gives $p_{sig}$ and $p_{rep}$ expressions as above, albeit calculated with sample slope $M$ replacing sample mean $\bar{X}$, predictor sum-of-squares (which we write as $Q$) replacing sample size $N$, and mean squared error of the response estimate replacing sample variance. This is because, with these replacements, such tests of independence are simply $t$-tests (see Appendix 2 for a derivation of these results). Note that in these correlation tests the sum of squares of the predictor variable is the continuous-valued analog of the discrete sample size $N$ in a $t$-test, and is treated as a controlled variable: where sample size gives the number of discrete measurements made in a $t$-test, predictor sum-of-squares gives the range of continuous measurements in a test of correlation. This means that the significance and replication probability of these tests depends on the choice of predictor and response variables: an estimate for the probability of replication of a given result in an experiment where $X$ is the predictor (and so assumed to be controlled in replications) will necessarily be different from the probability of replication of that result when $Y$ is the predictor and the $Y$ sum of squares is assumed to be controlled in replications (because the two replication experiments themselves are different).

Code to calculate all these tests of distributional significance and replication is available online at https://osf.io/ep86y. This code also tests the distributional model’s approach to significance and replication against the Many Labs 1 replication dataset, as described in the next section.
2.4 Comparing with point-form approaches to replication

How does this distributional model compare with other approaches to replication? The most influential method for estimating the probability of replication $p_{rep}$ is that of Killeen (Killeen, 2005a, b, 2007; Sanabria and Killeen, 2007), which for a number of years was recommended by the journal *Psychological Science* as an alternative to standard hypothesis tests. This approach does not estimate the probability of obtaining a statistically significant result in a second experiment: instead it estimates the probability of obtaining a result in a second experiment that is the same sign as the original result. In a one-sample test with sample size $N$ and effect $d = \bar{X}/S$, Killeen’s $p_{rep}$ calculates the probability of obtaining a result of the same sign as $d$ by estimating the variance of the original effect as $\sigma_d^2 \sim N/(N-4)$, taking the variance in the ensemble of original and replication to be $2\sigma_d^2$, and assuming that effects are normally distributed, so that Killeen’s $p_{rep}$ for a given $d$ is approximately

$$
\Phi\left(\frac{|d|}{\sqrt{2}\sigma_d}\right) = \Phi\left(\frac{|ar{X}|}{\sqrt{2}S \left[ 1 - \frac{4}{N} \right]}\right)
$$

Researchers have pointed out a number of fundamental problems with this approach to replication: that there are errors in the derivation of Killeen’s $p_{rep}$ (Doros and Geier, 2005); that Killeen’s $p_{rep}$ is simply a function of the point-form $p$ and so gives no further information (Maraun and Gabriel, 2010); that Killeen’s $p_{rep}$ estimates an aggregated probability over all results and experiments, rather than the probability of a given result being replicated in a particular experiment (Miller, 2009; Miller and Schwarz, 2011); that replication probabilities must be estimated based on a prior distribution (Macdonald, 2005);
that Killeen’s $p_{rep}$ assumes all effect sizes are equally likely and so assumes a priori that the null hypothesis is false (Iverson et al., 2010b); and finally that the claims associated with Killeen’s $p_{rep}$ are easily misinterpreted (Iverson et al., 2009a,b, 2010a).

Our distributional null hypothesis expression for $p_{rep}$ resolves the problems in Killeen’s approach. Our $p_{rep}$ is not simply a function of the point-form $p$ and is an estimate for replication in a particular experiment (in that it depends on the ratio of between-experiment to within experiment variance $b$, the ratio of within-experiment variance in the original experiment and the replication $c$, and the sample sizes of the original and replication experiments). Our $p_{rep}$ is specifically based on a prior distribution for the null hypothesis, does not assume all effect sizes are equally likely (the larger an effect size the less likely it is under this prior distribution), and does not assume the null hypothesis is false. Finally, since our result is based on well-known properties of the Normal and $t$ distributions, errors in the derivation are (hopefully) unlikely, and the associated claims have a clear interpretation.

3 Predicting Replication in the Many Labs 1 Dataset

We test this distributional approach using data from the first ‘Many Labs’ replication project (Klein et al., 2014). This involved the replication of 16 different experiments investigating a variety of classic and contemporary psychological effects. Each experiment was originally published in the cognitive or social psychology literature, and was replicated by researchers in around 36 different sites (25 in the US, 11 international): each individual instance of one of these tasks thus had around 35 replications with the same design but with varying sample size and sample variance values (some tasks had less than 36 experiments;
there were 574 experiments in total, with 400 occurring at US sites). We chose to use this dataset to test the distributional null approach because the raw response data for all experiments at all sites is available, allowing us to compute the various estimators required in the distributional model, and because the large number of replications of each individual task allows an accurate estimate of the actual replication rate for these experiments, which we can use to test the replication probability predicted for those experiments by our model.

These experiments covered a wide range of topics, including the impact of question phrasing on whether speeches for or against democracy should be allowed/forbidden; the effect of ‘anchoring’ on estimates of the distance from San Francisco to NYC, the number of babies born per year in the US, the population of Chicago, or the height of Mount Everest; agreement with quotes depending on they are attributed to George Washington/Osama Bin Laden; the effect of priming with the US flag/currency on political opinions; and the effect of imagined contact with Muslims on reductions in prejudice. A number of these topics were US-specific, and so experimental “replications” of these results in non-US sites are subject to clear confounds (we would expect there to be differences between US and non-US sites in knowledge about US distances and US city populations, and in attitudes towards George Washington and the US flag or currency, for example\(^1\)). For this reason we limit our analysis to results from US sites only.

\(^1\)Such differences are evident even in knowledge about the height of Mount Everest: on average fewer than 2% of estimates at US sites fell within 1% of the true height, with all US sites having less than 6% of estimates in that range. Of the 11 international sites, however, one had 35% of estimates within 1% of the true height, one 26% and one 20%, and on average more than 10% of international estimates were within 1% of the true height.
3.1 Methods

All data, analysis and visualisation code is publicly available on the OSF repository at [https://osf.io/ep86y](https://osf.io/ep86y). Data were analyzed using R, version 4.0.5 [R Core Team 2021] and the packages ggplot2 version 3.3.5 (Wickham 2016) and xtable 1.8.4 (Dahl et al. 2019). The R analysis script downloads the Many Labs 1 dataset from the project’s OSF repository and carries out all analyses described below.

Experiments in the Many Labs dataset varied widely in significance, with some having significant results in all or almost all replications, and others having only a few significant results. In our analysis we use the independent and dependent measures from the Many Labs 1 tasks (and the corresponding criteria for inclusion/exclusion of responses as flagged in the dataset); Table 1 gives summary information on these tasks for US sites.

For every individual experiment, in this script we calculated the within-experiment sample variance $S^2$; for each experimental task we calculated the between-experiment sample variance $S^2_0$ (in terms of sample means $\bar{X}$ or slopes $\hat{M}$). To assess the distributional model of significance against these experimental results, we used these sample variances to calculate the distributional significance estimate $p_{sig}$ for each experiment, and compared against the point-form significance $p$ for each experiment.

To assess the distributional model of replication, we grouped all experiments for a given task into ‘predictor-target’ pairs and used the results of the predictor experiment to calculate the probability of replication $p_{rep}$ for that particular target experiment (and a given value $\alpha$). We then compared the predicted replication probability for each target experiment against the observed rate of successful replication in those target experiments.
Table 1: Summary information for US sites in Many Labs 1 replication project. The table also gives the estimated sample variance of the means across experiments in each task \( (S_0^2) \), the proportion of experiments in each task that were statistically significant in two-sided point-form and distributional tests \( (p \text{ or } p_{\text{sig}} \text{ less than } 0.05) \) and where the effect in the same direction as in the original experiment (this is equivalent to significance at 0.025 in a one-sided point-form or distributional test with the direction of the test corresponding to that of the original effect). The \( p \) and \( p_{\text{sig}} \) values of the aggregated dataset for each experimental task are also shown (with between-experiment variance for a given task taken to be \( S_0^2 \) and within-experiment variance calculated from the aggregated dataset for that task).

| Task                                                 | Total participants | expts | test       | \( S_0^2 \) | \( \bar{b} \) (mean) | proportion | \( p \)   | \( p_{\text{sig}} \) | \( p \)   | \( p_{\text{sig}} \) |
|------------------------------------------------------|--------------------|-------|------------|-------------|-----------------------|------------|-----------|----------------|------------|----------------|
| 1 Allowed/forbidden                                   | 4934               | 25    | \( \chi^2 \) | 0.007       | 0.06                  | 1.00       | 1.00      | 10^{-325}      | 10^{-9}    |
| 2 Anchoring - babies born                            | 4481               | 25    | t          | \( 8.5 \times 10^6 \) | 0.08                  | 1.00       | 1.00      | 10^{-325}      | 0.0005     |
| 3 Anchoring - Mt. Everest                            | 4575               | 25    | t          | \( 1.1 \times 10^7 \) | 0.13                  | 1.00       | 1.00      | 10^{-325}      | 0.002      |
| 4 Anchoring - Chicago                                 | 4302               | 25    | t          | \( 1.0 \times 10^{11} \) | 0.10                  | 1.00       | 1.00      | 10^{-325}      | 0.006      |
| 5 Anchoring - distance to NYC                         | 4422               | 25    | t          | \( 6.9 \times 10^4 \) | 0.07                  | 1.00       | 0.60      | 10^{-267}      | 0.05       |
| 6 Relation between Implicit and Explicit math attitudes | 4383               | 25    | r          | 0.02        | 0.09                  | 0.88       | 0.12      | 10^{-148}      | 0.10       |
| 7 Retrospective gambler fallacy                       | 4690               | 25    | t          | 0.77        | 0.14                  | 0.88       | 0.04      | 10^{-99}       | 0.35       |
| 8 Low vs High category scales                        | 4664               | 25    | \( \chi^2 \) | 0.006       | 0.11                  | 0.80       | 0.44      | 10^{-58}       | 0.04       |
| 9 Gain vs. loss framing                               | 4925               | 25    | \( \chi^2 \) | 0.01        | 0.05                  | 0.84       | 0.80      | 10^{-92}       | 0.01       |
| 10 Sex differences in implicit math attitudes         | 4558               | 25    | t          | 0.02        | 0.08                  | 0.76       | 0.00      | 10^{-57}       | 0.40       |
| 11 quote attribution                                  | 4964               | 25    | t          | 0.34        | 0.08                  | 0.56       | 0.00      | 10^{-36}       | 0.50       |
| 12 sunk costs                                         | 4967               | 25    | t          | 0.17        | 0.05                  | 0.36       | 0.00      | 10^{-19}       | 0.48       |
| 13 norm of reciprocity                                | 4928               | 25    | \( \chi^2 \) | 0.01        | 0.06                  | 0.44       | 0.24      | 10^{-28}       | 0.20       |
| 14 imagined contact                                   | 4973               | 25    | t          | 0.17        | 0.05                  | 0.16       | 0.00      | 10^{-7}        | 0.73       |
| 15 Flag priming                                       | 4896               | 25    | t          | 0.03        | 0.03                  | 0.00       | 0.00      | 0.38           | 0.93       |
| 16 Currency priming                                   | 4970               | 25    | t          | 0.03        | 0.04                  | 0.00       | 0.00      | 0.84           | 0.99       |

### 3.2 Distribution of means across experiments

To test the assumption that experimental means vary between experiments following a Normal distribution, for each task we calculate \( \bar{X}_0 \) (the average of sample means) for
Figure 1: (Left) Histogram of the standardised sample means, $z = (\bar{X}_i - \bar{X}_0)/S_0$, for US sites for each task in the Many Labs 1 replication dataset, in bins of size 0.5 with colour representing task. The line shows the standard Normal distribution $\mathcal{N}(0, 1)$, scaled by bin size $\times$ number of observations to match the histogram scale. (Right) QQ plot showing quantiles of the standardised sample means, $z = (\bar{X}_i - \bar{X}_0)/S_0$, for US sites for each task against quantiles of the standard Normal distribution.

each replication of that task; for correlation tests we take $\bar{X}_i = \hat{M}_i$ and $S_0^2$ (the sample estimate of the variance of means or slopes $\mu_i$ around the overall mean $\mu_0$), and normalise to $z = (\bar{X} - \bar{X}_0)/S_0$.

Figure 1(left) plots a histogram of these $z$ values and shows consistent variance in experimental means $\bar{X}$ for all tasks, with $z$ scores for means following the standard Normal distribution. Figure 1(right) plots the quantiles of these $z$ values for each individual task against quantiles of the standard Normal distribution, confirming that individual ex-
Experimental means for each task follow this distribution. Shapiro-Wilk tests showed no significant evidence against the Normal distribution for all but 1 task (point-form \( p > 0.05 \) for all but 1 task, which had \( p = 0.04 \); note that since the specific model here is one where experimental means \( \mu_i \) are normally distributed around a point-form mean \( \mu_0 \), the point-form test for normality is appropriate in this case). Together these results support the distributional model’s assumption that means of experimental replications vary randomly following an approximately Normal distribution.

### 3.3 Comparing point-form and distributional significance

Statistical significance in this dataset was originally assessed in a two-sided test relative to the point-form \( p \) at \( \alpha = 0.05 \), with a given experimental result counted as significant when it was both significant in this two-sided test and where the effect was the same direction as that seen in the originally published experiment. We follow this definition for distributional significance, with results being counted as significant when \( p_{\text{sig}} < \alpha = 0.05 \) and with effect direction matching the original direction.

As an initial check we used numerical integration methods to calculate, for each experiment, the theoretical value \( p_{\text{sig}}(t|\hat{b}) \) given that experiment’s \( t \) value and the \( \hat{b} \) estimate for that task, and compared against the closed-form expression \( p_{\text{sig}} \) for that experiment. \( p_{\text{sig}}p(t|\hat{b}) \) and \( p_{\text{sig}} \) values were almost identical (correlation \( r = 0.99 \)), supporting the closed-form approximations, and so we used only the closed-form approximation \( p_{\text{sig}} \) in our analysis.

To compare point-form and distributional measures of significance (\( p \) and \( p_{\text{sig}} \)) we cal-
calculate, for each task, the $p$ value for results from each US site and record the percentage of sites which have $p \leq 0.05$. Taking $\hat{b} = S_0^2 / S^2$ for each task and experiment we similarly calculate $p_{sig}$ values for each site and record the percentage of sites with $p_{sig} \leq 0.05$. Table 1 compares, for US sites, the percentage of successful replications of a given task at the $\alpha = 0.05$ level under point-form ($p$) and distributional ($p_{sig}$) tests, and also reports the $p$ and $p_{sig}$ values for the aggregated data (across all US sites) for each task. Point-form $p$ values for aggregated data are unreasonably extreme: 4 tasks had $p < 10^{-325}$ (the computational minimum); a task with only 16% successful replications relative to the point-form $p$ had aggregate significance of $p < 10^{-7}$. Distributional significance values $p_{sig}$ were orders of magnitude more conservative, both in terms of proportion of successful replications and in the aggregate measure.

We also compared $p_{sig}$ and point-form $p$ values for each individual result on a log$_{10}$ scale (see Figure 2(Left)). There are many extremely low $p$ values, with 38% of experiments having $p < 10^{-5}$ and 21% of experiments having $p < 10^{-15}$. Distributional $p_{sig}$ values were again orders of magnitude more conservative (94% greater than $10^{-5}$ and all greater than $10^{-10}$). Many results were significant under point-form but not distributional tests: 42% of results with $p < 0.05$ had $p_{sig} > 0.05$ and 17% of results with $p < 10^{-5}$ had $p_{sig} > 0.05$. Even apparently highly significant results (in point-form tests) turn out to be consistent with the null hypothesis when between-experiment variation is taken into account.
Figure 2:  **(Left)** Scatterplot of $\log_{10}$ distributional $p_{sig}$ against $\log_{10}$ point-form $p$ for all experiments in all tasks in the Many Labs 1 replication dataset for US sites (note the difference in scales). Lines indicate statistical significance at levels $\alpha = 0.05$ (dotted), $\alpha = 0.025$ (dashed) and $\alpha = 0.01$ (solid).  **(Right)** Analogous scatterplot of $\log_{10}$ distributional $p_{sig}$ against $\log_{10}$ Bayes Factor $BF_{10}$. Horizontal lines indicate Bayes Factor levels of 3 (dotted: $BF_{10} \geq 3$ being typically interpreted as moderate evidence against the null), 10 (dashed: strong evidence against the null) and 30 (solid: extremely strong evidence against the null). Points for 9 experiments, all with $p < 10^{-40}$ ($BF_{10} > 10^{40}$) and ranging as low as $p < 10^{-325}$ ($BF_{10} > 10^{325}$), are not shown.

### 3.4 Comparing predicted and observed replication probabilities

To assess the distributional model of replication, for each of the 16 tasks we generated every possible pair of experiments from two different US sites and calculated the replication probability $p_{rep}$ for the second or target experiment in each pair based on the result $t$ in the first or predictor experiment. This calculation used the between-experiment variance of means for the task overall, $S_0^2$, the within-experiment variance in the predictor experiment
Significance and Replication 37

$S^2$ and the sample size of the predictor experiment $N$, and, given these values, generating the probability of replication for an experiment with the sample size $N_r$ of the paired target experiment. This calculation assumed $c = 1$ and so did not make use of the sample variance of the target experiment (and so represents the calculation a researcher would carry out when they have observed a surprising result in an experiment with sample size $N$ and within-experiment variance $S^2$, and are estimating the probability of replicating that result in a planned replication with sample size $N_r$ but unknown within-experiment variance). We calculated this replication probability for a range of commonly used significance levels $\alpha = 0.1, 0.05, 0.01, 0.005, 0.001$. For each target experiment and each level $\alpha$ we compared this predicted replication probability against a dichotomous successful replication variable ($p_{\text{sig}} \leq \alpha$) which indicated whether the target experiment did, in fact, replicate successfully at level $\alpha$.

As an an initial check we calculated, for each pair of experiments in a given task, both the closed-form approximation $p_{\text{rep}}$ and the double-integral expression $p_{\text{rep}}(t|\hat{b})$. As before, these were almost identical (correlation $r = 0.96$) supporting the closed-form approximations, and so we primarily make use of the closed-form approximation $p_{\text{sig}}$ in our analysis (Figure 2 gives a visual comparison of $p_{\text{rep}}$ and $p_{\text{rep}}(t|\hat{b})$ values).

Correlation between $p_{\text{rep}}$ values and dichotomous successful replication values ($p_{\text{sig}} \leq \alpha$) was $r = 0.80$ across the entire set with a slope of 0.94. Point form $p$ for these correlations between predicted and observed replication was less than $10^{-325}$ (the computational minimum) in all cases. Table 2 gives the correlation, significance and replication values for each level of $\alpha$ and overall. The table also gives the necessary statistics for future calculations of
Table 2: Correlation between predicted and observed replication rates at each level of α, with distributional significance \( \hat{p}_{\text{sig}}(B = 1) \) and replication probability \( \hat{p}_{\text{rep}}(B = 1, \alpha = 0.05) \) for these correlations. The table also gives the relevant parameters characterising each correlation: slope, predictor sum-of-squares \( Q \) and response variation or error \( S^2 \).

| α   | N  | % significant \( (p_{\text{sig}} < \alpha) \) | correlation \( r \) for \( p_{\text{sig}} \) vs \( p_{\text{rep}} \) | \( p_{\text{sig}} \) slope \( \hat{p}_{\text{sig}} \) | \( p_{\text{rep}} \) slope \( \hat{p}_{\text{rep}} \) | \( Q \)  | \( S^2 \) |
|-----|----|---------------------------------|-----------------|--------------|--------------|-----|------|
| 0.1 | 9600 | 46%                          | 0.77            | 0.004        | 1             | 0.91 | 1703.0 | 0.10 |
| 0.05| 9600 | 39%                          | 0.80            | 0.002        | 1             | 0.93 | 1680.6 | 0.09 |
| 0.01| 9600 | 30%                          | 0.83            | 0.0001       | 1             | 0.96 | 1500.0 | 0.06 |
| 0.005| 9600 | 26%                          | 0.82            | 0.0001       | 1             | 0.96 | 1365.0 | 0.06 |
| 0.001| 9600 | 16%                          | 0.75            | 0.0005       | 1             | 0.85 | 1008.6 | 0.06 |
| all | 48000 | 31%                          | 0.81            | 0.0006       | 1             | 0.94 | 7626.2 | 0.08 |

between-experiment variance using these results (the sample slope, sum of squares of the predictor variable, and sample variance or error of the response variable).

To illustrate the relationship visually, we combined the sets of predictor-target pairs for these values of α into a single collection, and grouped those pairs into bins of size 1/40 by level of \( p_{\text{rep}} \) and task: each bin contained a set of predictor-target pairs involving the same task with approximately the same replication probability \( p_{\text{rep}} \) produced from the predictor experiment for the target (for the value \( \alpha \) initially applied to that pair). To distinguish between predictions from statistically significant and non-significant predictor experiments, we carried out this grouping process once for all pairs for which the predictor experiment was significant at \( p_{\text{sig}} \leq \alpha \), and a second time for all pairs where the predictor experiment was non-significant. To estimate the true rate of successful replication for target experiments in each bin we calculated the proportion of pairs in each bin for which the target experiment was significant (\( p_{\text{sig}} \leq \alpha \) held for the pair’s assigned value of \( \alpha \)). We excluded
Figure 3: Predicted vs observed replication rate (for $\alpha = 0.1, 0.05, 0.01, 0.005, 0.001$) for target experiments in the Many Labs 1 replication dataset for US sites, grouped by $p_{rep}$ in bins of size $1/40$. Bubble size represents the number of predictor-target pairs in each bin (sizes range from 40 pairs for the smallest to 2800 for the largest bubble). Hollow bubbles contain only non-significant and solid bubbles only significant predictor experiments. The left graph shows results for the double-integral $p_{rep}(t|\hat{b})$ replication estimate, the right for the closed-form $p_{rep}$ estimate. Correlation between predicted and observed replication rates for bubbles was high for $p_{rep}(t|\hat{b})$ ($r = 0.93, \hat{p}_{sig} < 10^{-11}$) and for $p_{rep}$ ($r = 0.91, \hat{p}_{sig} < 10^{-7}$, $\hat{p}_{rep} = 1.0$ with $\alpha = 0.05$ and $B = 1$ for both expressions).

Bins containing less than 40 predictor-target pairs, to allow a relatively accurate estimate of the actual replication rate for experiments in each bin (and to produce a matched level of resolution for predicted and observed replication rates). Figure 3 shows a bubbleplot of predicted and observed replication rates for the double integral $p_{rep}(t|\hat{b})$ and for $p_{rep}$. As the figure shows there was a reliable linear relationship between observed and predicted
replication rates across bins.

One concern is that the observed relationship between predicted and observed replication probabilities could simply be an artefact of the differences in significance rates across different tasks. To see the problem, assume that a statistically significant experiment necessarily produces a high predicted replication probability, while a non-significant experiment necessarily produces a low predicted replication probability. In this situation a task where all or almost all experiments were statistically significant would produce both a high predicted replication rate and (since every experiment is significant) a high observed replication rate (for the same reason), while a task where all or almost all experiments were non-significant would produce both a low predicted replication rate and a low observed replication rate. Figure 3 shows that this artefact does not explain these results: predicted and observed replication probabilities were related at the centre of the probability scale, as well as at the boundaries.

3.5 Sensitivity to estimates of between-experiment variance

The predicted probability of replication in the distributional model, \( p_{\text{rep}} \), depends on an estimate of between-experiment variance. In this section we ask how sensitive the accuracy of this predictive probability is to the between-variance estimate used in making the prediction. To test this we re-ran our replication assessment on the US sites in the Many Labs 1 dataset just as above, but with the between-experiment variance estimate \( \hat{\sigma}^2 \) for each task multiplied by a scaling value \( e \). In the first sensitivity analysis we set \( e = 0.5 \) for all tasks (simulating a situation where the between-experiment variance used in calculating \( p_{\text{rep}} \) is
Figure 4: Sensitivity analysis. Each graph shows the predicted vs observed replication rate (for $\alpha = 0.05, 0.025, 0.01, 0.005, 0.001$) for target experiments in the Many Labs 1 replication dataset for US sites as in Figure 3, but with between-experiment variation $S^2_0$ multiplied by scale $e$. 
underestimated by 50% relative to the actual experimental value for each task); in subsequent analyses we set \( e \) to 0.75, 1.25 and 1.5 (calculating \( p_{rep} \) with between-experiment variance estimates of 75%, 125% or 150% of the actual value).

Correlations between \( p_{rep} \) values and dichotomous successful replication values for target experiments, combined across all \( \alpha \) levels, were \( r = 0.77 \) or higher for all values of \( e \), indicating that even with significant over- or underestimation of between-experiment variance, \( p_{rep} \) reliably predicts replication rates. Figure 4 shows the predicted/observed replication rates produced in these analyses; correlation between predicted and observed replication rates for bubbles was above \( r = 0.84 \) for all values of \( e \) (\( \hat{p}_{sig} < 10^{-5}, \hat{p}_{rep} = 1 \), with \( \alpha = 0.05 \) and \( B = 1 \)). As the figure demonstrates, replication probability tended to be underestimated when between-experiment variance was underestimated (\( e < 1 \)) but overestimated when between-experiment variance was underestimated (\( e > 1 \)), with the degree of under/overestimation in replication increasing with the degree of under/overestimation in between-experiment variance. This pattern follows from the relationship between type 1 and 2 error rates and the value of \( b \). There was relatively little difference in prediction accuracy for \( e = 0.75 \) and \( e = 1.25 \), suggesting that the \( p_{rep} \) is not overly sensitive to error in estimates of between-experiment variance.

4 Comparing with Bayesian approaches

Our primary focus here is on a comparison of point-form and distributional null approaches to testing a single hypothesis, via the \( t \)-test. Here we briefly compare our distributional null model against approaches taken in Bayesian statistics. Advocates of the Bayesian approach
may consider that, in the words of one reviewer, we are ‘teetering on the edge of Bayes already’ and ask why we do not ‘go all the way’. Our view is that the frequentist/Bayesian divide is artificial, because both approaches are simply mathematical tools we can use to reason about experimental results, and not particularly helpful, because restricting ourselves to one set of tools by going ‘all the way’ Bayesian (or all the way frequentist) will limit our ability to reason effectively about those results. In our distributional approach we’ve tried to use these tools as a single unified framework; to avoid this artificial division, we’ve minimised use of frequentist/Bayesian terminology as much as possible in presenting our model. In this section we address these issues by, first, comparing the distributional model against perhaps the best-known and most commonly used Bayesian approach to null hypothesis testing, the Bayesian or JZS \( t \)-test \cite{Rouder2009}; and second, by pointing out the similarities and differences between our approach and the Bayesian approach generally.

## 4.1 JZS Bayesian \( t \)-test

Given some observed data \( y \) the Bayes Factor \( BF_{10} \) comparing two hypotheses \( H_1 \) and \( H_0 \) is the ratio of the marginal likelihood of \( y \) given \( H_1 \) to the marginal likelihood of \( y \) given \( H_0 \):

\[
BF_{10} = \frac{p(y|H_1)}{p(y|H_0)}
\]

The greater this value \( BF_{10} \), the more data \( y \) gives Bayesian evidence in favour of \( H_1 \) rather than \( H_0 \).

To use this Bayes Factor approach to assess evidence for or against a null hypothesis
requires specifying two hypotheses about the parameter of interest: the null $H_0$ and the alternative $H_1$. In the JZS Bayesian $t$-test (Rouder et al., 2009) the parameter of interest is the sample mean $\bar{X}$ and the general model is that individual measurements $X$ follow a normal distribution with unknown mean $\mu$ and unknown variance $\sigma^2$, so that the sample mean follows the distribution

$$\bar{X} \sim N(\mu, \sigma^2/N)$$

The null hypothesis $H_0$ is the standard point-form null

$$H_0 : \bar{X} \sim N(0, \sigma^2)$$

with unknown variance $\sigma$, and in the Bayesian approach the probability of observing a result $\bar{X}$ given $H_0$ (that is, the density of the probability distribution at $\bar{X}$) is

$$p(\bar{X}|H_0) = \int_0^\infty N(\bar{X}|0, \sigma^2)f_\sigma(\sigma)d\sigma$$

where $f_\sigma$ is the density of the assumed prior for $\sigma$ (which in the JZS test is the Jeffreys prior).

The alternative hypothesis is that the unknown mean $\mu$ itself follows a Normal distribution $\mu \sim N(0, \sigma_\mu^2)$, so that the parameter of interest follows the distribution

$$H_1 : \bar{X} \sim N(0, \sigma^2/N + \sigma_\mu^2)$$

(identical to our distributional null model) and the probability of a result $t$ given $H_1$ is

$$p(\bar{X}|H_1) = \int_0^\infty \int_0^\infty N(\bar{X}|0, \sigma^2/N + \sigma_\mu^2)f_\sigma(\sigma)f_{\sigma_\mu}(\sigma_\mu)d\sigma d\sigma_\mu$$
where $f_{\sigma_{\mu}}$ is the prior density of $\sigma_{\mu}$.

The Bayes Factor $BF_{10}$ against the null for a given experiment can then be expressed in terms the observed mean $\bar{X}$. However $BF_{10}$ is typically expressed in terms of $t = \bar{X}/(S/\sqrt{N})$, giving

$$p(t|H_0) = \int_{0}^{\infty} f_{\nu}(t)f_{\sigma}(\sigma) d\sigma$$

and

$$p(t|H_1) = \int_{0}^{\infty} \int_{0}^{\infty} f_{\nu} \left( \frac{t}{\sqrt{1 + \frac{\sigma^2}{\sigma_{\mu}^2} N}} \right) f_{\sigma}(\sigma) f_{\sigma_{\mu}}(\sigma_{\mu}) d\sigma d\sigma_{\mu}$$

where $f_{\nu}$ is the density of the $T$ distribution with $\nu$ degrees of freedom, so that

$$BF_{10} = \frac{p(t|H_1)}{p(t|H_0)}$$

This Bayesian $t$-test implemented in the R BayesFactor package via the function ‘ttest.tstat’ (Morey and Rouder, 2021).

To compare this approach against our distributional null proposal, we used this package to calculate $BF_{10}$ for every experiment in the Many-Labs dataset, and compared these $BF_{10}$ values against the distributional significance $p_{sig}$ for that result on a log_{10} scale (Figure 2(Right)). This comparison gave results almost identical those seen in the earlier point-form $p$ comparison. There were many extremely high $BF_{10}$ values, with 33% of experiments having $BF_{10} > 10^5$ and 17% of experiments having $BF_{10} > 10^{15}$. Distributional $p_{sig}$ values were again orders of magnitude more conservative. Many results gave strong or very strong

Note that this distribution is typically presented in term of a reparameterisation to effect size $\delta$ with unknown variance $\sigma_{\delta}^2$, where $\sigma_{\delta}^2$ is assumed to have an inverse $\chi^2(1)$ prior. This reparameterisation has no effect, of course, on the associated density: we retain the expression in terms of $\mu$ to allow readers to compare with our analogous expression for the distributional null.
evidence against the null in the Bayesian test while not reaching the minimum level of significance in the distributional test: 28% of results with $BF_{10} > 30$ (very strong evidence against the null) had $p_{sig} > 0.05$. Even results with apparently very strong evidence against the null (in the Bayesian t-test) turn out to be consistent with the null hypothesis when between-experiment variation is taken into account.

The left and right scatterplots in Figure 2 are extremely similar, suggesting that the logs of the point-form $p$ and the Bayes Factor $BF_{10}$ are related; or more precisely (since Figure 2(Left) has a negative base-10 log scale on the $y$ axis) that $\log_{10}(BF_{10})$ and $\log_{10}(1/p)$ are related. A comparison of values of $\log_{10}(BF_{10})$ versus $\log_{10}(1/p)$ across experiments and tasks in the Many Labs dataset and confirms that these measures have an almost perfect linear relationship, with a correlation of $r = 0.9999$ and with the line of best fit being $\log_{10}(BF_{10}) = 0.99 \log_{10}(1/p) - 1.6$. This means that the point-form and the Bayesian $t$-test convey essentially the same information, at least in this dataset.

To see why this $BF_{10} \sim 1/p$ relationship holds, we first note that

$$p(t|H_0) = \int_0^\infty f_\nu(t)f_\sigma(\sigma)d\sigma = f_\nu(t)$$

is necessarily true for all priors $f_\sigma$, simply because $t$ is by construction independent of $\sigma$. We next note that the Mills ratio approximation relates the cumulative standard Normal $\Phi$ to the standard Normal density $\phi$ as

$$\Phi(-|t|) \approx \frac{\phi(t)}{|t|}$$

(an approximation which is relatively accurate for $|t| > 3$; see e.g. Small, 2010, p. 43).
Since the $T$ distribution approximates the Normal distribution, this means that

$$T_\nu(-|t|) \approx \frac{f_\nu(t)}{|t|}$$

also holds. From this we get

$$p(t|H_0) \approx |t|T_\nu(-|t|) = \frac{|t|p}{2}$$

and

$$p(t|H_1) \approx |t| \int_0^\infty T_\nu \left( \frac{X/S}{\sqrt{1/N + \frac{\sigma_0^2}{\sigma^2}}} \right) \frac{f_{\sigma,\mu}(\sigma_\mu)}{\sqrt{1 + \frac{\sigma_0^2}{\sigma^2}N}} \, d\sigma_\mu$$

so that

$$BF_{10} \approx 2 \frac{p}{p} \int_0^\infty T_\nu \left( \frac{X/S}{\sqrt{1/N + \frac{\sigma_0^2}{\sigma^2}}} \right) \frac{f_{\sigma,\mu}(\sigma_\mu)}{\sqrt{1 + \frac{\sigma_0^2}{\sigma^2}N}} \, d\sigma_\mu$$

The value of the cumulative $T$ in this integral only varies with effect size $d = X/S$. Values of $BF_{10}$ across experiments are therefore dictated primarily by values of $p$ (which change with $d\sqrt{N}$), and so we see that $BF_{10} \sim 1/p$ is expected to hold across experiments.

We conclude our assessment by noting a further problem with the JZS Bayesian $t$-test as a test of the null hypothesis; a problem arising because, in that approach, both the null $H_0$ and the alternative $H_1$ assume that $X$ is distributed around a mean of 0 (with the two models differing only in the degree of variance around that mean). The fact that both hypotheses assume a mean of 0 means this form of Bayesian $t$-test cannot tell us anything about whether the population mean differs from 0 (that is, from the null hypothesis of no effect): any evidence in favour of $H_1$ tells us only that our result is less likely under a model where $X$ varies around 0 in the way described in $H_0$ (the point-form null model).
and is more likely under a model where $\mathbf{X}$ varies around 0 in the way described in $H_1$ (which is analogous to the distributional null model). For a more detailed account of this relationship between point-form significance tests and Bayes Factor hypothesis tests, and of related issues with the Bayesian $t$-test approach, see Costello and Watts (2022).

### 4.2 Bayesian approaches in general

Our distributional approach to hypothesis testing draws on both the frequentist and the Bayesian approaches to statistical inference, using hypothesis testing (typically frequentist) for rejecting the null and parameter updating (typically Bayesian) for estimating replication probabilities. In this section we illustrate the artificial nature of this frequentist/Bayesian division by considering the three forms of our replication probability $p_{\text{rep}}$ and where they fall on the frequentist-to-Bayesian spectrum.

We first consider the theoretical ‘double integral’ estimate of $p_{\text{rep}}(t|\hat{b})$, which assumes that the variance ratio $b$ follows an $F$ distribution scaled by our sample estimate $\hat{b}$, and the ratio $c$ analogously follows an unscaled $F$. The line of reasoning here is essentially Bayesian, involving as it does the updating of a ‘prior’ distribution (the distributional null hypothesis) and calculating the posterior predictive distribution by using $F$ distributed priors on these variance ratios that are informed by sample data. The primary deviation from the Bayesian approach lies in the use of the cumulative distribution function for hypothesis testing, which some researchers argue is inconsistent with the Bayesian perspective (because it leads us to make decisions based on results we have not observed: those in the tail of the distribution). Note, however, that the Mills ratio approximation mentioned above
undermines this objection, at least for statistical models based on the Normal distribution (because the cumulative and the probability density are linearly related), and that modern Bayesian workflow proposals typically involve a posterior predictive check which is analogous to our ‘double integral’ estimate of $p_{rep}$ (though involving the cumulative function of the posterior predictive distribution up to the observed data $t$, rather than to a critical value $t_{crit}$).

We next consider the closed-form estimate, $p_{rep}$. This estimate involves a test against the cumulative $T$ distribution, exactly equivalent to that in a standard $t$-test (though with $t_0$ being equal to the sample mean $\bar{X}$ divided by the estimated between-experiment variance in means $S^2_0$ rather than the within-experiment sample variance of the mean $S^2/\sqrt{N}$), and so is fully and completely frequentist in approach. The fact that these frequentist-style estimates $p_{rep}$ agree closely with the Bayesian-style estimates $p_{rep}(t|\hat{b})$ illustrates the commonalities of the two approaches, with the Bayesian approach dealing with the unknown variance $\sigma^2$ by integrating over its prior distribution while the frequentist approach deals with this unknown variable in terms of the $\chi^2$ distribution relating $\sigma^2$ to its sample value $S^2$.

We finally consider our bounding replication probability $\hat{p}_{rep}$, which applies when no estimate for the between-experiment variance $\sigma^2_0$ (and so the variance ratio $b$) is available. The form of this estimate again corresponds to that of a Bayesian posterior predictive distribution. In the Bayesian approach the lack of an estimate for $b$ would be dealt with by placing some uninformative prior $f_b$ on this parameter, giving an estimate for significance of

$$\int_0^{\infty} 2T_\nu \left(-|t|/\sqrt{1 + bN}\right) f_b(b) db$$
and for replication of

\[
\int_0^\infty \int_0^\infty T_{\nu_r} \left( \frac{|t| \sqrt{N_r} - T_{\nu_r}^{-1} \left( 1 - \alpha/2 \right) \sqrt{c(1 + bN_r)} \sqrt{c + bN_r/(1 + bN)} \right) f_{\nu,\nu}(c)f(b) \, db \, dc
\]

This, however, is not appropriate in the hypothesis testing context, because with this prior the distributional null hypothesis becomes a compound of two proposals: that individual experimental means \( \mu \) vary around the null value \( \mu_0 = 0 \), and that \( \sigma_0 \), the variance of these values \( \mu \) around that null, is distributed according to our uninformative prior \( f_b \), scaled by \( \sigma^2 \). In this situation a rejection of the distributional null may arise when \( \mu_0 \neq 0 \) (suggesting a real effect) or equally when \( \mu_0 = 0 \) but \( \sigma_0^2 \neq \sigma^2 f_b \) (no real effect, but an incorrect assumption about \( \sigma_0^2 \)): and so the significance test no longer plays its role of distinguishing possible real effects from random variation. Our bounding approach addresses this problem by assuming much less information about \( \sigma_0^2 \) than carried by the uninformative prior \( f_b \): rather than assuming some probability distribution for \( b \), we simply assume that \( b \) is between 0 and some extreme value \( B \) (without saying anything about its distribution in that range), and show that \( p_{sig}(t|b) \) is less than \( \hat{p}_{sig} \) and \( p_{rep}(t|b) \) is greater than \( \hat{p}_{rep} \) for all \( b \) in that range.

5 Conclusions

The above results give evidence in favour of the distributional approach to significance testing, supporting its assumptions about Normally-distributed between-experiment variance of means, showing that many results that appear statistically significant under the point-form approach are identified as consistent with with random (between-experiment)
variation in the distributional approach, and showing that the predicted replication probabilities generated for target experiments in the distributional approach are closely related to the actual observed probability of successful replication in those experiments, at least in the Many Labs 1 dataset.

We believe this distributional approach has a number of advantages over standard point-form significance testing. First, this distributional approach more accurately reflects the various random factors that do, in fact, influence all experimental outcomes and so gives a more accurate estimate of the degree to which a given outcome is unexpected or surprising under a null model of random variation but no real effect. Second, this approach addresses well-known problems with sample size that arise in the standard approach, where the probability of a significant result rises with sample size irrespective of any real effect. This issue is particularly important in research involving hypothesis testing on large data sets (increasingly common in the ‘big data’ era), and so the distributional approach should be useful in this form of research. Third, because the distributional model includes between-experiment variation in statistical analysis, it gives a natural account for the rate at which significant results will replicate in future experiments (an account which the point-form model cannot provide, because that model does not allow for cross-experiment variation in the experimental mean). Finally, this approach also gives a useful perspective on commonly used measures of the statistical power of an experiment to detect effects, showing that in the presence of between-experiment variation some effects simply cannot be detected reliably, no matter how large the sample.

We expect a number of objections to our argument for a distributional approach to
hypothesis testing. The first objection concerns the use of a distributional representation of the null hypothesis. ‘These distributional nulls are just Bayesian priors in another form’ we imagine the objection goes, ‘and Bayesian priors are subjective measures of belief, not objective probability estimates. Subjective beliefs cannot enter into objective frequentist hypothesis testing’.

It is true that our distributional nulls have a mathematical form that is identical to a Bayesian prior. It is not true, however, that these distributional nulls represent subjective measures of belief. Instead, these distributional nulls play the same role that point-form nulls play in standard significance testing: for a given (distributional or point-form) null hypothesis we say ‘result t would have a low probability of occurrence if null hypothesis were true, and so result t is unlikely to be simply a consequence of random processes’. Such assertions do not require or reflect any subjective belief in the null hypothesis. To put this response another way: since the logic of significance testing is independent of the form of null hypothesis being used, our use of distributional rather than point nulls does not change the objective nature of such hypothesis testing.

A second objection concerns statistical testing against distributional null hypotheses characterised by the parameter b (representing the between-experiment to within-experiment variance ratio). ‘Researchers can adjust the distribution of this parameter b until they find a null hypothesis against which their observed results are statistically significant’ we imagine the objection goes. ‘But this is simply a form of data-dredging or p-hacking: an attempt to find patterns in data that can be presented as statistically significant when in fact there is no real underlying effect’.
Our response here is to point out that this value $b$ is not picked arbitrarily: instead, $b$ is estimated from experimental data on replications (and we give unbiased estimators for that situation). More generally, even if researchers were arbitrarily picking values for this parameter $b$, the use of distributional testing systematically reduces the occurrence of statistically significant results, relative to the point-form null. This is because the rejection region for a null hypothesis falls monotonically with the value of this ratio $b$: and so the maximum rejection region (and so the greatest chance of a statistically significant result) arises with the point-form null. A better characterisation of this process of testing against distributional nulls is one where we attempt to reduce the chance of finding statistically significant results: where we are conservative in results as statistically significant, taking into account both between-experiment and within-experiment variance.

A third possible objection concerns the availability of alternative hypothesis-testing methods, such as the Bayesian $t$-test (commonly put forward as a replacement for the significance testing approach). ‘While significance testing was appropriate in the last century’, we imagine the objection goes, ‘today we have better statistical methods; we don’t need to test for significance’. Our response here is to note that the classical (point-form) $t$-test and the JZS Bayesian $t$-test against a point-form null appear to be almost exactly equivalent in order of magnitude, at least in the Many Labs 1 data, and so replacing significance testing against a point-form null with this form of Bayesian $t$-test may not, therefore, represent a meaningful advance.

While useful, our distributional approach is subject to various caveats. First, our approach assumes normally distributed variation or error both within and between experi-
ments. This assumption is reasonable for simple experiments involving one or two variables (t-tests, tests of correlation or contingency) but does not hold in more complex experimental designs involving multiple variables, such as ANOVAs, multiple regression analyses, and mixed models. This is because the internal structure in such designs can cause random between-experiment differences to have systematic non-normal effects on between-experiment variability. Applying our distributional approach to between-experiment variation in this more complex setting would be challenging, requiring a statistical model of between-experiment variance in each component of the experimental design and how that variance affects the overall between-experiment distribution of results.

Second, while our distributional approach allows us to estimate the probability of replication of given experimental results, is not a ‘magic bullet’ that resolves all problems of replication. In particular, our approach does not address the important problem of publication bias. The distributional approach works best with some estimate for the between-experiment variability of means for a given experimental task, $S_0^2$. This can only be estimated from available (that is, published) data on experimental means. If this set of available means is restricted in some way as a consequence of selective publication (if, for example, published means tend to be further from 0 than unpublished means), this will lead to a systematic underestimation of between-experiment variation. This problem of publication bias does not apply to the Many Labs 1 dataset results: while the experimental tasks examined in that dataset were selected because they investigate well-known classic and contemporary effects in psychology (and so the original papers describing those effects were subject to some degree of publication bias), the results from all 36 replications of those
effects were ‘published’ irrespective of their experimental means. This problem clearly does apply, however, if between-experiment variability is estimated from a set of individually published experimental results. This problem of publication bias is best addressed by continuing replication studies in various fields. Such studies are additionally important because they will give useful estimates of the degree of between-experiment variation in experiments of different types, allowing researchers to assess the approximate probability of replication of new results in similar experiments.
References

Amrhein, V. and Greenland, S. (2018). Remove, Rather Than Redefine, Statistical Significance. *Nature Human Behaviour*, 2(1):4.

Berger, J. O. and Pericchi, L. R. (1996). The Intrinsic Bayes Factor for Model Selection and Prediction. *Journal of the American Statistical Association*, 91(433):109–122.

Bishop, C. M. (2006). *Pattern Recognition and Machine Learning*. Springer.

Camerer, C. F., Dreber, A., Holzmeister, F., Ho, T.-H., Huber, J., Johannesson, M., Kirchler, M., Nave, G., Nosek, B. A., Pfeiffer, T., et al. (2018). Evaluating the Replicability of Social Science Experiments in Nature and Science Between 2010 and 2015. *Nature Human Behaviour*, 2(9):637–644.

Carver, R. (1978). The Case Against Statistical Significance Testing. *Harvard Educational Review*, 48(3):378–399.

Christensen, R. (2005). Testing Fisher, Neyman, Pearson, and Bayes. *The American Statistician*, 59(2):121–126.

Cohen, J. (1992). A Power Primer. *Psychological Bulletin*, 112(1):155.

Cohen, J. (2013). *Statistical Power Analysis for the Behavioral Sciences*. Routledge.

Costello, F. and Watts, P. (2022). Why Bother With the Bayes Factor. *Submitted*. 
Dahl, D. B., Scott, D., Roosen, C., Magnusson, A., and Swinton, J. (2019). *Xtable: Export Tables to LaTeX or HTML*. R package version 1.8-4.

Diaconis, P. et al. (1991). [Replication and Meta-Analysis in Parapsychology]: Comment. *Statistical Science*, 6(4):386–386.

Doros, G. and Geier, A. B. (2005). Probability of Replication Revisited: Comment on An Alternative to Null-Hypothesis Significance Tests. *Psychological Science*, 16(12):1005–1006.

Fritz, C. O., Morris, P. E., and Richler, J. J. (2012). Effect Size Estimates: Current Use, Calculations, and Interpretation. *Journal of Experimental Psychology: General*, 141(1):2.

Hunter, J. E. (1997). Needed: A Ban on the Significance Test. *Psychological Science*, 8(1):3–7.

Iverson, G. J., Lee, M. D., and Wagenmakers, E.-J. (2009a). Prep Misestimates the Probability of Replication. *Psychonomic Bulletin & Review*, 16(2):424–429.

Iverson, G. J., Lee, M. D., and Wagenmakers, E.-J. (2010a). The Random Effects Prep Continues to Mispredict the Probability of Replication. *Psychonomic Bulletin & Review*, 17(2):270–272.

Iverson, G. J., Lee, M. D., Zhang, S., and Wagenmakers, E.-J. (2009b). Prep: An Agony in Five Fits. *Journal of Mathematical Psychology*, 53(4):195–202.
Iverson, G. J., Wagenmakers, E.-J., and Lee, M. D. (2010b). A Model-Averaging Approach to Replication: The Case of Prep. Psychological Methods, 15(2):172.

Kelley, K. and Preacher, K. J. (2012). On Effect Size. Psychological Methods, 17(2):137.

Killeen, P. R. (2005a). An Alternative to Null-Hypothesis Significance Tests. Psychological Science, 16(5):345–353.

Killeen, P. R. (2005b). Replicability, Confidence, and Priors. Psychological Science, 16(12):1009–1012.

Killeen, P. R. (2007). Replication Statistics. Best Practices in Quantitative Methods, pages 103–124.

Klein, R. A., Ratliff, K. A., Vianello, M., Adams Jr, R. B., Bahník, Š., Bernstein, M. J., Bocian, K., Brandt, M. J., Brooks, B., Brumbaugh, C. C., et al. (2014). Investigating Variation in Replicability. Social Psychology, 45(3):142–152.

Klein, R. A., Vianello, M., Hasselman, F., Adams, B. G., Adams Jr, R. B., Alper, S., Aveyard, M., Axt, J. R., Babalola, M. T., Bahník, Š., et al. (2018). Many Labs 2: Investigating Variation in Replicability Across Samples and Settings. Advances in Methods and Practices in Psychological Science, 1(4):443–490.

Lipsey, M. W., Puzio, K., Yun, C., Hebert, M. A., Steinka-Fry, K., Cole, M. W., Roberts, M., Anthony, K. S., and Busick, M. D. (2012). Translating the Statistical Representation of the Effects of Education Interventions Into More Readily Interpretable Forms. National Center for Special Education Research.
Macdonald, R. R. (2005). Why Replication Probabilities Depend on Prior Probability Distributions. *Psychological Science-Cambridge*, 16(12):1007.

Mandel, J. (2012). *The Statistical Analysis of Experimental Data*. Courier Corporation.

Maraun, M. and Gabriel, S. (2010). Killeen’s (2005) Prep Coefficient: Logical and Mathematical Problems. *Psychological Methods*, 15(2):182.

McShane, B. B., Gal, D., Gelman, A., Robert, C., and Tackett, J. L. (2019). Abandon Statistical Significance. *The American Statistician*, 73(sup1):235–245.

Meehl, P. E. (1990a). Appraising and Amending Theories: The Strategy of Lakatosian Defense and Two Principles That Warrant It. *Psychological Inquiry*, 1(2):108–141.

Meehl, P. E. (1990b). Why Summaries of Research on Psychological Theories Are Often Uninterpretable. *Psychological Reports*, 66(1):195–244.

Miller, J. (2009). What Is the Probability of Replicating a Statistically Significant Effect? *Psychonomic Bulletin & Review*, 16(4):617–640.

Miller, J. and Schwarz, W. (2011). Aggregate and Individual Replication Probability Within an Explicit Model of the Research Process. *Psychological Methods*, 16(3):337.

Morey, R. D. and Rouder, J. N. (2011). Bayes Factor Approaches for Testing Interval Null Hypotheses. *Psychological Methods*, 16(4):406.

Morey, R. D. and Rouder, J. N. (2021). *BayesFactor: Computation of Bayes Factors for Common Designs*. R package version 0.9.12-4.3.
Murphy, K. P. (2007). Conjugate Bayesian Analysis of the Gaussian Distribution. Technical report, University of British Columbia.

Open Science Collaboration et al. (2015). Estimating the Reproducibility of Psychological Science. *Science*, 349(6251):aac4716.

Orben, A. and Lakens, D. (2020). Crud (Re) Defined. *Advances in Methods and Practices in Psychological Science*, 3(2):238–247.

Pashler, H. and Wagenmakers, E.-J. (2012). Editors’ Introduction to the Special Section on Replicability in Psychological Science: A Crisis of Confidence? *Perspectives on Psychological Science*, 7(6):528–530.

R Core Team (2021). *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria.

Rouder, J. N., Speckman, P. L., Sun, D., Morey, R. D., and Iverson, G. (2009). Bayesian T Tests for Accepting and Rejecting the Null Hypothesis. *Psychonomic Bulletin & Review*, 16(2):225–237.

Sanabria, F. and Killeen, P. R. (2007). Better Statistics for Better Decisions: Rejecting Null Hypotheses Statistical Tests in Favor of Replication Statistics. *Psychology in the Schools*, 44(5):471–481.

Small, C. G. (2010). *Expansions and Asymptotics for Statistics*. Chapman and Hall/CRC.

Snedecor, G. W. and Cochran, W. G. (1989). Statistical Methods.
Thompson, B. (1998). In Praise of Brilliance: Where That Praise Really Belongs. *American Psychologist, 53*(7):799–800.

Wickham, H. (2016). *Ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York.
6 Appendix 1

Assuming $c = 1$ and $N_r = N$ (an exact replication), for a given $t$-statistic and a between-experiment variance ratio $b$ we can rewrite $p_{rep}(t|b)$ as

$$p_{rep}(t|b) = T_{\nu} \left( \frac{bN \left[ \frac{|t|}{\sqrt{1+bN}} - T_{\nu}^{-1}(1-\alpha/2) \right] - T_{\nu}^{-1}(1-\alpha/2)}{\sqrt{1+2bN}} \right)$$

$$= T_{\nu} (|t| f(bN))$$

where the function $f(z)$ is

$$f(z) = \frac{1}{\sqrt{2z+1}} \left( \frac{z}{\sqrt{z+1}} - \frac{z+1}{\tau} \right)$$

with $\tau = |t|/T_{\nu}^{-1}(1-\alpha/2)$ (which is positive for $\alpha < 0.5$ and $t \neq 0$, both of which we assume).

The derivative of this probability with respect to $b$ is

$$\frac{\partial}{\partial b} p_{rep}(t|b) = |t|NT_{\nu}'(|t| f(bN)) f'(bN),$$

and since $T_{\nu}$ is a monotonically increasing function of its argument, this derivative will vanish only when $f'(bN)$ is zero. A quick computation gives

$$f'(z) = \frac{1}{(2z+1)^{3/2}} \left( \frac{3z+2}{2(z+1)^{3/2}} - \frac{z}{\tau} \right)$$

and therefore $f$ – and thus $p_{rep}(t|b)$ – reaches its extremal value(s) at $z_0/N$, where

$$f'(z_0) = \frac{1}{(2z_0+1)^{3/2}} \left( \frac{3z_0+2}{2(z_0+1)^{3/2}} - \frac{z_0}{\tau} \right) = 0.$$
The above will be satisfied when
\[
\frac{3z_0 + 2}{2(z_0 + 1)^{3/2}} - \frac{z_0}{\tau} = 0
\]
which can be rearranged to give the quintic equation
\[
z_0^5 + 3z_0^4 + 3z_0^3 + \left(1 - \frac{9\tau^2}{4}\right)z_0^2 - 3\tau^2z_0 - \tau^2 = 0. 
\] (7)

No matter what value \(\tau\) takes, there is only one sign change between the coefficients of the polynomial on the left-hand side, so by Descartes’ Rule of Signs, there is exactly one positive solution to this quintic; it can be shown that it is a maximum of \(f(z)\), so we call it \(z_{\text{max}}\). It is this solution we use to obtain \(b_{\text{max}} = z_{\text{max}}/N\), the value of \(b\) which maximises \(p_{\text{rep}}(t|b)\).

To obtain a bound on \(b_{\text{max}}\), we put \(z_0 = \tau\) into the quintic polynomial in (7) and obtain
\[
\tau^5 + 3\tau^4 + 3\tau^3 + \left(1 - \frac{9\tau^2}{4}\right)\tau^2 - 3\tau^2 - \tau^2 = \tau^5 + \tau^4 + \frac{\tau^4}{4}
\]
which is necessarily positive. Since the quintic in (7) has the negative value of \(-\tau^2\) when \(z_0 = 0\), it is zero for some value of \(z_0\) between 0 and \(\tau\) and so \(z_{\text{max}} \leq \tau\) and
\[
b_{\text{max}} \leq \frac{|t|}{NT^{-1}(1 - \alpha/2)} = \frac{|d|}{\sqrt{NT^{-1}(1 - \alpha/2)}}
\]
where \(d\) is the sample effect size. Since this expression falls with \(\sqrt{N}\), we see that \(b_{\text{max}}\) is necessarily close to 0 for all but very large effect sizes.

7 Appendix 2

Here we consider an experiment involving two variables, a predictor variable \(X\) and a response variable \(Y\). For pairs \((X_i, Y_i)\) we assume that values of the predictor variable \(X_i\)
are fixed, and that values of the response variable follow the distribution

\[ Y_i = \mathcal{N}(\mu X_i + a, \sigma^2) \]  

(8)

for unknown slope \( \mu \), offset \( a \) and variance \( \sigma^2 \) (where \( \sigma^2 \) is the variance of random within-experiment error in the response variable; these are the standard assumptions of linear regression).

We wish to test for independence of \( X \) and \( Y \). In the point-form null model, this involves testing the hypothesis that the slope \( \mu = 0 \). In the distributional model, this involves assuming that the slope \( \mu \) varies randomly across experiments in a normal distribution \( \mu \sim \mathcal{N}(\mu_0, b\sigma^2) \), and testing for independence involves testing the hypothesis that that \( \mu_0 = 0 \).

Suppose we have \( N \) pairs of estimates in our experiment. We take

\[ Q = \sum_{1}^{N} (X_i - \bar{X})^2 \]

to represent the sum-of-squares for the predictor variable \( X \). For a given pair of values \((X_i, Y_i)\) we define \( M_i = (X_i - \bar{X})Y_i \) as the estimate for the slope \( \mu \) for that pair, and so take

\[ \bar{M} = \frac{\sum_{1}^{N} (X_i - \bar{X})Y_i}{Q} \]

be our overall estimate for the slope \( \mu \). Then the least-squares regression line for that experiment is

\[ \hat{Y}_i = \bar{Y} + \bar{M}X_i \]
Within a single experiment the variable $\bar{M}$ is distributed around the unknown slope $\mu$ in that experiment as

$$N\left(\bar{M}|\mu, \frac{\sigma^2}{Q}\right)$$

Letting

$$S^2 = \frac{\sum_{i=1}^{N} (Y_i - \hat{Y}_i)^2}{(N - 2)}$$

be the mean squared error between observed and predicted values of the response variable $Y$ and, given the assumption of a linear relationship between $X$ and $Y$, the variable

$$\frac{(N - 2) S^2}{\sigma^2}$$

has a $\chi^2$-distribution with $\nu = N - 2$ degrees of freedom. Then as before, under our distributional null hypothesis we have

$$\bar{M} \sim N\left(0, \frac{(\sigma^2/Q)(1 + bQ)}{}\right)$$

where $b = \sigma^2_0/\sigma^2$ (and so $b$ represents the ratio of between-experiment variance in the slope to within-experiment variance in the response variable) and letting

$$t = \frac{\bar{M} S}{\sqrt{Q}}$$

the variable

$$\frac{t}{\sqrt{1 + bQ}}$$

has a $t$ distribution with $\nu$ degrees of freedom. These variables $\bar{M}, Q, S^2$ and $t/\sqrt{1 + bQ}$ for correlation thus have identical distributions and relationships as the corresponding
variables $X, N, S^2$ and $t/\sqrt{1+bN}$ for the t-test, and so estimates for significance, replication and between-experiment variance $S^2_0$ hold as given in the previous section (with these variable substitutions). For example: given a set of $K$ replications of some similar correlation experiment, each with sample slope $\bar{M}_i$, predictor sum of squares $Q_i$, mean squared response error $S^2_i$, and degrees of freedom $\nu_i$, this means that our estimate for the between-experiment variance of the slope is

$$\langle S^2_0 \rangle = \frac{1}{K-1} \sum_{i=1}^{K} (\bar{M}_i - \bar{M}_0)^2 + \frac{1}{K} \sum_{i=1}^{K} \frac{\nu_i S^2_i}{Q_i(\nu_i - 2)}$$

where $\bar{M}_0$ is the mean of those sample slopes, and $S^2_0$ follows an approximately $\chi^2$ distribution with degrees of freedom $\nu_0 = K - 1$. Taking $\hat{b} = S^2_0 / S^2$ as our estimate for the ratio $b = \sigma^2_0 / \sigma^2$ this means that we have a theoretical expression for significance of

$$p_{\text{sig}}(r|\hat{b}) = \int_0^\infty 2T_{\nu} \left( -|t| / \sqrt{1 + \hat{b}Q} \right) f_{\nu,\nu_0}(b) db$$

and a theoretical expression for replication (in a replication experiment with predictor sum-of-squares $Q_r$ and degrees of freedom $\nu_r$) of

$$p_{\text{rep}}(r|\hat{b}) = \int_0^\infty \int_0^\infty T_{\nu_r} \left( \frac{|t| \sqrt{\hat{b}QQ_r}}{1 + \hat{b}Q} - T_{\nu_r}^{-1} (1 - \alpha/2) \sqrt{c(1 + \hat{b}Q_r)} \right) f_{\nu,\nu_0}(b) f_{\nu_r,\nu}(c) db dc$$

From this we get closed-form expressions for significance and replication of

$$p_{\text{sig}} = 2T_{\nu_0} \left( -\frac{|t|}{\sqrt{\hat{b}Q}} \right)$$

$$p_{\text{rep}} = T_{\nu_r} \left( \sqrt{\frac{\hat{b}QQ_r}{Q + Q_r}} \left[ -\frac{|t|}{\sqrt{\hat{b}Q}} - T_{\nu_r}^{-1} (1 - \alpha/2) \sqrt{\frac{1}{\hat{b}Q} + \frac{\nu_0}{\nu_0 - 2}} \right] \right)$$
and generic estimates of

\[ \hat{p}_{\text{sig}} = 2T_{\nu} \left( -|t| / \sqrt{1 + BQ} \right) \]

\[ \hat{p}_{\text{rep}} = \int_0^\infty T_{\nu, r} \left( \frac{|t| B\sqrt{Q_{\nu, r}} - T_{\nu, r}^{-1} (1 - \alpha/2) \sqrt{c(1 + BQ_{\nu, r})}}{\sqrt{c + BQ_{\nu, r} / (1 + BQ)}} \right) f_{\nu, \nu}(c) dc \]

Note that in these correlation tests the sum of squares of the predictor variable \( Q \) is the continuous-valued analog of the discrete sample size \( N \) in a \( t \)-test: where sample size gives the number of discrete measurements made in a \( t \)-test, predictor sum-of-squares gives the range of continuous measurements in a test of correlation. We’ve derived these expressions in a experimental design investigating how values of a response variable \( Y \) are related to those of a predictor \( X \) whose values are fixed by the experimenter. However, this approach extends naturally to the situation where both \( X \) and \( Y \) are random variables. To measure evidence for replication in this situation, however, it is necessary to select one of these variables as the predictor and the other as the response: an estimate for the probability of replication of a given result \( r \) in an experiment where \( X \) is the predictor and the \( X \) sum of squares is assumed to have a particular controlled value will necessarily be different from the probability of replication of that result in an experiment where \( Y \) is the predictor the \( Y \) sum of squares is assumed to have a particular controlled value.

We extend this approach to tests of independence in \( 2 \times 2 \) contingency tables by considering an experiment involving \( N \) pairs of outcomes from two dichotomous or binary variables, a predictor variable \( X \) and a response variable \( Y \), where we are interested in the degree of association between variable \( X \) and variable \( Y \). The standard approach here is to count the number of times each pair of values for these variables occurs and apply Pearson’s
\( \chi^2 \)-squared test to the resulting contingency table, testing against the null hypothesis of no association between the two variables. Letting \( n_{ij} \) represent the number of pairs where \( X = i \) and \( Y = j \), this test asks whether the \( \phi \) measure of association

\[
\phi = \frac{n_{11}n_{00} - n_{10}n_{01}}{\sqrt{(n_{11} + n_{10})(n_{11} + n_{01})(n_{00} + n_{01})(n_{00} + n_{10})}}
\]

is significantly different from 0. For \( 2 \times 2 \) contingency table, however, this test is identical to a \( Z \)-test of proportions \( \text{[Snedecor and Cochran 1989]} \), and so does not take sample size into account. This means that our analysis of replication (which depends on sample size or an analogous measure) cannot apply to the Pearson’s \( \chi^2 \)-squared test.

Note, however, that the correlation coefficient \( r \) is given by

\[
r = \frac{N \sum X_i Y_i - \sum X_i \sum Y_i}{\sqrt{N \sum X_i^2 - (\sum X_i)^2} \sqrt{N \sum Y_i^2 - (\sum Y_i)^2}}
\]

Since for two binary variables we have \( N = n_{11} + n_{10} + n_{01} + n_{00} \), \( \sum x_i y_i = n_{11} \), \( \sum x_i = n_{10} + n_{11} \), and so on, by substitution and rearrangement we see that \( r = \phi \). Further, for large enough \( N \) significance relative to the null hypothesis \( \phi = 0 \) in Pearson’s \( \chi^2 \)-squared test is equivalent to significance relative to the null hypothesis of \( r = 0 \) in a test of linear correlation. To use our distributional null model in experiments involving pairs of outcomes from dichotomous variables, we thus apply the correlation and linear regression approach described in the previous section to these dichotomous variables \( X \) and \( Y \).