Detecting $p$-hacking*  

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Abstract  

We analyze what can be learned from tests for $p$-hacking based on distributions of $t$-statistics and $p$-values across multiple studies. We analytically characterize restrictions on these distributions that conform with the absence of $p$-hacking. This forms a testable null hypothesis and suggests statistical tests for $p$-hacking. We extend our results to $p$-hacking when there is also publication bias, and also consider what types of distributions arise under the alternative hypothesis that researchers engage in $p$-hacking. We show that the power of statistical tests for detecting $p$-hacking is low even if $p$-hacking is quite prevalent.

Keywords: $p$-hacking, publication bias, $p$-curve, $t$-curve  

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1 Introduction

A researchers’ ability to explore various ways of analyzing and manipulating data and then selectively report the ones that yield statistically significant results, commonly referred to as p-hacking, undermines the scientific credibility of reported results. To assess the extent of this problem researchers have begun to examine distributions of t-statistics (t-curves) and p-values (p-curves) across studies in various fields, with mixed results (e.g., Bishop and Thompson, 2016; Brodeur et al., 2016, 2018; Gerber and Malhotra, 2008; Head et al., 2015; Jager and Leek, 2013; Simonsohn et al., 2014; Vivalt, 2019). This paper examines more closely what can be learned from these distributions, and whether or not these tests are likely to be informative about the extent to which p-hacking occurs.

Missing from the literature is a careful understanding of the restrictions on distributions of t-tests and p-values in the absence or presence of various types of p-hacking. We provide analytically under general assumptions the set of distributions implied in the absence of p-hacking and use these results to determine the null hypothesis to be tested. The null set of distributions of p-values are distributions that are non-increasing under a wide set of distributions of the true parameters of the model. Assumptions required for this result rule out non-similar tests but hold under a wide set of testing situations. No such restriction is available for the null set of distributions of t-statistics. We further show that, unless there is extreme excess bunching, humps in the t-curve generated by p-hacking cannot be distinguished from humps generated by the distribution of alternatives, suggesting that testing for p-hacking based on humps in the t-curve can be problematic.

In practice, the observed distribution of p-values or t-statistics is typically sample selected through only observing published papers, a situation referred to in the literature as publication bias.1 We extend our analytical results to

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1This paper is concerned with the testable implications of p-hacking in the presence and absence of publication bias. Our analysis thus complements the literature on the identification and correction of publication bias (e.g., Andrews and Kasy, 2018).
situations where there is publication bias. This involves additional assumptions to ensure the same set of distributions imply the null hypothesis of no \( p \)-hacking. Without such additional restrictions, tests for \( p \)-hacking must be re-interpreted as joint tests for \( p \)-hacking and publication bias.

We also analytically derive impacts of \( p \)-hacking of restricted forms to help understand reasonable alternative hypotheses. There are a broad set of approaches to \( p \)-hacking, from judicious covariate selection, searching over choices in nuisance parameter estimation to searching over data sources and decisions on cleaning the data. Our results examine the first of these. This helps provide an understanding of how powerful tests might be against reasonable characterizations of \( p \)-hacking and also understand then the extent to which these tests are likely to be able to detect \( p \)-hacking in typical empirical applications. Our theoretical results further show that in realistic settings non-rejections of the null hypothesis are compatible with \( p \)-hacking. In this sense, \( p \)-hacking is a refutable but non-verifiable hypothesis.

The restrictions on the set of distributions under the null hypothesis suggest tests not previously employed in testing for \( p \)-hacking, which we evaluate for this purpose and compare to existing procedures. Through Monte Carlo analysis we examine plausible \( p \)-hacking scenarios and how well tests are able to detect \( p \)-hacking. We find that \( p \)-hacking of the forms examined is difficult to detect unless a substantial fraction of results is \( p \)-hacked.

We apply the tests to assess the prevalence of \( p \)-hacking in economics and other disciplines based on two large datasets of \( p \)-values. The first dataset, collected by Brodeur et al. (2016), contains test statistics and \( p \)-values from papers published in the American Economic Review, the Quarterly Journal of Economics, and the Journal of Political Economy between 2005 and 2011. The second dataset, collected by Head et al. (2015), contains text-mined \( p \)-values from all articles publicly available in the PubMed database and allows us to investigate the extent of \( p \)-hacking across different fields. There are several important practical issues involved in testing for \( p \)-hacking, including the choice and aggregation of \( p \)-values, the dependence between \( p \)-values within
papers, and rounding by researchers. We discuss these issues based on our
two applications and explore different approaches for addressing them. Our
empirical results are sensitive to the choice of tests as well as the particular
approaches used to deal with the aforementioned practical issues.

The remainder of the paper is structured as follows. In Section 2, we in-
troduce the setup and a simple running example. Section 3 characterizes the
testable restrictions of \( p \)-hacking. In Section 4, we develop new tests for \( p \)-
hacking and discuss tests currently in use. Section 5 provides Monte Carlo
evidence on the finite sample size and power properties of these tests. In Sec-
tion 6, we present two empirical applications. Section 7 concludes by discussion
the implications of our results for empirical practice and data collection. The
appendix contains detailed derivations and some additional results.

2 Setup

Consider a test statistic \( T \) which is distributed according to a distribution
with cumulative distribution function (cdf) \( F_h \), where \( h \) indexes parameters
of either the exact or asymptotic distribution of the test. The parameters \( h \)
contain the parameters of interest and possibly nuisance parameters. Suppose
researchers are testing the hypothesis

\[
H_0 : h \in \mathcal{H}_0 \quad \text{against} \quad H_1 : h \in \mathcal{H}_1,
\]

where for the parameters of interest \( \mathcal{H}_0 \cap \mathcal{H}_1 = \emptyset \). Let \( \mathcal{H} = \mathcal{H}_0 \cup \mathcal{H}_1 \). Denote as
\( F \) the cdf of the chosen null distribution from which critical values are deter-
mined. We will assume that the test rejects for large values and denote the crit-
ical value for level \( p \) as \( cv(p) \). For any \( h \) we denote \( \beta(p, h) = P(T > cv(p) \mid h) \)
as the rejection rate of a level \( p \) test with parameters \( h \). For \( h \in \mathcal{H}_1 \) this is
the power of the test. Then

\[
\beta(p, h) = P(T > cv(p) \mid h) = 1 - F_h(cv(p))
\]
In this paper, we are interested in the distribution of the $p$-values across studies, where we compute $p$-values from a distribution of $T$ given values for $h$, which themselves are drawn from a probability distribution $\pi$. For the cdf of the $p$-values, we are interested in

$$G(p) = \int_{\mathcal{H}} P(T > cv(p) \mid h) \, d\pi(h)$$

$$= \int_{\mathcal{H}} \beta(p, h) \, d\pi(h)$$

If the level of the test is equal to its size (say for a simple null hypothesis with continuous random variables, or a test that is similar) then for situations where the null is always true, $h \in \mathcal{H}_0$ and $\beta(p, h) = P(T > cv(p) \mid h) = p$, which implies that

$$G(p) = \int_{\mathcal{H}_0} P(T > cv(p) \mid h) \, d\pi(h)$$

$$= p \int_{\mathcal{H}_0} d\pi(h)$$

$$= p$$

and we have the well-known uniform distribution of $p$-values result. For non-similar tests this result does not hold in general and the exact shape of $G$ depends on $\beta(p, h)$ and $\mathcal{H}_0$.

2.1 An illustrative example: one-sided $t$-test

Here we introduce a simple running example which we will return to throughout the paper. Consider the problem of testing a one-sided hypothesis concerning a scalar parameter $\theta$:

$$H_0 : \theta = \theta_0 \quad \text{against} \quad H_1 : \theta > \theta_0$$

We estimate $\theta$ using a sample of $n$ observations. Suppose that the estimator $\hat{\theta}$ is normally distributed

$$\sqrt{n} \left( \hat{\theta} - \theta \right) \sim N \left( 0, \sigma^2 \right),$$

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where $\sigma^2$ is assumed to be known. To test hypothesis (2), we employ a $t$-test with

$$T = t := \sqrt{n} \frac{\hat{\theta} - \theta_0}{\sigma}.$$

Defining $h := \sqrt{n}((\theta - \theta_0)/\sigma)$, we obtain the following testing problem

$$H_0 : h = 0 \quad \text{against} \quad H_1 : h > 0.$$

In the notation of our general setup, $\mathcal{H}_0 = \{0\}$ and $\mathcal{H}_1 = (0, \infty)$. The assumed normality of $\hat{\theta}$ (Equation 3) implies that $F_h(x) = \Phi(x - h)$, where $\Phi$ is the cdf of the standard normal distribution. The chosen null distribution is the standard normal distribution, $F = \Phi$. A level $p$ test rejects the null hypothesis when $\hat{t}$ is larger than the $(1 - p)$-quantile of the normal distribution, $cv(p) = \Phi^{-1}(1 - p)$. Then

$$\beta(p, h) := P(\hat{t} > cv(p) \mid h)
= 1 - F_h(cv(p))
= 1 - \Phi(\Phi^{-1}(1 - p) - h).$$

Since the one-sided $t$-test is similar, $p$-values are uniformly distributed if all null hypotheses are true:

$$G(p) = \int_{\mathcal{H}_0} P(\hat{t} > cv(p) \mid h) \, d\pi(h)
= 1 - \Phi(\Phi^{-1}(1 - p))
= 1 - (1 - p)
= p.$$ 

This conclusion is no longer true for non-similar tests. To illustrate, consider the following slightly modified testing problem

$$H_0 : h \leq 0 \quad \text{against} \quad H_1 : h > 0, \quad (4)$$

where now $\mathcal{H}_0 = (-\infty, 0]$ and $\mathcal{H}_1 = (0, \infty)$. We choose the $F$ to be the standard normal distribution, $F = \Phi$. Suppose that $\pi$ is the standard normal
distribution truncated from above at zero. Figure 1 plots the distribution of
p-values for this case and shows that the uniform distribution result no longer
holds for non-similar tests.

![Figure 1: Cdf of p-values under the null hypothesis](image)

3 Testable restrictions of p-hacking

3.1 The shape of the p-curve in the absence of p-hacking

In this section, we study the shape of the p-curve, the density of p-values,
g(p), in the absence of p-hacking. The following assumption ensures that g(p)
is well-defined and differentiable.

Assumption 1 (Regularity). F and F_h are twice continuously differentiable
with uniformly bounded first and second derivatives f, f', f_h and f'_h. f(x) > 0
for all x ∈ {cv(p) : p ∈ (0,1)}, where cv(p) = F^{-1}(1 - p). For h ∈ Η,
supp(f) = supp(f_h).^2

A necessary condition for Assumption 1 is the absolute continuity of F
and F_h. This is not too restrictive since in many cases F and F_h are the
asymptotic distributions of test statistics which typically satisfy this condition.

^2For a function ϕ, supp(ϕ) is defined as the closure of \{x : ϕ(x) ≠ 0\}.

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Further, in cases where the test statistics have a discrete distribution, size does not typically equal level which could lead to $p$-curves that violate non-increasingness as we illustrate below.

Assumption 1 holds for many tests with parametric $F$ and $F_h$, including $t$-tests and Wald-tests. Under Assumption 1, the $p$-curve is

$$g(p) = \int_{\mathcal{H}} \frac{\partial \beta (p, h)}{\partial p} d\pi(h).$$

(5)

As discussed in Section 2, for similar tests, the distribution of $p$-values is uniform when the null hypothesis is always true. Based on analytical and numerical examples, several studies have argued that $g$ is right-skewed and decreasing if some of the alternatives are true (e.g., Hung et al., 1997; Simonsohn et al., 2014). These results rely on specific choices of $\pi$. However, for testing purposes we need to characterize distributions over all possible sets of alternatives. One contribution of this paper is to clearly define the shape of $g$.

To test the null hypothesis of “no $p$-hacking”, we therefore seek a characterization of the shape of $g$ which holds for a very general class of $\pi$. Under Assumption 1, the derivative of $g$ is

$$g'(p) := \frac{dg(p)}{dp} = \int_{\mathcal{H}} \frac{\partial^2 \beta (p, h)}{\partial p^2} d\pi(h).$$

(6)

Because $\pi$ is a probability measure, the sign of $g'(p)$ is determined by the second derivative of the power function $\partial^2 \beta (p, h) / \partial p^2$. The following condition is sufficient for $\partial^2 \beta (p, h) / \partial p^2$ to be weakly negative.

**Assumption 2.** For all $(x, h) \in \{cv(p) : p \in (0, 1)\} \times \mathcal{H}$, $f'_h(x)f(x) \geq f'(x)f_h(x)$.

When $\mathcal{H}_0 = \{0\}$ and $F = F_0$ (as in our illustrative example), Assumption 2 is of the form of a monotone likelihood ratio property, which relates the shape of the density of $T$ under the null to the shape of the density of $T$ under alternative $h$. The next lemma shows that this condition holds for many popular tests.
Lemma 1. Assumption 2 holds when

(i) $F(x) = \Phi(x), \ F_h = \Phi(x - h), \ \mathcal{H}_0 = \{0\}, \ \mathcal{H}_1 = (0, \infty)$ (e.g., one-sided $t$-test; cf. Section 2.1)

(ii) $F$ is the cdf of a half normal with scale parameter 1, $F_h$ is the cdf of a folded normal with location parameter $h$ and scale parameter 1, $\mathcal{H}_0 = \{0\}, \ \mathcal{H}_1 = \mathbb{R}\setminus\{0\}$, (e.g., two-sided $t$-test)

(iii) $F$ is the cdf of a $\chi^2$ distribution with degrees of freedom $k$, $F_h$ is the cdf of a noncentral $\chi^2$ distribution with degrees of freedom $k$ and noncentrality parameter $h$, $\mathcal{H}_0 = \{0\}, \ \mathcal{H}_1 = (0, \infty)$, (e.g., Wald test)

Proof. See Appendix D. 

We emphasize that all tests in Lemma 1 are similar. Similarity is crucial for the $p$-curve to be decreasing. Below, based on our illustrative example, we show that the $p$-curve can be increasing in the absence of $p$-hacking when the tests are non-similar.

The following theorem shows that, under the maintained assumptions, the $p$-curve is non-increasing on $\mathcal{P} := [p, \overline{p}]$, where $0 < p < \underline{p} < 1$.

Theorem 1 (Main testable restriction of $p$-hacking). Under Assumptions 1–2, $g$ is non-increasing on $\mathcal{P}$:

$$g'(p) \leq 0, \quad p \in \mathcal{P}.$$ 

Proof. Recall that

$$\beta(p, h) = 1 - F_h(cv(p)),$$

where $cv(p) = F^{-1}(1 - p)$. Under Assumption 1, the derivative of $\beta(p, h)$ with respect to $p$ is

$$\frac{\partial \beta(p, h)}{\partial p} = \frac{f_h(cv(p))}{f(cv(p))} \geq 0.$$
The second derivative is
\[ \frac{\partial^2 \beta(p, h)}{\partial p^2} = \frac{f_h'(cv(p))cv'(p)f(cv(p)) - f'(cv(p))cv'(p)f_h(cv(p))}{f(cv(p))^2} \]
\[ = \frac{cv'(p)}{f(cv(p))^2} \left[ f_h'(cv(p))f(cv(p)) - f'(cv(p))f_h(cv(p)) \right] \]

The result now follows by Assumption 2 and because \( cv'(p)/f(cv(p))^2 \leq 0 \).

The result in Theorem 1 holds for many commonly-used statistical tests, suggesting that, in many empirically relevant settings, the p-curve will be non-increasing in the absence of p-hacking. Theorem 1 constitutes our main testable restriction and the basis for developing better tests for p-hacking and evaluating methods currently in use in Section 4.

**Remark 1.** When testing for the presence of p-hacking, we often focus on the p-curve over a subinterval \( \mathcal{A} = [a, \bar{a}] \subset \mathcal{P} \),
\[ g_{\mathcal{A}}(p) = \frac{1}{G(\bar{a}) - G(a)} \int_{\mathcal{H}_m} \frac{\partial \beta_m(p, h)}{\partial p} d\pi_m(h), \quad p \in \mathcal{A}. \]
Therefore, under the conditions of Theorem 1, \( g_{\mathcal{A}} \) is non-increasing on \( \mathcal{A} \).

**Remark 2.** We are often interested in testing p-hacking based on aggregate data obtained from different statistical tests and hypotheses about different parameters of interest. Suppose that there are \( M \) different methods indexed by \( m \in \{1, \ldots, M\} \) and \( L \) different parameters of interest indexed by \( l \in \{1, \ldots, L\} \). The p-curve for method \( m \) and parameter \( l \) is given by
\[ g_{ml}(p) = \int_{\mathcal{H}_{ml}} \frac{\partial \beta_{ml}(p, h)}{\partial p} d\pi_{ml}(h), \]
where \( \mathcal{H}_{ml}, \beta_{ml} \) and \( \pi_{ml} \) denote the support of \( h \), the power function, the distribution of \( h \) for the statistical test \( m \) and parameter \( l \). Denote by \( w_{ml} \) the proportion of statistical tests using method \( m \) for making inference about parameter \( l \). The aggregate density of p-values is a finite mixture with density
\[ g(p) = \sum_{m=1}^{M} \sum_{l=1}^{L} g_{ml}(p)w_{ml}. \]
The derivative of \( \bar{g} \) is

\[
\bar{g}'(p) = \sum_{m=1}^{M} \sum_{l=1}^{L} g'_{ml}(p) w_{ml}.
\]

As a consequence, if the conditions of Theorem 1 hold for all \((m, l) \in \{1, \ldots, M\} \times \{1, \ldots, L\} \), \( \bar{g}' \) is non-increasing in the absence of \( p \)-hacking. \( \square \)

**Illustrative example (continued).** In our illustrative example, we can directly use the properties of the normal distribution to establish that the \( p \)-curve is decreasing. Recall that

\[
\beta(p, h) = 1 - \Phi(cv(p) - h),
\]

where \( cv(p) = \Phi^{-1}(1 - p) \). Let \( \phi \) denote the density of the standard normal distribution. Using that \( \partial cv(p)/\partial p = -1/\phi(cv(p)) \) and \( \partial \phi(x)/\partial x = -x\phi(x) \), we obtain

\[
\frac{\partial \beta(p, h)}{\partial p} = \exp \left( hcv(p) - \frac{h^2}{2} \right),
\]

\[
\frac{\partial^2 \beta(p, h)}{\partial p^2} = -\frac{h \exp \left( hcv(p) - \frac{h^2}{2} \right)}{\phi(cv(p))}.
\]

It is easy to see that, for all \( h \in [0, \infty) \),

\[
-\frac{h \exp \left( hcv(p) - \frac{h^2}{2} \right)}{\phi(cv(p))} \leq 0.
\]

For specific parametric choices of \( \pi \) it is possible to obtain closed-form expressions for the \( p \)-curve (e.g., Hung et al., 1997). A particularly simple analytical expression can be obtained by choosing \( \pi \) to be a half-normal distribution with scale parameter \( \sigma \):

\[
g(p) = \int_0^{\infty} \exp \left( hcv(p) - \frac{h^2}{2} \right) \sqrt{\frac{2}{\pi \sigma^2}} \exp \left( -\frac{h^2}{2\sigma^2} \right) dh
\]

\[
= \frac{2}{\sqrt{1 + \sigma^2}} \exp \left( \frac{cv(p)^2}{2(1 + \sigma^{-2})} \right) \Phi \left( \frac{cv(p)}{\sqrt{1 + \sigma^{-2}}} \right).
\]
The derivative is given by

\[ g'(p) = -2\sigma \exp \left( \frac{cv(p)^2}{2(1+\sigma^{-2})} \right) \left( \Phi \left( \frac{cv(p)}{\sqrt{1+\sigma^{-2}}} \right) \frac{cv(p)}{\sqrt{1+\sigma^{-2}}} + \phi \left( \frac{cv(p)}{\sqrt{1+\sigma^{-2}}} \right) \right) \leq 0. \]

Figure 2 plots the \( p \)-curves for this analytical example for different values of \( \sigma \). We note the prevalence of very small \( p \)-values, which is characteristic for the \( p \)-curves in our empirical application in Section 6.

Finally, we illustrate the role of similarity. Consider the testing problem (4) with \( F = \Phi \) for which the \( t \)-test is non-similar. Suppose that \( \pi \) is a normal distribution with mean \( \mu \) and variance 1. Figure 3 plots the \( p \)-curve for \( \mu \in \{-2.5, 0\}^3 \). The \( p \)-curve is monotonically decreasing on \((0, 0.1]\) when \( \mu = 0 \) but non-monotonic when \( \mu = -2.5 \).

### 3.2 The shape of the \( p \)-curve under \( p \)-hacking

There is a broad set of approaches to \( p \)-hacking, from judicious covariate selection, searching over choices in nuisance parameter estimation to searching over

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\[ \text{The expression for the } p \text{-curve in this example is given by } g(p; \mu) = \int_{-\infty}^{\infty} \exp \{hcv(p) - h^2/2\} \phi(h - \mu) \, dh = \exp \{cv(p)^2 + 2\mu cv(p) - \mu^2)/4\} / \sqrt{2}, \text{ where } cv(p) = \Phi^{-1}(1 - p). \]
data sources and decisions on cleaning the data. Different forms of p-hacking will lead to different shapes of the p-curve under the alternative. These shapes might differ from common intuition of a hump near $p = 0.05$. Here we analytically characterize the shape of the p-curve from using judicious covariate selection. This helps provide an understanding of how powerful tests might be against reasonable characterizations of p-hacking and also understand then the extent to which empirical studies are likely to be able to detect p-hacking. In Section 5, we build on the theoretical analysis here to simulate the alternative distributions in the Monte Carlo simulations.

Suppose that researchers are interested in estimating the effect of a scalar variable $x_i$ on an outcome $y_i$. The data are generated according to the following linear model:

$$y_i = x_i \beta + u_i, \quad i = 1, \ldots, n,$$

where $x_i$ is non-stochastic and $u_i \sim iid \mathcal{N}(0, 1)$. In addition, there are two non-stochastic control variables, $z_{1i}$ and $z_{2i}$. The researchers are interested in testing

$$H_0 : \beta = 0 \quad \text{against} \quad H_1 : \beta > 0.$$

For simplicity, assume that the variables are scale normalized such that $n^{-1} \sum_{i=1}^n x_i^2 = n^{-1} \sum_{i=1}^n z_{1i}^2 = n^{-1} \sum_{i=1}^n z_{2i}^2 = 1$, that $n^{-1} \sum_{i=1}^n z_{1i} z_{2i} = 0$, and that $n^{-1} \sum_{i=1}^n x_i z_{1i} = n^{-1} \sum_{i=1}^n x_i z_{2i} = \gamma$, where $|\gamma| \in (0, 1/\sqrt{2})$. Define $h := \sqrt{n} \beta / \sqrt{1 - \gamma^2}$, where
$h$ is drawn from a distribution of alternatives $\pi$ with support $\mathcal{H} = [0, \infty)$.

Consider the following form of $p$-hacking.

1. The researchers run a regression of $y_i$ on $x_i$ and $z_{1i}$ and report the corresponding $p$-value, $p_1$, if $p_1 \leq \alpha$.

2. If $p_1 > \alpha$, the researchers run a regression of $y_i$ on $x_i$ and $z_{2i}$ instead of $z_{1i}$, which yields $p$-value, $p_2$. They report $\min\{p_1, p_2\}$.

The reported $p$-value, $p_r$, is

$$p_r = \begin{cases} p_1, & \text{if } p_1 \leq \alpha. \\ \min\{p_1, p_2\}, & \text{if } p_1 > \alpha. \end{cases}$$

In Appendix B, we show that, for $p \in (0, \alpha]$, 

$$g(p) = \int_{\mathcal{H}} \frac{\phi(z_h(p))C'(p, h; \alpha, \rho)}{\phi(z_0(p))} d\pi(h),$$

where $z_h(p) = \Phi^{-1}(1 - p) - h$, $\rho = \frac{1 - 2\gamma^2}{1 - \gamma^2}$ and $C(p, h; \alpha, \rho) = 1 - \Phi(z_h(\alpha)) + \Phi\left(\frac{z_h(\alpha) - \rho z_h(p)}{\sqrt{1 - \rho^2}}\right)$. The derivative is

$$g'(p) = \int_{\mathcal{H}} \frac{\phi(z_h(p)) \left[ \frac{\rho}{\sqrt{1 - \rho^2}} \phi\left(\frac{z_h(\alpha) - \rho z_h(p)}{\sqrt{1 - \rho^2}}\right) - hC'(p, h; \alpha, \rho) \right]}{[\phi(z_0(p))]^2} d\pi(h).$$

Note that $\rho$ is always positive and if all nulls are true, i.e., $\pi$ assigns probability one to $h = 0$, then $g'(p) > 0$.

In general, the shape of the $p$-curve and, in particular, whether or not it is non-decreasing, depends on the distribution of alternatives, $\pi$. To illustrate, take $\alpha = 0.05$, $\gamma = 0.3$, and let $\pi$ be a half-normal distribution with scale parameter $\sigma$. Figure 4 shows that the $p$-curve is monotonically decreasing (when $\sigma = 1.5$) and non-monotonic (when $\sigma = 0.6$).

Our analysis has important implications for the testability of $p$-hacking. First, it shows that a possibly prevalent form of $p$-hacking can lead to non-monotonic $p$-curves. Second, it illustrates the importance of the distribution
of alternatives for testing $p$-hacking: the exact same form of $p$-hacking can lead to both monotonically decreasing and non-monotonic $p$-curves, depending on the distribution of alternatives. Finally, it shows that $p$-hacking can be fully compatible with non-increasing $p$-curves, which highlights an important limitation on the learnability of $p$-hacking: a decreasing $p$-curve never allows to confirm the hypothesis of “no $p$-hacking”.\footnote{We refer to Bruns and Ioannidis (2016) and Ulrich and Miller (2015) for alternative examples of $p$-hacking that lead to non-increasing $p$-curves.} In this sense, $p$-hacking is a refutable but non-verifiable hypothesis.

![Figure 4: P-curves for different values of $\sigma$.](image)

**3.3 $P$-hacking and publication bias**

So far, we have assumed that the true distribution of $p$-values is observed. However, in practice, we often only have access to data on $p$-values from published papers. This creates a sample selection problem affecting the properties of the $p$-curve which will depend critically on exactly how this sample selection works. This section extends our analysis to settings where not all papers get published.

Let $S$ denote a binary indicator that takes value $S = 1$ if a study is published and $S = 0$ otherwise. Instead of the true distribution of $p$-values, $g(p)$,
we observe the distribution conditional on publication, \( g_{S=1}(p) := g(p \mid S = 1) \).

If the publication indicator \( S \) is independent of \( p \)-values (i.e., if the publication probability does not depend on the reported \( p \)-values), we have that \( g_{S=1}(p) = g(p) \). Thus, under independence, all our previous results directly apply. However, independence is a very strong assumption and may not be plausible in many settings. For example, using data from experimental economics (Camerer et al., 2016) and psychology replication studies (Open Science Collaboration, 2015), Andrews and Kasy (2018) estimate that results that are significant at the 5% level are over 30 times more likely to get published than insignificant results. We now turn to this case.

By Bayes’ rule we have

\[
g_{S=1}(p) = \frac{P(S = 1 \mid p)g(p)}{P(S = 1)}.
\]

Since the denominator does not depend on \( p \), all our understanding of the slope of \( g_{S=1} \) comes from the product in the numerator. Assuming differentiability, we have that

\[
g'_{S=1}(p) = \frac{1}{P(S = 1)} \left( \frac{\partial P(S = 1 \mid p)}{\partial p}g(p) + P(S = 1 \mid p)g'(p) \right).
\]  

(8)

Thus, whether or not the \( p \)-curve is non-increasing depends on the derivative of the publication probability with respect to the \( p \)-value.

On the one hand, it is often plausible to assume that the conditional publication probability is decreasing in \( p \) (i.e., more significant results are more likely to get published), which implies that \( g'_{S=1} \) is non-increasing under the assumptions of Theorem 1. In Appendix A, we present a simple reduced form model in the spirit of Brodeur et al. (2016), which provides a formal justification for a decreasing publication probability.\(^5\) In this case, \( g_{S=1} \) is non-increasing whenever \( g \) is non-increasing. On the other hand, equation (8)\(^5\)However, we emphasize that the assumption of a decreasing publication probability is not innocuous. For instance, the publication probability may be non-monotonic because journals value precisely estimated zero results; see Brodeur et al. (2016) for a further discussion of this issue.

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shows that $g_{S=1}$ may not be monotonically decreasing even if $g$ is monotonically decreasing.

Whether or not the publication probability is assumed to be such that $g_{S=1}$ is non-increasing affects the interpretation of our null and alternative hypothesis. When the publication probability is assumed to be such that $g_{S=1}$ is non-increasing, tests for non-increasingness of $g_{S=1}$ are tests for $p$-hacking by the researchers. By contrast, when the publication probability is left unrestricted, these tests are generally not able to distinguish $p$-hacking from publication bias and, thus, are joint tests for $p$-hacking and publication bias.

### 3.4 The shape of the $t$-curve

This section analyzes the shape of the density of $t$-values, the $t$-curve. Consider the one-sided testing problem of Section 2.1. The $t$-curve is given by

$$g_t(t) = \int_{\mathcal{H}} \phi(t-h)d\pi(h), \quad (9)$$

where $\mathcal{H} = [0, \infty)$ and its derivative is

$$g'_t(t) = \int_{\mathcal{H}} (h-t)\phi(t-h)d\pi(h).$$

We note that sign of the derivative will depend on the threshold $t$ and on the distribution of alternatives $\pi$ in general.

Next, we analyze the distribution of the absolute value of the $t$-statistic. Consider the following two-sided hypothesis testing problem

$$H_0 : \theta = \theta_0 \quad \text{against} \quad H_1 : \theta \neq \theta_0. \quad (10)$$

Since $\hat{t} \sim N(h, 1)$, the $|\hat{t}|$ is distributed according to a folded Normal with location parameter $h$ and scale parameter 1. The $t$-curve is

$$g_{|\hat{t}|}(t) = \int_{\mathcal{H}} (\phi(t+h) + \phi(t-h)) d\pi(h)$$
with derivative
\[ g'_{[\hat{t}]}(t) = \int_{\mathcal{H}} [(h - t)\phi(t - h) - (t + h)\phi(t + h)] d\pi(h). \]

As for the one-sided $t$-test, the sign $g'_{[\hat{t}]}(t)$ will generally depend on $\pi$. Note that, if one is willing to impose additional restrictions on $\pi$, it is possible to show that the $t$-curve is decreasing. For instance, we show in Appendix C that the $t$-curve is decreasing if the distribution of alternatives admits a unimodal density that is symmetric around zero.

To illustrate the general result, suppose that the distribution of alternatives, $\pi$, is a mixture of two normals, $\tau \cdot \phi(x) + (1 - \tau) \cdot \phi((x - 2.5)/0.25)/0.25$. Figure 5 plots $g_{[\hat{t}]}$ for $\tau \in \{0.3, 0.4, 0.5, 0.6\}$. We can see that, depending on $\pi$, the $t$-curve takes many different forms. This simple numerical example further demonstrates that the distribution of alternatives can induce humps around 1.96, as documented empirically for instance by Gerber and Malhotra (2008), Brodeur et al. (2016, 2018) and Vivalt (2019), even if there is no $p$-hacking. Thus, humps generated by $p$-hacking cannot be distinguished from humps generated by the distribution of alternatives, which suggests that testing for $p$-hacking based on the shape of the $t$-curve around 1.96 (or any other significance threshold) can be problematic. For one-sided tests, Andrews and Kasy (2018) show that the specific structure of $g_{t}$ (Equation (9)) implies other testable restrictions that could be used to test for $p$-hacking: smoothness of $t$-curve and the impossibility of extreme bunching and spikes. We do not explore tests based on these testable restrictions here.

4 Statistical tests for $p$-hacking

In this section, we consider statistical tests for $p$-hacking based on the testable restriction derived in Theorem 1:

\[ H_0 : g \text{ is non-increasing} \quad \text{against} \quad H_1 : g \text{ is not non-increasing} \quad (11) \]

We explore novel tests for the hypothesis testing problem (11), a histogram-based test for monotonicity and tests for concavity of the cdf of $p$-values, and
compare them to the most popular tests currently in use, Fisher’s test (e.g., Simonsohn et al., 2014) and the Binomial test (e.g., Simonsohn et al., 2014; Head et al., 2015).

4.1 Histogram-based test

Here we adopt the approach for testing for monotonicity proposed by Romano and Wolf (2013) to our problem.\footnote{Romano and Wolf (2013) formulate the alternative hypothesis as “strict monotonicity” and the null as the negation of the alternative. By contrast, to test “no p-hacking” against “no p-hacking”, our null is “non-increasingness” and the alternative is the negation of the null.} Let $p = x_0 < x_1 < \cdots \leq x_J = \alpha \leq p$ be an equidistant partition of the $[p, \alpha]$ interval and define

$$\tilde{p}_i = \int_{x_{i-1}}^{x_i} g(p) dp \quad \text{and} \quad \Delta_i = \tilde{p}_{i+1} - \tilde{p}_i, \quad i = 1, \ldots, J,$$

where $g(p)$ is a true density of $p$-values. When $g$ is non-increasing, $\Delta_i$ should be non-positive for all $i$. Therefore, the testing problem (11) can be reformulated as

$$H_0 : \max_i \Delta_i \leq 0 \quad \text{against} \quad H_1 : \max_i \Delta_i > 0. \quad (12)$$
We estimate $\Delta_i$ based on the sample proportions $\hat{p}_i$, $\hat{\Delta}_i = \hat{p}_{i+1} - \hat{p}_i$, and consider the test statistic

$$t_{\text{max}} \equiv \max_i \frac{\hat{\Delta}_i}{\hat{\sigma}_i},$$

where $\hat{\sigma}_i^2$ is an estimator of the variance of $\hat{\Delta}_i$. To determine the critical value, we set $\Delta_i = 0$ for all $i \in \{1, \ldots, J\}$ and approximate the null distribution using simulations.\(^7\) To do this, we draw 50,000 independent samples of a given size from uniform distribution and calculate $t_{\text{max}}$-statistic in each sample.

### 4.2 LCM tests

Under the null hypothesis (11), the cdf of $p$-values is concave. This observation allows us to use tests based on the least concave majorant (LCM) (e.g., Hartigan and Hartigan, 1985; Carolan and Tebbs, 2005; Beare and Moon, 2015). The key idea of LCM-based tests is to assess concavity based on the distance between the empirical distribution function of $p$-values, $\hat{G}$, and its LCM, $\mathcal{M}\hat{G}$, where $\mathcal{M}$ is the LCM operator.\(^8\) We consider the following test statistic

$$M^n_p = \sqrt{n}\|\mathcal{M}\hat{G} - \hat{G}\|_p,$$

where $\|\cdot\|_p$ is the $L^p$-norm with respect to the Lebesgue measure and $p \in [1, \infty]$.

It can be shown that the uniform distribution is least favorable for LCM tests (cf. Kulikov and Lopuhaä, 2008). When the true distribution of $p$-values is uniform $M^n_p$, converges weakly to $\|\mathcal{M}B - B\|_p$, where $B$ is a standard Brownian Bridge on $[0, 1]$. For strictly concave distributions, such as the null distributions in our simulation study, $M^n_p$ converges in probability to zero (Beare and Moon, 2015, Theorem 3.1).\

\(^7\)Following Romano and Wolf (2013), we also experimented with a bootstrap procedure and found very similar results.

\(^8\)The least concave majorant of a function, $f$, is the smallest concave function, $g$, such that $g(x) \geq f(x)$ for any $x$. 

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4.3 Fisher’s test

To test for skewness of the $p$-curve, Simonsohn et al. (2014) propose to apply Fisher’s test. This test is based on the observation that, if the $p$-curve is uniformly distributed on $(0, \alpha)$, the “$p$-value of $p$-value”, $pp := p/\alpha$, has the uniform distribution on $(0, 1)$. In this case, the test statistic $-2 \sum_{i=1}^{n} \log(pp_i)$ has a $\chi^2$-distribution with $2n$ degrees of freedom, $\chi^2(2n)$. In our context, where the $p$-curve under the null hypothesis is non-increasing, it is not possible to directly apply Fisher’s test. Therefore, we use the modified test statistic $-2 \sum_{i=1}^{n} \log(1 - pp_i)$ for which the uniform distribution is least favorable such that we can use $\chi^2(2n)$ critical values.\(^9\)

4.4 Binomial test

Binomial tests (e.g., Simonsohn et al., 2014; Head et al., 2015) allow for testing $p$-hacking at a pre-specified threshold $\alpha$, for example, $\alpha = 0.05$. For $\ell \in (0, 1)$ divide the $p$-values in the interval $[\alpha \ell, \alpha]$ into two groups, “high” ($> \alpha(\ell+1)/2$) and “low” ($\leq \alpha(\ell+1)/2$).\(^{10}\) The Binomial test exploits that, in the absence of $p$-hacking, $p_{\text{high}} = P(\alpha(\ell+1)/2 < p_i \leq \alpha)/P(p_i \in [\alpha \ell, \alpha])$ cannot exceed 0.5, which suggests the following hypothesis testing problem:

$$H_0 : p_{\text{high}} = 0.5 \quad \text{against} \quad H_1 : p_{\text{high}} > 0.5$$

(13)

Critical values are obtained using exact Binomial tests.

\(^9\)To see this note that when $p_i$ has decreasing density function, the distribution function of $-\log(1 - pp_i)$ is $F(1 - \exp(-t))$ for $t \in [0, \infty)$, where $F$ is concave on $[0, 1]$. Therefore, $F(1 - \exp(-t)) > 1 - \exp(-t), t \in [0, \infty)$. The latter function is the CDF of $-\log(1 - pp_i)$ when $p_i$ is distributed uniformly on $(0, \alpha)$. This implies that for any decreasing density of $p_i$, the quantiles of $-\log(1 - pp_i)$ are weakly smaller than in case of uniformly distributed $p_i$. Since $p$-values are assumed to be independent, this is also true for $-2 \sum_{i=1}^{n} (\log(1 - pp_i))$.

\(^{10}\)Some authors, for example Head et al. (2015), apply the Binomial test on the open interval $(\alpha \ell, \alpha)$. When the $p$-values are continuously distributed, the Binomial tests based on $[\alpha \ell, \alpha]$ and $(\alpha \ell, \alpha)$ are asymptotically equivalent. However, as we discuss in Section 6, the choice between both tests matters in the presence of rounding.
4.5 Discussion

Here we discuss some key differences between the tests introduced in Sections 4.1–4.4. First, the tests differ with respect to the extent to which they exploit the testable implication in Theorem 1. The Romano-Wolf test, the LCM tests, and Fisher’s test fully exploit the testable implication, whereas the Binomial test is a “local” test at a pre-specified threshold $\alpha$. Thus, by construction, the Binomial test exhibits lower power against certain alternatives because it is unable to detect violations of the null outside of $[\alpha \ell, \alpha]$. Moreover, while choosing $\alpha = 0.05$ may be a natural starting point (e.g., Head et al., 2015), it is often plausible that $p$-hacking also occurs at other salient significance thresholds such as $\alpha = 0.01$ or $\alpha = 0.1$. Even under exact knowledge of the thresholds that the researchers are targeting when $p$-hacking, the Binomial test cannot account for multiple cutoffs. By contrast, all other tests accommodate and aggregate information across different cutoffs, irrespective of whether or not the location of these cutoffs is known. Finally, different from the other tests which are based on the entire sample, the Binomial test only uses a subset of the data such that collecting a sufficiently large sample to guarantee good power properties may be difficult.

Second, unlike the LCM tests and Fisher’s test, the Romano-Wolf test and the Binomial test both rely on binning the $p$-values. As a consequence, these two tests are not able to detect violations of the null which offset within bins and thus, by construction, exhibit lower power against certain alternatives.

Finally, the tests differ in whether they rely on tuning parameters. The LCM tests and Fisher’s test are tuning-free, whereas the Romano-Wolf test and the Binomial test require the choice of the number of bins and of the local interval $[\alpha \ell, \alpha]$, respectively. Unfortunately, no theoretical guidance is available for choosing these tuning parameters and the empirical applications in Section 6 show that both tests are quite sensitive to the practical choice of the tuning parameters.
5 Monte Carlo evidence

In this section, we investigate the finite sample properties of the tests in Section 4 using a Monte Carlo simulation study, which is based on an extended version of the analytical example in Section 3.2.

Suppose researchers have access to a random sample of size 100 generated by the model

\[ y_i = x_i \beta + u_i, \quad i = 1, \ldots, 100, \]

where \( x_i \sim \mathcal{N}(0, 1) \) and \( u_i \sim \mathcal{N}(0, 1) \) are independent of each other. In addition, they have access to a vector of \( K \) control variables, \( z_i = (z_1, \ldots, z_k)' \), where

\[ z_{ki} = \gamma_k x_i + \sqrt{1 - \gamma_k^2} \epsilon_{z_k,i}, \quad \epsilon_{z_k,i} \sim \mathcal{N}(0, 1), \quad k = 1, \ldots, K. \]

We set \( \beta = h / \sqrt{100} \), where \( h \) is drawn from a half-normal distribution with scale parameter 1, and generate the correlation parameter as \( \gamma_k \sim U[-0.8, 0.8] \).

Researchers first regress \( y_i \) on \( x_i \) and \( z_i \) and then use a \( t \)-test to test

\[ H_0 : \beta = 0 \quad \text{against} \quad H_1 : \beta > 0. \]

A fraction \( \tau \) of researchers \( p \)-hack. They employ the following strategy. If \( p \leq 0.05 \), they report the \( p \)-value. If \( p > 0.05 \), they run regressions of \( y_i \) on \( x_i \) including all \((K - 1) \times 1\) subvectors of \( z_i \) and select the result corresponding to the minimum \( p \)-value. If there is no significant result, they explore all \((K - 2) \times 1\) subvectors of \( z_i \) and so on. The remaining fraction \( 1 - \tau \) of researchers do not \( p \)-hack and simply regress \( y_i \) on \( x_i \) and \( z_i \) and report the results.

We generate the distribution of \( p \)-values as a mixture:

\[ g(p) = \tau \cdot g^p(p) + (1 - \tau) \cdot g^{np}(p), \]

where \( g^p \) is the distribution under \( p \)-hacking and \( g^{np} \) is the distribution in the absence of \( p \)-hacking. \( g^p \) is generated based on the \( p \)-hacking strategy described before and \( g^{np} \) is the distribution of \( p \)-values from the initial regression of \( y_i \).
on $x_i$ and $z_i$. In the simulations, we vary the prevalence of $p$-hacking ($\tau$) and the number of controls ($K$). Figure 10 in Appendix E displays $g^p$ and $g^{np}$ for $K \in \{5, 7, 9\}$. We can see that $p$-hacking with a larger set of controls leads to more pronounced violations of non-increasingness.

**Figure 6: Empirical rejection rates. Simulations are based on 10,000 replications.**

Figure 6 reports the empirical rejection rates for the Binomial test on $g^p$ and $g^{np}$. Then, to construct samples on every Monte Carlo iteration, we draw with replacement from these data.
Romano-Wolf tests with 5 and 10 bins, LCM tests with $p = 2$ and $p = \infty$, and Fisher’s test for samples of size $n \in \{100, 500, 1000\}$. The nominal level is set to 5%. We find that, while all tests control size, they exhibit low power unless $\tau$ is large and either $K$ or $n$ (or both) are large. A comparison between the different methods shows that, while there are no notable differences in power when $\tau$ is small, both LCM tests are often substantially more powerful than the other procedures when $\tau$ is large. Our results further illustrate the sensitivity of the Romano-Wolf test to the choice of the number of bins. The power of the test with five bins is consistently higher than that of the test with ten bins. Finally, we can see that, across all designs, the “local” Binomial test exhibits very low power not exceeding 50% even in the most “extreme” case when $K = 9$ and $\tau = 1$. This is because the particular type of $p$-hacking considered here does not lead to a clear hump near nominal size, highlighting the drawbacks of tests that do not fully exploit the testable restriction.

6 Empirical applications

In this section, we apply the statistical tests of Section 4 to assess the prevalence of $p$-hacking in two large samples of $p$-values.

6.1 $P$-Values from three top economics journals

In our first application, we use the data on test statistics and $p$-values collected by Brodeur et al. (2016). This dataset contains information on 50,078 tests reported in 641 papers published in the American Economic Review, the Quarterly Journal of Economics, and the Journal of Political Economy between 2005 and 2011. We exclude 240 observations from the analysis for which it was not possible to construct $p$-values based on the reported information.\footnote{The dataset is available here: https://www.aeaweb.org/articles?id=10.1257/app.20150044}
In addition, as explained below, we focus on “main hypotheses” such that the final dataset contains 35,083 tests from 625 papers.

For each test, we observe the value of the point estimate, its standard deviation, the $p$-value of the test or the absolute value of the corresponding $t$-statistic. In what follows, we convert all $t$-statistics into $p$-values associated with two-sided $t$-tests based on the standard normal distribution.

An important practical issue is the choice of $p$-values. A natural starting point is to use the raw data on all $p$-values. However, there are several potential issues with this approach. (1) Papers typically contain different types of $p$-values, including $p$-values associated with main hypotheses and $p$-values associated with robustness checks. (2) The number of $p$-values differs substantially across papers such that a few papers with many $p$-values could drive the results. (3) While it is often plausible to assume that $p$-values are independent across papers, it may not be plausible to assume independence between $p$-values within papers. Correlation between $p$-values poses substantial statistical challenges for the tests in Section 4. For example, it precludes the application of exact tests.

To address (1), we exclusively focus on main hypotheses, which is possible because the data contain an indicator variable for “main hypothesis”. To deal with (2) and (3), we explore and compare two different approaches. First, we randomly draw one $p$-value per paper and apply our tests to the random subsample. Second, we consider aggregate $p$-values that are obtained as weighted averages of the $p$-values for the main hypotheses within each paper. Our weights are constructed as in Brodeur et al. (2016), accounting for the fact that the number of collected $p$-values differs across papers and tables. Both approaches mitigate (2) and (3), but exhibit potential drawbacks. Analyzing random subsamples of $p$-values may result in low power because not all the data are being used and the distribution of aggregate $p$-values may not be non-increasing under the conditions of Theorem 1, even when the $p$-values are only know that the statistic of interest is below a threshold (e.g, $p$-value < 0.01).
independent.\footnote{For example, if all null hypotheses are true, the distribution of the average of two \( p \)-values has a triangular shape. Moreover, by a CLT, the distribution of the average of many independent \( p \)-values is approximately normal.}

Figure 7 presents the results. A common feature of all histograms is the large number of very small \( p \)-values, which is sometimes interpreted as indicative of evidential value (e.g., Simonsohn et al., 2014). As discussed in Brodeur et al. (2016), natural numbers that can be expressed as ratios of small integers are overrepresented because of the low precision used by some of the authors. As a result, the data exhibit a noticeable mass point at \( \hat{t} = 2 \) (there are 427 such observations in the original data, our final dataset of “main hypotheses” contains 318 of them), which translates into a mass point in the \( p \)-curve at \( p = 0.046 \). We note that the mass point could also be due to \( p \)-hacking if \( \hat{t} = 2 \) is a “focal point”. To analyze the impact of rounding, we apply the tests to the de-rounded data provided by Brodeur et al. (2016). Figure 8 presents the results.
Based on the original (rounded) data on all p-values, the Binomial test on [0.04, 0.05] rejects the null in all three (sub)samples and the LCM with \( p = \infty \) test rejects for both the overall sample and microeconomics. None of the other tests rejects the null at the conventional significance levels. We find
very different results for the de-rounded data. Neither the Binomial nor the LCM test with \( p = \infty \) or any other test reject the null, which suggests that the rejections based on the original data are due to the mass point just below \( p = 0.05 \). We emphasize that the Binomial test is particularly sensitive to

Figure 8: Testing results (derounded data)
rounding. Because of the particular location of the mass point, the Binomial test on \([0.04, 0.05]\) rejects almost by construction, whereas more local versions, for example, on \([0.045, 0.05]\), would not reject. Rounding does not impact the results for the random samples of \(p\)-values; none of tests reject the null neither based on the original nor based on the de-rounded data. For the aggregated rounded \(p\)-values, only the Binomial test on \([0.08, 0.10]\) (for macroeconomics) and the LCM test with \(p = 2\) (for microeconomics) reject the null at the 10%-level level (the LCM test with \(p = \infty\) almost rejects at the 10%-level). After de-rounding, the null is only rejected for microeconomics and only based on the two LCM tests.

6.2 \(P\)-Values from different disciplines

In this section, we investigate the prevalence of \(p\)-hacking across different disciplines using the dataset collected by Head et al. (2015).\(^{15}\) This dataset contains \(p\)-values obtained from text-mining all open access papers available in the PubMed database. The authors collected \(p\)-values from ten different disciplines. Here, we focus on six of them: biology, chemistry, education, engineering, medical and health sciences, and psychology and cognitive science.\(^{16}\)

The dataset contains two different types of \(p\)-values: \(p\)-values from abstracts and \(p\)-values from the result section in the main text. We use the \(p\)-values obtained from the abstracts as these \(p\)-values are more salient and thus presumably more likely to be \(p\)-hacked. Since there are multiple \(p\)-values per paper, for our analysis we use the random subsample with one \(p\)-value per abstract contained in the publicly available dataset.\(^{17}\) Table 1 (last row) reports the number of observations for each discipline.

\(^{15}\)The dataset is available here: https://datadryad.org/resource/doi:10.5061/dryad.79d43.

\(^{16}\)Unfortunately, the data do not contain any information on the types of tests underlying the \(p\)-values. Therefore, we cannot verify that all the tests satisfy the conditions of Theorem 1.

\(^{17}\)As in the previous application, we exclude from our analysis \(p\)-values reported as being lower or higher than a threshold.
Panel (a) of Figure 9 displays a histogram of the raw data on p-values for the medical and health sciences (the largest subsample). A substantial fraction of p-values are rounded to two decimal places. As a consequence, there are sizable mass points at 0.01, 0.02, 0.03, and 0.04 (the authors excluded p-values at 0.05 from the sample). One important reason for prevalence of rounding relative to the Brodeur et al. (2016) dataset is that Head et al. (2015) directly collected p-values through text mining, while Brodeur et al. (2016) also collected data on test statistics, estimates, and standard errors, which allows us to construct more precise p-values.

Table 1 presents the results from applying the tests to the original (rounded) data. By construction, the Binomial test is very sensitive to rounding and the choice of the interval matters a lot. We therefore report the results for [0.04, 0.05) (including the mass point at 0.04) and (0.04, 0.05) (not including the mass point at 0.04). Both LCM tests and the RW test (10 bins) reject the null hypothesis for two or more disciplines, whereas as none of the other tests rejects at the conventional significance levels.

To mitigate the effect of rounding, we deround the data by adding random
noise to the $p$-values.\textsuperscript{18} Panel (b) of Figure 9 displays the histogram of raw $p$-values for the medical and health sciences after de-rounding and Table 2 presents results for all tests and disciplines based on the de-rounded data. The differences are striking. Only the LCM sup-norm test (for medical and health sciences) and the Romano-Wolf test with 10 bins (for psychology and cognitive sciences) reject the null hypothesis at the 5% and 10%-level, respectively.

Table 1: Results for different sciences: rounded data

<table>
<thead>
<tr>
<th>Discipline</th>
<th>Test</th>
<th>Biological sciences</th>
<th>Chemical sciences</th>
<th>Education</th>
<th>Engineering</th>
<th>Medical and health sciences</th>
<th>Psychology and cognitive sciences</th>
</tr>
</thead>
<tbody>
<tr>
<td>Binomial on (0.04, 0.05)</td>
<td>0.277</td>
<td>0.500</td>
<td>1.000</td>
<td>0.891</td>
<td>0.976</td>
<td>0.855</td>
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<tr>
<td>Binomial on [0.04, 0.05)</td>
<td>1.000</td>
<td>0.887</td>
<td>1.000</td>
<td>1.000</td>
<td>1.000</td>
<td>0.989</td>
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<tr>
<td>LCM (2-norm)</td>
<td>0.000</td>
<td>0.940</td>
<td>0.404</td>
<td>0.129</td>
<td>0.000</td>
<td>0.456</td>
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</tr>
<tr>
<td>LCM (sup-norm)</td>
<td>0.000</td>
<td>0.291</td>
<td>0.196</td>
<td>0.013</td>
<td>0.000</td>
<td>0.219</td>
<td></td>
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<tr>
<td>Romano-Wolf (5 bins)</td>
<td>1.000</td>
<td>0.986</td>
<td>0.962</td>
<td>0.944</td>
<td>1.000</td>
<td>0.966</td>
<td></td>
</tr>
<tr>
<td>Romano-Wolf (10 bins)</td>
<td>0.000</td>
<td>0.539</td>
<td>0.016</td>
<td>0.000</td>
<td>0.000</td>
<td>0.072</td>
<td></td>
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<tr>
<td>Fisher’s Method</td>
<td>1.000</td>
<td>1.000</td>
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<td>1.000</td>
<td>1.000</td>
<td>1.000</td>
<td></td>
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<tr>
<td>Obs in (0.04, 0.05)</td>
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<td>2</td>
<td>6</td>
<td>1506</td>
<td>8</td>
<td></td>
</tr>
<tr>
<td>Obs in (0, 0.05)</td>
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<td>11</td>
<td>21</td>
<td>2727</td>
<td>13</td>
<td></td>
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<tr>
<td>Obs in (0, 0.05)</td>
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<td>106</td>
<td>111</td>
<td>174</td>
<td>24927</td>
<td>134</td>
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Table 2: Results for different sciences: derounded data

<table>
<thead>
<tr>
<th>Discipline</th>
<th>Test</th>
<th>Biological sciences</th>
<th>Chemical sciences</th>
<th>Education</th>
<th>Engineering</th>
<th>Medical and health sciences</th>
<th>Psychology and cognitive sciences</th>
</tr>
</thead>
<tbody>
<tr>
<td>Binomial on [0.04, 0.05)</td>
<td>0.973</td>
<td>0.726</td>
<td>1.000</td>
<td>0.999</td>
<td>1.000</td>
<td>0.828</td>
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<tr>
<td>LCM (2-norm)</td>
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<td>1.000</td>
<td>1.000</td>
<td>0.857</td>
<td>0.963</td>
<td>0.934</td>
<td></td>
</tr>
<tr>
<td>LCM (sup-norm)</td>
<td>0.845</td>
<td>0.994</td>
<td>0.994</td>
<td>0.721</td>
<td>0.039</td>
<td>0.723</td>
<td></td>
</tr>
<tr>
<td>Romano-Wolf (5 bins)</td>
<td>1.000</td>
<td>0.850</td>
<td>0.986</td>
<td>0.157</td>
<td>1.000</td>
<td>0.932</td>
<td></td>
</tr>
<tr>
<td>Romano-Wolf (10 bins)</td>
<td>0.983</td>
<td>0.834</td>
<td>0.637</td>
<td>0.148</td>
<td>1.000</td>
<td>0.071</td>
<td></td>
</tr>
<tr>
<td>Fisher’s Method</td>
<td>1.000</td>
<td>1.000</td>
<td>1.000</td>
<td>1.000</td>
<td>1.000</td>
<td>1.000</td>
<td></td>
</tr>
<tr>
<td>Obs in [0.04, 0.05)</td>
<td>198</td>
<td>11</td>
<td>5</td>
<td>14</td>
<td>2127</td>
<td>10</td>
<td></td>
</tr>
<tr>
<td>Obs in (0, 0.05)</td>
<td>2438</td>
<td>107</td>
<td>111</td>
<td>175</td>
<td>25355</td>
<td>137</td>
<td></td>
</tr>
</tbody>
</table>

\textsuperscript{18}We de-round the data as follows. To each observed $p$-value rounded up to the $k$th decimal point we add a random number generated from the uniform distribution supported on the interval $[−0.5, 0.510] \cdot 10^{−k}$. Some $p$-values become negative after de-rounding. To resolve this issue we set them equal to the smallest positive value observed in the data.
7 Concluding remarks

This paper provides the first general results on distributions of p-values across scientific studies, providing conditions under which a null set of distributions can be identified. We extend the results to sample selection through observing p-values of published papers only. Since p-hacking can take many forms, the alternatives of interest also take many forms. We characterize analytically one likely important alternative, that of specification search across controls in a linear regression, and show possible alternative distributions.

For the empirical researcher, the analysis both provides constructive understanding of the problem of detecting p-hacking as well as some cautionary notes. In the absence of sample selection, for many popular tests, regardless of whether or not the hypotheses being tested are true and regardless of the actual value of the parameters being tested, the null hypothesis contains all p-curve distributions that are non-increasing. Such results are not available for distributions of t-tests. Unfortunately, as has been shown in simple settings and we show in a more realistic setting, detecting p-hacking via the p-curve is a refutable but non-verifiable hypothesis. The characterization of the null set leads directly to considering tests that make use of the entire distribution of p-values, some such tests are in use and we suggest others here, rather than focusing on the intuitive idea of a “hump” in the p-curve directly below 5%. Disappointingly however, our simulations of p-hacking through covariate selection show that there needs to be a very large number of researchers engaged in this type of p-hacking for tests to have enough power that we are likely to detect p-hacking in practice.

Lastly, we provide some recommendations for data collection. First, to enable a careful selection of p-values, a detailed classification, which distinguishes main hypotheses, robustness checks, and other analyses, is indispensable. Second, to assess the dependence structure between p-values, we suggest to not only collect indicators for papers but also for tables within papers. Third, to avoid rounding issues, p-values should be collected at the highest possible pre-
cision level. It may be useful to gather data on estimates, standard errors, and test statistics to increase the precision. Finally, to gauge whether the $p$-curve is non-increasing in the absence of $p$-hacking, one needs to collect information on the particular types of tests and on how the $p$-values were computed.
References


A simple model of publication bias

In this section, we present a simple model for publication bias similar to the one presented in Brodeur et al. (2016, Section III.B.). We show that the publication probability can be decreasing in \( p \) in settings where the publication decision is not only a function of \( p \)-values, but also of other random factors.

Suppose that there is a unique journal that attaches value \( f(p, \varepsilon) \) to each submitted paper. Here \( p \) can be interpreted as the \( p \)-value on the main hypothesis and \( \varepsilon \) is an unobserved error term, which captures various unobserved factors that affect the publication decision. Journals accept papers if their value exceeds a certain threshold, \( \bar{f} \).

\[
S = 1 \{ f(p, \varepsilon) > \bar{f} \}
\]

This implies that

\[
P(S = 1 | p) = P(f(p, \varepsilon) > \bar{f} | p)
\]

We impose the following two assumptions.

**Assumption 3.** \( f \) is strictly decreasing in its first argument and strictly increasing in its second argument.

**Assumption 4.** \( \varepsilon \) is independent of \( p \).

Assumption 3 states that, ceteris paribus, journals attach higher value to papers with lower \( p \)-values. Assumption 4 requires that \( p \)-values are independent of all other factors that affect publication, which essentially amounts to abstracting from any other forms of systematic publication bias.

Under Assumption 3, there exists a unique \( \tilde{f}(p) \) such that \( f(p, \varepsilon) > \bar{f} \iff \varepsilon > \tilde{f}(p) \), where \( \tilde{f}(p) \) is increasing in \( p \) (the higher the \( p \)-value, the higher the \( \varepsilon \) required to pass the threshold to get published). Hence, under Assumptions 3–4, we can write

\[
P(S = 1 | p) = P(\varepsilon > \tilde{f}(p) | p)
\]

\[
= 1 - F_{\varepsilon|p}(\tilde{f}(p) | p)
\]

\[
= 1 - F_{\varepsilon}(\tilde{f}(p)),
\]

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which implies that $P(S = 1 \mid p)$ is decreasing in $p$.

**B Detailed derivations for Section 3.2**

Let $\hat{\sigma}_j$ be the standard error of the estimate of $\beta$ when we use $z_j$ as a control ($j = 1, 2$). Given our assumptions and since the variance of $u$ is known, it can be shown that

$$\hat{\sigma}_j^2 = \frac{1}{1 - \gamma^2}, \quad j = 1, 2.$$ 

It follows that the $t$-statistic for testing $H_0 : \beta = 0$ has the following distribution

$$T_j = \frac{\sqrt{n}\hat{\beta}_j}{\hat{\sigma}_j} \sim t \left( \frac{W_{xu} - \gamma W_{zju}}{\sqrt{1 - \gamma^2}} \right), \quad j = 1, 2,$$

where

$$\begin{pmatrix} W_{xu} \\ W_{z1u} \\ W_{z2u} \end{pmatrix} \sim \mathcal{N} \left( \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix}, \begin{pmatrix} 1 & \gamma & \gamma \\ \gamma & 1 & 0 \\ \gamma & 0 & 1 \end{pmatrix} \right).$$

This means that, conditional on $h$, $T_1$ and $T_2$ are jointly normal with common mean equal to $h$, unit variances and correlation $\rho = (1 - 2\gamma^2)/(1 - \gamma^2)$.

Fix $h$ for now and let $z_h(p) = z_0(p) - h$, where $z_0(p) = \Phi^{-1}(1 - p)$. Then the cdf of $p_r$ on $(0, \alpha]$ interval is given by

$$G_h(p) = P(p_r \leq p)$$

$$= P(p_1 \leq p \mid p_1 \leq \alpha)P(p_1 \leq \alpha) + P(\min\{p_1, p_2\} \leq p \mid p_1 > \alpha)P(p_1 > \alpha)$$

$$= P(p_1 \leq p \mid p_1 \leq \alpha)P(p_1 \leq \alpha) + P(p_1 > \alpha, p_2 \leq p)$$

$$= P(T_1 \geq z_0(p))P(T_1 \geq z_0(\alpha)) + P(T_1 < z_0(\alpha), T_2 \geq z_0(p))$$

$$= (1 - \Phi(z_h(p)))(1 - \Phi(z_h(\alpha))) + \int_{z_h(\alpha)}^{+\infty} \int_{z_h(p)}^{+\infty} f(x, y; \rho) dxdy,$$

where $f(x, y; \rho) = \frac{1}{2\pi\sqrt{1-\rho^2}} \exp\left\{-\frac{x^2-2\rho xy+y^2}{2(1-\rho^2)}\right\}$ and $p \in (0, \alpha]$.  

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Differentiate $G_h(p)$ with respect to $p$:

\[
\frac{dG_h(p)}{dp} = \frac{dz_h(p)}{dp} \left[ -\phi(z_h(p))(1 - \Phi(z_h(\alpha))) - \int_{-\infty}^{z_h(\alpha)} f(z_h(p), y; \rho) dy \right] = \frac{\phi(z_h(p))[1 - \Phi(z_h(\alpha))] + \Phi \left( \frac{z_h(\alpha) - \rho z_h(p)}{\sqrt{1 - \rho^2}} \right)}{\phi(z_0(p))}
\]

Finally, the density function of $p$-values on the $(0, \alpha]$ interval is given by

\[
g(p) = \int_{\mathcal{H}} \frac{dG_h(p)}{dp} d\pi(h) = \int_{0}^{\infty} \frac{\phi(z_h(p)) \left[ 1 - \Phi(z_h(\alpha)) \right] + \Phi \left( \frac{z_h(\alpha) - \rho z_h(p)}{\sqrt{1 - \rho^2}} \right)}{\phi(z_0(p))} d\pi(h)
\]

and its derivative is

\[
g'(p) = \int_{\mathcal{H}} \frac{\phi(z_h(p))[z_h(p) - z_0(t)]C(p, h; \alpha, \rho) + \phi \left( \frac{z_h(\alpha) - \rho z_h(p)}{\sqrt{1 - \rho^2}} \right) - \rho}{[\phi(z_0(p))]^2} d\pi(h),
\]

where $C(p, h; \alpha, \rho) = 1 - \Phi(z_h(\alpha)) + \Phi \left( \frac{z_h(\alpha) - \rho z_h(p)}{\sqrt{1 - \rho^2}} \right)$. To get the final expression for $g'(p)$ note that $z_h(p) - z_0(p) = -h$.

C The $t$-curve is decreasing if $\pi$ is symmetric around zero

If one is willing to impose additional restrictions on the distribution of alternatives, $\pi$, it is possible to show that the $t$-curve is decreasing. For example, this is the case if $\pi$ admits a density $f_\pi$ that is symmetric around zero and unimodal, i.e., if $f_\pi(h) = f_\pi(-h)$ and $\partial f_\pi(h)/\partial h \leq 0$ for $h > 0$.

The distribution of the absolute $t$-statistic is given by

\[
g(t) = \int_{-\infty}^{\infty} (\phi(h+t) + \phi(h-t)) f_\pi(h) dh = 2 \int_{0}^{\infty} (\phi(h+t) + \phi(h-t)) f_\pi(h) dh, t \geq 0
\]

Assuming that we can interchange differentiation and integration, the derivative of $g$ is

\[
g'(t) = 2 \int_{0}^{\infty} (\phi'(h+t) - \phi'(h-t)) f_\pi(h) dh,
\]
where \( \phi'(x) = -x\phi(x) \). Note that

\[
\int_{0}^{\infty} \phi'(h + t)f_\pi(h)dh = \int_{t}^{\infty} \phi'(x)f_\pi(x - t)dx = -\int_{t}^{\infty} x\phi(x)f_\pi(x - t)dx
\]

and

\[
\int_{0}^{\infty} \phi'(h - t)f_\pi(h)dh = \int_{-t}^{\infty} \phi'(x)f_\pi(x + t)dx = -\int_{-t}^{\infty} x\phi(x)f_\pi(x + t)dx
\]

\[
= -\int_{-t}^{0} x\phi(x)f_\pi(x + t)dx - \int_{0}^{t} x\phi(x)f_\pi(x + t)dx - \int_{t}^{\infty} x\phi(x)f_\pi(x + t)dx
\]

\[
= \int_{0}^{t} x\phi(x)f_\pi(t - x)dx - \int_{0}^{t} x\phi(x)f_\pi(x + t)dx - \int_{t}^{\infty} x\phi(x)f_\pi(x + t)dx
\]

Hence,

\[
g'(t) = 2 \left( \int_{0}^{t} x\phi(x)[f_\pi(t + x) - f_\pi(t - x)]dx + \int_{t}^{\infty} x\phi(x)[f_\pi(x + t) - f_\pi(x - t)]dx \right)
\]

\[
\leq 0,
\]

where the last inequality holds since \( f_\pi(t + x) \leq f_\pi(t - x) \) for \( x \in (0, t) \) and \( f_\pi(x + t) \leq f_\pi(x - t) \) for \( x \in (t, \infty) \).

**D  Proof of Lemma 1**

Note that for all tests, \( \{cv(p) : p \in (0, 1)\} = (0, \infty) \).

(i) The assumption for one-sided \( t \)-test was verified in Section 3.1.

(ii) In this case \( f(x) = 2\phi(x) \) and \( f_h(x) = \phi(x - h) + \phi(x + h) \), where \( x \geq 0 \).

After taking derivatives and collecting terms we get

\[
f'(x)f_h(x) - f'_h(x)f(x) = 2\phi(x)h(\phi(x + h) - \phi(x - h))
\]

\[
= 2\phi(x)\phi(x - h)(e^{-2xh} - 1)
\]

\[
\leq 0,
\]

since \( h(e^{-2xh} - 1) \leq 0 \) for any \( h \).
(iii) In this case $f(x) = f(x; k) = \frac{1}{2^{k/2} \Gamma(k/2)} x^{k/2-1} e^{-x^2/2}$ and

$$f_h(x) = \sum_{j=0}^{\infty} \frac{e^{-h/2} (h/2)^j}{j!} f(x; k + 2j),$$

where $x > 0$. Note that $f'(x; k) = f(x; k) ((k - 2)x^{-1} - 1)$. After taking derivatives and collecting terms we get

$$f'(x)f_h(x) - f'_h(x)f(x) = \sum_{j=0}^{\infty} \frac{e^{-h/2} (h/2)^j}{j!} f(x; k + 2j) f(x; k) \left[ ((k - 2)x^{-1} - 1) - ((k + 2j - 2)x^{-1} - 1) \right]$$

$$= -\sum_{j=0}^{\infty} \frac{e^{-h/2} (h/2)^j}{j!} f(x; k + 2j) f(x; k) 2jx^{-1} \leq 0,$$

since every term in the last sum is non-negative.
E Additional figures

(a) $K = 5$, no $p$-hacking  
(b) $K = 5$, with $p$-hacking

(c) $K = 7$, no $p$-hacking  
(d) $K = 7$, with $p$-hacking

(e) $K = 9$, no $p$-hacking  
(f) $K = 9$, with $p$-hacking

Figure 10: $P$-hacked and non-$p$-hacked distributions.