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Detecting and avoiding likely false-positive findings – a practical guide

Wolfgang Forstmeier[1]*, Eric-Jan Wagenmakers[2] and Timothy H. Parker[3]

[1]*Department of Behavioural Ecology and Evolutionary Genetics, Max Planck Institute for Ornithology, 82319 Seewiesen, Germany*
[2]*Department of Psychology, University of Amsterdam, PO Box 15906, 1001 NK Amsterdam, The Netherlands*
[3]*Department of Biology, Whitman College, Walla Walla, WA 99362, U.S.A.*

ABSTRACT

Recently there has been a growing concern that many published research findings do not hold up in attempts to replicate them. We argue that this problem may originate from a culture of 'you can publish if you found a significant effect'. This culture creates a systematic bias against the null hypothesis which renders meta-analyses questionable and may even lead to a situation where hypotheses become difficult to falsify. In order to pinpoint the sources of error and possible solutions, we review current scientific practices with regard to their effect on the probability of drawing a false-positive conclusion. We explain why the proportion of published false-positive findings is expected to increase with (*i*) decreasing sample size, (*ii*) increasing pursuit of novelty, (*iii*) various forms of multiple testing and researcher flexibility, and (*iv*) incorrect *P*-values, especially due to unaccounted pseudoreplication, i.e. the non-independence of data points (clustered data). We provide examples showing how statistical pitfalls and psychological traps lead to conclusions that are biased and unreliable, and we show how these mistakes can be avoided. Ultimately, we hope to contribute to a culture of 'you can publish if your study is rigorous'. To this end, we highlight promising strategies towards making science more objective. Specifically, we enthusiastically encourage scientists to preregister their studies (including *a priori* hypotheses and complete analysis plans), to blind observers to treatment groups during data collection and analysis, and unconditionally to report all results. Also, we advocate reallocating some efforts away from seeking novelty and discovery and towards replicating important research findings of one's own and of others for the benefit of the scientific community as a whole. We believe these efforts will be aided by a shift in evaluation criteria away from the current system which values metrics of 'impact' almost exclusively and towards a system which explicitly values indices of scientific rigour.

Key words: confirmation bias, HARKing, hindsight bias, overfitting, *P*-hacking, power, preregistration, replication, researcher degrees of freedom, Type I error.

CONTENTS

I. Introduction 1942
II. Problems 1943
(1) The argument of Ioannidis and some extensions 1943
(2) Multiple testing in all of its manifestations 1946
(*a*) The temptation of selective reporting 1948
(*b*) Cryptic multiple testing during stepwise model simplification 1949
(*c*) A priori hypothesis testing versus *HARKing: Does it matter?* 1949
(*d*) Researcher degrees of freedom: (1) stopping rules 1950
(*e*) Researcher degrees of freedom: (2) flexibility in analysis 1951
(3) Incorrect *P*-values 1952
(*a*) Pseudoreplication at the individual level 1953
(*b*) Pseudoreplication due to genetic relatedness 1954
(*c*) Pseudoreplication due to spatial and temporal autocorrelation 1955
(*d*) Pseudoreplication renders *P*-curve analysis invalid 1956

* Address for correspondence (Tel.: +49-8157-932346; E-mail: forstmeier@orn.mpg.de).

(4) Errors in interpretation of patterns 1956
(*a*) Overinterpretation of apparent differences 1956
(*b*) Misinterpretation of measurement error 1957
(5) Cognitive biases 1958
III. Solutions 1959
(1) Need for replication and rigorous assessment of context dependence 1959
(*a*) Obstacles to replication 1959
(*b*) Overcoming the obstacles 1960
(*c*) Interpretation of differences in findings 1960
(*d*) Is the world more complex or less complex than we think? 1961
(2) Collecting evidence for the null and the elimination of zombie hypotheses 1961
(3) Making science more objective 1962
(*a*) Why should I preregister my next study? 1962
(*b*) Badges make good scientific practice visible 1962
(*c*) Blinding during data collection and analysis 1963
(*d*) Objective reporting of non-registered studies 1963
(*e*) Concluding recommendations for funding agencies 1963
IV. Conclusions 1964
V. Glossary 1964
VI. Acknowledgements 1966
VII. References 1966

I. INTRODUCTION

Several research fields appear to be in crisis of confidence (McNutt, 2014; Nuzzo, 2014, 2015; Horton, 2015; Parker *et al.*, 2016) as evidence emerges that the majority of published research findings cannot be replicated (Ioannidis, 2005; Pereira & Ioannidis, 2011; Prinz, Schlange & Asadullah, 2011; Begley & Ellis, 2012; Open Science Collaboration, 2015). According to a recent survey in *Nature* (Baker, 2016), 52% of researchers believe that there is 'a significant crisis', 38% see 'a slight crisis', and only 3% see 'no crisis'. This suggests that many scientists are starting to contemplate the following key questions: (*i*) to what extent are the findings in my field reliable? (*ii*) How shall I judge the existing literature? (*iii*) Can I distinguish findings that are likely false from those that are likely true? (*iv*) How can I avoid building my own research project on earlier findings that are false? (*v*) How do I avoid repeating the mistakes that others seem to have made? (*vi*) Which statistical approaches minimize my risk of drawing false conclusions?

This review has the goal of providing guidance towards answering these important questions. This requires a good understanding of some basic statistical principles. To serve as a practical guide for those less experienced or less versed in statistics, we make an effort to explain basic concepts in an easily accessible way (see also the Glossary in Section V), and we choose a conversational style of writing to motivate the reader to work through this important material. We have compiled a collection of common pitfalls and illustrate them with accessible examples. Our hope is that these examples will prime our readers to recognize weaknesses or mistakes when they critically examine the literature or review manuscripts and help them avoid these mistakes when they design their own studies and analyse their own data.

Our examples originate from our own research experiences in behavioural ecology and evolutionary genetics, but the same statistical issues occur across a wide range of probabilistic scientific disciplines such as ecology, physiology, neuroscience, medical sciences, and psychology. Statistical analyses have been important in biology since the development of tools like analysis of variance in the early decades of the 20th century (Fisher, 1925), and statistical tools remain essential and continue to proliferate (e.g. advanced Bayesian statistics) across the biological sciences. Yet, no matter whether you are running a simple *t*-test or a restricted maximum likelihood animal model, there is always a risk of getting it wrong [for examples of mistakes that lead to over-confidence see Hadfield *et al.* (2010) and Valcu & Valcu (2011)]. Hence, our first point is that there are some common mistakes in the use of statistical tools and that these mistakes often lead to nominal significance ($P < 0.05$), yet the *P*-value is often incorrect and (frequently) too small, thereby contributing to false-positive claims in the literature. Our second point is more philosophical but is a complement to our first point. Statistically significant findings typically seem more interesting than non-significant findings and are thus easier to publish. This has created our current scientific culture of actively seeking statistical significance, often with practices that lead to misleading results. We hence try to raise the general awareness of psychological biases that we need to keep in check in order to ensure an objective reporting of research outcomes. We believe that these two issues explain much of the current crisis in science, and that we need to rethink critically some of our common research practices.

The pitfalls we outline are unlikely to be equally serious in all fields of science, so we want to avoid creating the false impression that all current science is fundamentally flawed. Our radical critique of the current research culture may leave

some readers frustrated and depressed, because it will be evident that making real scientific progress is much harder than iconic research papers seem to suggest. However, instead of frustration and depression we hope to offer optimism. We invite our readers to be among the first to implement new standards that will dramatically improve the reliability and objectivity of research. This should be appealing and exciting not only because researchers would like to have confidence in the reliability of their own work, but also because new tools allow them to signal the reliability of their research findings to others. As this signalling (Gintis, Smith & Bowles, 2001) becomes more widespread, it will be harder for others to cut corners and present results that are likely wrong.

Section II of our article outlines the existing problems. We begin by reviewing the statistical parameters (prior probability, realized α and β) that determine which proportion of the published positive findings will be false-positives (Section II.1). We show that unaccounted-for multiple testing is a major source of false-positive findings, and we present examples that illustrate how easily this source of error creeps into our research if we fail to develop a clear predetermined research plan. Flexibility in defining and testing our hypotheses, combined with selective reporting of apparent cases of success hence leads to a high risk of publishing false-positive findings (Section II.2). This risk increases further if we fail to acknowledge that the data points we collected may not be independent of each other. *P*-values derived from such pseudoreplicated data will often mislead us into seeing patterns where none exist (Section II.3). Sections II.2 and II.3 make up the bulk of the present article because there are quite a few statistical pitfalls to avoid. False-positive conclusions can also arise from over-interpretation of differences or from misinterpretation of measurement error, which we address in Section II.4. Finally, we briefly touch on cognitive biases that render it difficult to collect and interpret data objectively (Section II.5).

Section III focuses on possible solutions. Only a few research fields have developed rigorous methodology that limits the extent of false-positive reporting and ensures that negative results are just as likely to get published as positive results; consequently, many scientific disciplines face a literature where it is difficult to distinguish likely truth from falsehood. We therefore highlight the need for rigorous replication studies (Section III.1) that help eliminate hypotheses that are likely to be false (Section III.2). We then conclude by discussing novel methods, like preregistration of studies, which promote greater objectivity and less bias in what gets reported in scientific publications (Section III.3).

II. PROBLEMS

(1) The argument of Ioannidis and some extensions

Approximately 10 years ago John Ioannidis famously explained 'Why Most Published Research Findings Are False' (Ioannidis, 2005). Although the title is somewhat misleading (Ioannidis did not actually prove that most findings are false), understanding his argument is essential for an intuitive feeling of how likely it is that any published positive finding is true or false. It is therefore worth following every step of the argument that we illustrate in Fig. 1 (see also Lakens & Evers, 2014).

Consider a thousand hypotheses H1 that we might wish to test (Fig. 1A). Many of these may not be true, so let us start with a scenario where only 10% of the hypotheses at hand are in fact true (Fig. 1B). This proportion of hypotheses being true is often described with the symbol π (here $\pi = 0.1$). When testing the 900 hypotheses that are not true (dark grey in Fig. 1B), we allow for 5% false-positive findings if we set our significance threshold at $\alpha = 0.05$ (the accepted level of making Type I errors). This means we will obtain 45 (i.e. 900×0.05) false-positive answers (red in Fig. 1C), where we state that our data provide significant support for the hypothesis H1 (or more formally speaking of 'evidence against the null hypothesis H0') even though that hypothesis H1 is false (and H0 is true). Now, when testing the 100 true hypotheses, we will sometimes fall short of the significance threshold, i.e. cases where we would conclude that the data do not support that hypothesis H1, although it is true and H0 is false (a false-negative or Type II error). The frequency with which our test of the empirical data falls short of reaching significance despite the hypothesis H1 being true is known as the probability β (the probability of making a Type II error). The probability β depends on sample size (and effect size). When the data set is very large, the risk of falling short of significance is small, so we speak of the study having high statistical power (which is defined as $1 - \beta$). In our example in Fig. 1D, we have a large sample size and hence a high power (80%) to support 80 out of the 100 true hypotheses correctly. In this case, β will be 20%, leading to 20 false-negative conclusions shown in black (i.e. where we reject the hypothesis despite it being true).

Here is the essential point of Ioannidis' argument (Ioannidis, 2005): when we consider only the subset of positive outcomes, where a hypothesis H1 has been supported by the data (the 45 red and the 80 blue cases in Fig. 1D), 36% (i.e. $45/(45+80)$) will not be true. This is the fraction of positive research findings (where data provided significant support for a hypothesis) that are false. This is also known as the false-positive report probability ($\mathrm{FPRP} = (\alpha(1-\pi)/[\alpha(1-\pi)+(1-\beta)\pi]$). Notably, this fraction is much higher than 5%. This highlights the fact that a 5% false positive rate (i.e. setting α at 0.05) does not mean that only 5% of significant research findings are false. The situation may get worse. In many studies, sample sizes are low, resulting in statistical power that is often as low as 20% (Møller & Jennions, 2002; Smith, Hardy & Gammell, 2011; Button *et al.*, 2013; Parker *et al.*, 2016). In this situation we will have 80 instead of 20 cases of false-negative results (black in Fig. 1E). If we then consider the positive outcomes only, we observe that 69% of the significant research findings are false [the red out of the red plus blue fraction in Fig. 1E; $45/(45+20) = 0.69$]. This disturbingly high proportion is what made Ioannidis (2005) claim that most findings are false.

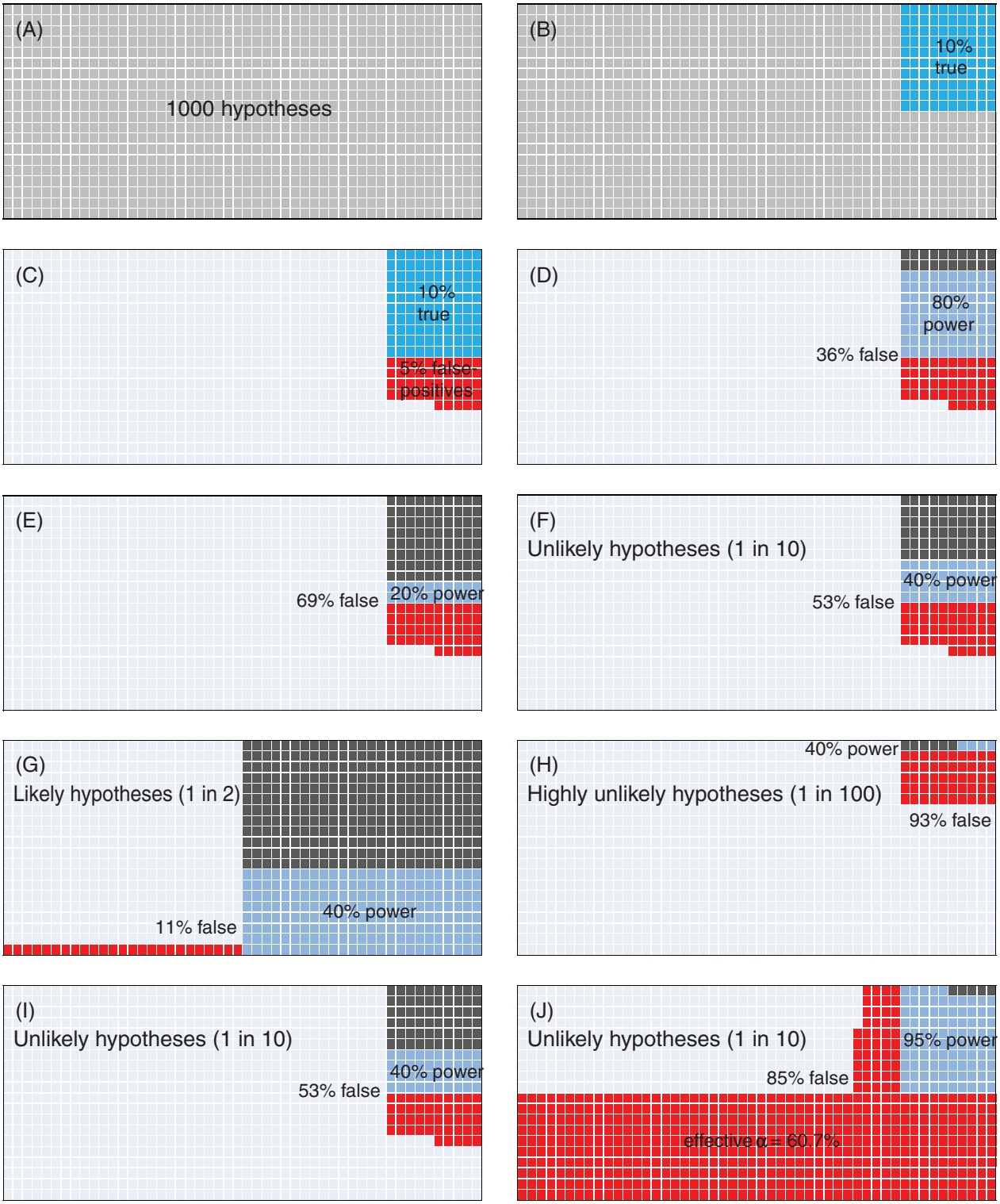

Fig. 1. Different scenarios of testing 1000 hypotheses, of which a limited proportion is true. The colours in panels (B and C) refer to hypotheses that are actually true (bright blue) or false (dark grey). The colours in panels (C–J) indicate false-positive findings (Type I error; red), true positive findings (pale blue), false-negative findings (Type II error; black), and true negative findings (light grey). For details see the main text. Illustration adopted and extended from http://www.economist.com/blogs/graphicdetail/2013/10/daily-chart-2.

For the following calculations, we will settle for an intermediate sample size (larger than is typical in ecology and evolution), which gives us a statistical power of 40%. Under this condition, 53% of the positive findings will be false (Fig. 1F). Now, it is essential to remember that we started with a scenario where only 10% of the hypotheses were actually true. That is, we were testing moderately unlikely hypotheses to begin with (Fig. 1F). If, in contrast, you are working in a research area where people mostly test hypotheses that are likely (every second hypothesis being actually true), the proportion of false-positive reports is quite small (Fig. 1G). We would obtain only 25 false positive reports (red in Fig. 1G), but as many as 200 true positives (blue in Fig. 1G). In this case, readers of publications that present positive findings will not often be misled (11% false). If, however, a research field is testing highly unlikely hypotheses (only one in a hundred being true) nearly all positive reports will be incorrect (93% false, Fig. 1H).

To illustrate one final point, let us return to a situation with moderately unlikely hypotheses (10% true) and still intermediate power ($1-\beta=40\%$), which is shown in Fig. 1I. Let us add a new dimension, which was brought up in a seminal publication of Simmons, Nelson & Simonsohn (2011). They stated that researchers actually have so much flexibility in deciding how to analyse their data that this flexibility allows them to coax statistically significant results from nearly any data set [for similar insights see Barber (1976), De Groot (1956/2014), Feynman (1974) and Gelman & Loken (2014)].

Simmons *et al.* (2011) called this flexibility 'researcher degrees of freedom'. We will address these researcher degrees of freedom in detail below, and we will give a range of illustrative examples. For now, imagine that researchers have to make many arbitrary decisions in data analysis, and if they are trying hard (even unintentionally through self-deception) to provide positive evidence for their hypothesis, at every arbitrary step they may always go for the option that produces the lowest *P*-value ('significance seeking'). Using simulations, Simmons *et al.* (2011) show that the combination of always choosing the better option in four consecutive arbitrary steps (each of which seems of minor importance, e.g. analysing yearlings and adults together *versus* separately) adds up to a dramatic effect of raising the α-level from $\alpha=0.050$ to 0.607. That means, if we systematically chose the option that reduces the *P*-value in each of the four steps, we will be able to present an effect of interest as being statistically significant ($P<0.05$) in 607 out of 1000 cases in which no real effect exists (hence the formulation 'allows presenting anything as significant'). If this scenario of raising α to 60.7% is applied to Ioannidis (2005) calculations, we would see 535 false positives (red in Fig. 1J) compared to approximately 95 true positives (blue in Fig 1J; note that this latter number is a rough guess and not based on simulations), which would mean that about 85% of all positive findings would be false.

According to the calculations illustrated in Fig. 1, the proportion of false-positive reports (out of all positive reports) will be highest for: (*i*) fields with mostly underpowered studies (small sample size); (*ii*) fields with unlikely hypotheses (driven by pursuit of novelty); (*iii*) fields that poorly guard against raising the level of α (significance seeking).

More can be said about each of these influential factors:

1 A comparison between Fig. 1D,E illustrates why low power produces relatively more false-positive findings. The absolute number of false positives stays the same (always 45 red cells), but we see fewer correct positives (20 rather than 80 blue cells) as power drops from 0.80 to 0.20. Hence the proportion of positive findings that are correct is decreasing. If you want to carry out your own calculations to see how the statistical power in your experiment depends on sample size, you will find suitable calculator tools online (e.g. GPower; Faul *et al.*, 2009), but they will always ask you about the size of the effect that you wish to detect. This is hard to know *a priori*. In the fields of ecology and evolution observed effect sizes are typically small (e.g. $r=0.19$; Møller & Jennions, 2002), which is still likely an overestimate (Hereford, Hansen & Houle, 2004; Parker *et al.*, 2016). Hence, large sample sizes are required to detect such effects (required $N=212$, for detecting $r=0.19$ with 80% power). While studies in animal behaviour have a reasonable power of around 70% for detecting a large effect of $r=0.5$, the power for detecting an effect of $r=0.19$ lies only around 15–20% [own calculations using GPower 3.1 (Faul *et al.*, 2009) based on results of Jennions & Møller (2003) and Smith *et al.* (2011)].
2 The relative proportion of false-positive reports is most strongly influenced by how likely one's hypothesis is to begin with (compare Fig. 1G with 1H). However, this quantity may be difficult to gauge. Most researchers would probably think (or at least hope) that they are testing relatively likely hypotheses (much closer to Fig. 1G than 1H). However, people's impressions may be deceiving. The existing literature is heavily biased towards stories of success (Parker *et al.*, 2016), with 84% of all publications finding support for their initial hypotheses (Fanelli, 2010). As we will see in Section II.2, this figure is far from an objective representation of all hypothesis tests that have been conducted, because null findings (non-significant results) are less likely to get published (Rosenthal, 1979; Simonsohn *et al.*, 2014), and because various common data-analysis practices increase the rate of false positives as well as the average strength of reported effects among those results that are published (Anderson, Martinson & De Vries, 2007; Simmons *et al.*, 2011; John, Loewenstein & Prelec, 2012; Parker *et al.*, 2016). Even without problematic data analysis, some (false) positive evidence can emerge for any hypothesis (Fig. 1H). Thus, just because we see support for a theory in the literature does not mean we should assume that our hypothesis, which is based on this theory, is likely to be true. Finally, one should realize that high-impact journals are always on the lookout for the most novel and surprising research findings.

Thus when researchers find evidence for surprising hypotheses (Fig. 1H) and manage to secure publication in these high-impact journals, other researchers may be tempted to test increasingly far-fetched (non-trivial, surprising) hypotheses. This could push a research field into an arms race that comes at the expense of tests for less-surprising hypotheses.

3 There are so many different ways in which the α-level can be raised above the conventional threshold of 5% (Fig. 1J) that this will keep us busy for most of this review. Conceptually it is helpful to distinguish between two problems. First (treated in Section II.2), there is the issue of multiple hypothesis testing that comes in various forms and can sometimes be deceivingly cryptic (Parker *et al.*, 2016). Here it is important to keep track of the extent of multiple testing. This may allow us to adjust α-levels accordingly, so that *P*-values can still be interpreted in a meaningful way. Second (treated in Section II.3), there are many ways of carrying out statistical tests incorrectly which often will yield highly significant *P*-values that are misleading and incorrect to an extent that cannot be adjusted for. The probably most important source of error here is the non-independence of data points (Milinski, 1997), which is typically referred to as pseudoreplication (independent data points are considered as proper replicates, while non-independent data points are considered as pseudoreplicates) or as clustered data (Weissgerber *et al.*, 2016).

Table 1 provides an overview of the statistical and psychological issues that will be addressed herein together with a collection of possible solutions.

(2) Multiple testing in all of its manifestations

In this chapter we will focus on how multiple testing and selective attention or reporting lead to inflated rates of Type I error. If researchers were forced to report the outcome of every single statistical test that they conduct, every obtained *P*-value could be taken at face value. With α set at 0.05, for each hypothesis H1 that is not true we would only have a 5% risk of drawing a false-positive conclusion. However, as soon as reporting becomes conditional on the outcome (typically: positive findings being more likely to get reported) or when we focus our attention on the promising outcomes (ignoring or forgetting about negative outcomes), the risk of a false-positive conclusion is much higher than 5% (e.g. 53% in Fig. 1F).

When the total number of statistical tests conducted is known (e.g. 10 tests), then it is possible to calculate the probability of obtaining at least one significant result by chance alone ($1-0.95^{10}=40\%$), and it is possible to adjust α-levels ($0.05/10=0.005$) for each test to ensure that the probability of making one or several Type I errors remains at about 5% ($1-0.995^{10}=4.9\%$). This adjustment is known as the classical Bonferroni correction (Dunn, 1961). While using such a strict α-threshold is effective in limiting Type I errors, it inevitably will increase the number of Type II errors (i.e. true effects that are discarded because they do not pass this threshold). Hence, if you are more worried about making Type II errors than about making Type I errors, you may well discard the Bonferroni correction (Nakagawa, 2004), or go for less-strict methods of correction based on false-discovery rate (Benjamini & Hochberg, 1995; Pike, 2011). Yet, whenever we allow our Type I error rate to rise in the interest of keeping the Type II error rate low, we will produce many false positives and thus need to seek to replicate these exploratory findings (Pike, 2011). For instance, if your aim is to discover a new treatment for a disease, you want to make sure that you do not miss out on something potentially interesting (and hence limit Type II errors). This is the exploratory part of science. It is essential and important. However, once you identified a potential treatment, you should be interested in making sure that you are right so as not to waste money or even cause harm, and hence you want to reduce Type I errors. This is the confirmatory part of science, the proper testing of *a priori* hypotheses.

Adjustments of α to multiple testing are typically called for when researchers present large tables containing numerous statistical tests, of which only a small fraction reaches significance ($P<0.05$). Such tables elicit skepticism in experienced researchers, who rightly worry that the content of the entire table may be consistent with the null hypothesis. As a pre-emptive response to such skepticism, authors may avoid presenting too many non-significant results alongside their positive findings. A threshold of $P<0.05$ seems fairly reasonable when only a few *P*-values are shown and these *P*-values mostly lie below the 0.05 threshold. By contrast, referees may request a more stringent threshold when many non-significant results are presented alongside, because the long list clearly reveals the extent of multiple testing. Problematically, when authors are free to choose which results to present in their publication, it becomes impossible to judge the appropriate statistical significance of the findings. When, for instance, the authors highlight a single significant finding from a pool of 10 tests they report, this inspires much less confidence in that finding than if it had arisen from a single planned test. This is a serious dilemma. Justified skepticism from reviewers creates an incentive for reduced transparency in scientific publications, thereby lowering the overall utility of the reported work. This problem could be mitigated if reviewers and editors would acknowledge and appreciate the greater scientific value of a paper that comprehensively reports all outcomes of a study compared to the minimalistic presentation of a single finding.

There is compelling evidence that many tests do, in fact, go unreported. As mentioned above, across scientific disciplines, 84% of all studies present positive support for their key hypothesis (Fanelli, 2010). Such a high success rate is impossible to obtain without selective reporting or biased attention that de-emphasizes non-significant findings or likely a combination of both (see Fig. 1G). Even if all tested hypotheses were true (which they are not), a statistical power of 84% (rarely ever achieved) would be required to yield

Table 1. Collection of problems and possible solutions

Section	Problems	Solutions
II.1	• Small sample size (e.g. data hard to obtain)	• Acknowledge preliminary nature • Multi-laboratory collaborations
II.1	• Novelty seeking	• Regard 'surprising' findings sceptically prior to replication
II.2*a*	• Multiple testing and selective reporting (e.g. due to too much trust in hypotheses, hindsight bias, pressure from referees)	• Avoid excessive testing (think before data exploration) • Keep track of number of tests conducted and report all tests • Bonferroni correction, false-discovery rate or emphasize preliminary nature of findings • Average effect sizes across conceptually similar tests • Referees and editors promote comprehensive and unbiased reporting
II.2*b*	• Multiple testing within models (stepwise model simplification)	• Report the initial full model • Global test of full model against null • Test a pre-determined subset of models • Average effects of individual variables across models
II.2*b*	• Overfitting of models (inflated significance)	• Keep $N > 3k$ for correct P-values, where k is number of parameters to be estimated ($N > 8k$ for reliable parameter estimates)
II.2*c*	• HARKing (hypothesizing after the results are known) and hindsight bias	• Preregister hypotheses • Keep track of number of tests conducted • Comprehensive reporting
II.2*d*	• Data collection ends with reaching $P < 0.05$	• Declare stopping rule • Adjust P-value for multiple testing
II.2*d*	• Discarding 'unsuccessful' experiments until an experiment 'works'	• Complete reporting of all experiments
II.2*e*	• Arbitrary decision in analysis (e.g. selective removal of outliers) are taken conditional on reaching significance (confirmation bias)	• Make decisions *a priori* (preregistration) • Ask colleagues to make decisions for you • Blinding yourself during data analysis • Specification-curve analysis: try all versions to examine robustness of findings
II.3	• Non-independence of data points (e.g. related individuals, temporal and spatial autocorrelation)	• Test for non-independence, autocorrelation • Fit grouping variables as random effects (intercepts, slopes, space, time, pedigrees) • Run analysis at the level where independence is met • Balance experiments for confounding effects
II.3*c*	• Overdispersed data	• Transform data • Control for overdispersion (random effects, quasi-likelihood)
II.4*a*	• Over-interpretation of apparent differences	• Test significance of interaction term • Test context dependence in follow-up study
II.4*b*	• Misinterpretation of regression to the mean	• Avoid allocating individuals to different treatment groups according to phenotype • Set up a control group • Model the expected effect
II.5	• Confirmation bias in data collection	• Blinding observers to treatment groups
III.1	• Lack of close replication studies	• Regard unreplicated findings as preliminary • Preferentially cite confirmatory replication studies as the most convincing evidence • Replicate own findings • Replicate important foundational studies as part of new research

♂ ♀	Time spent with females	Latency to pair × −1	Number of females	Female fecundity
Size of ornament	0.03	0.03	-0.02	0.11
Hue	-0.08	0.12	-0.18	-0.03
Saturation	0.07	-0.03	0.06	-0.15
Brightness × −1	-0.02	0.04	-0.07	0.07
Colour PC1	-0.06	0.05	-0.01	0.01
Colour PC2	0.06	0.23*	-0.11	-0.09

Fig. 2. A fictional table of correlation coefficients between measures of male ornamentation and measures of male success in pairing with females. The asterisk highlights a significant correlation. Some parameters were multiplied by −1, such that positive correlations indicate higher mating success for more ornamented males.

this rate of success. Hence, this means that most disciplines presumably sit on a huge pile of 'failed' experiments and unpublished null results that are inaccessible because they are hidden in the file-drawers of the experimenters [known as the 'file-drawer problem' (Rosenthal, 1979)].

In the following we will discuss various forms of multiple testing by giving typical examples to increase principle awareness of problematic situations.

(*a*) *The temptation of selective reporting*

Imagine you study mate choice in species xy, and you would like to understand why males of species xy have a colourful plumage ornament that is absent in females. Hence, on the side of males, you measure the size of the ornament as well as its colour in terms of hue, saturation, and brightness, and you also summarize the measures of the reflectance spectra in two principal component scores. To assess female choice, you measure how much time females spend close to each male, the latency for males to secure a female partner, the number of females each male sires offspring with, and the number of eggs laid by females after pairing with a male of a given ornamentation. You then look for positive correlations between the degree of male ornamentation and their success in attracting and pairing with females (Fig. 2).

The longer you look at this table of correlations with one association being significant, the more tempting it may become to convince yourself that, maybe, principal component analysis actually represents the most objective way of summarizing complex colour information, and that maybe the latency to pair is the most meaningful measure of male pairing success in this study species. Surely this significant finding must be a true positive effect, since why else would males have evolved these beautiful colours. Also the use of Bonferroni correction has often been criticized (Nakagawa, 2004) for being too conservative and leading to many false-negative outcomes (Type II errors). Hence, we might be tempted to publish only the association of 'latency to pair' with 'Colour PC1' and 'Colour PC2' without mentioning the remaining 22 null results (focussing on PC2 only without reporting on PC1 would be too extreme). We might not even perceive this as unscientific conduct because we have convinced ourselves of the biological and statistical logic behind our 'discovery'. As we convince ourselves that the biology is right, we presumably feel an obligation to share our discovery. Thus our personal focus on discovery motivates us to publish this as a positive finding. Humans are highly efficient at finding *post-hoc* justifications for their choices (Trivers, 2011) if those choices produce a more desirable outcome [positive results are likely easier to publish than null findings (Franco, Malhotra & Simonovits, 2014)].

When we selectively report only 2 out of the 24 correlations shown in Fig. 2, we often forget that the remaining 22 correlations actually represented equally valid tests of our hypothesis that greater ornamentation enhances mating success. A more objective approach would be to average the 24 correlation coefficients to yield an estimate of the overall effect of ornamentation. This can be done because all variables were coded in such a way that high values always refer to increased ornamentation and increased mating success, meaning that positive correlations count as support for the hypothesis. In our example, the average correlation between ornamentation and mating success is exactly zero (the mean of all positive and negative correlations is $r = 0.00$). Hence, if we started with the aim of objectively quantifying something (rather than discovering something) we should face less of a risk of misleading ourselves and our colleagues and of having wasted efforts for the short-term benefit of possibly publishing in a higher-ranking journal.

This hypothetical case clearly shows that 'data do not always speak for themselves'. Without knowing the context of why the author decided to focus on principle component analysis and on 'latency to pair', we cannot judge the statistical significance of the finding. We will explore other examples of deceiving statistical results below.

The literature on sexual selection acting on ornamental traits is plagued by this problem of potential selective reporting (not every study is biased, but there is no label that would identify unbiased reporting). Since we have no way of telling the extent of reporting bias, it is not clear how we could draw a general conclusion about the strength of sexual selection on ornaments from several decades of work (Parker, 2013). This illustrates how inefficient research can sometimes be if it fails to ensure maximal objectivity in reporting. Meta-analyses that summarize all published effects are not able to take into account these arbitrary decisions made by authors (Ferguson & Heene, 2012). Although any meta-analytic summary would certainly reveal a strong effect of ornaments on mating success, it is unclear whether or to what extent this is evidence for a theory as opposed to evidence of selective reporting driven by a theory. There are probably more than a few research areas where we might benefit from a new round of empirical investigation in which all results were made available. If we all begin now with studies adhering to a standard of unbiased reporting and we make such studies identifiable with the use of

badges (see Section III.3*b*), in a few years' time we could conduct meta-analysis comparing studies with and without such badges to confirm or refute our past work.

(*b*) *Cryptic multiple testing during stepwise model simplification*

A table like that shown in Fig. 2 immediately reminds researchers that they have to be aware of the issue of multiple testing. A much less obvious form of multiple testing happens when researchers fit complex models to explain variation in a dependent variable by a combination of multiple predictors. This has been termed 'cryptic multiple hypotheses testing' (Forstmeier & Schielzeth, 2011).

Imagine you are trying to explain variation in a variable of interest with a set of six possible predictors. Besides the six main effects that you are interested in, there is also the possibility that any pair of two predictors might interact with each other in influencing the dependent variable. To explore all these possibilities you start by fitting a rather complex full model where the dependent variable is a function of 6 predictors plus their 15 two-way interactions, and you then carry out a standard procedure of model simplification where, at each step, you always delete the least significant term from the model until you have only significant predictors (main effects or interactions) left in the minimal model. Such extensive data exploration minimizes the risk that you overlook a potentially complex combination of factors that affects your variable of interest. However, this widespread procedure (recommended by some standard statistical textbooks, e.g. Crawley, 2002) comes with a very high risk of Type I error. In a simulation study it was shown (Forstmeier & Schielzeth, 2011), that when all null hypotheses are true (using randomly generated data), the chance of finding at least one significant effect lies close to 70%). This means that most of the time you will be able to present a significant minimal model that seems to reveal an interesting pattern [see also Mundry & Nunn (2009) and Whittingham *et al.* (2006)]. Many researchers seem unaware that they have actually examined 21 different hypotheses at once, and that a Bonferroni correction of setting α to $0.05/21 = 0.0024$ would be required to keep the false-positive rate at the desired 5%.

This Bonferroni correction works reliably as long as the full model was built on a reasonably sized data set. However, when sample size becomes low relative to the number of parameters to be estimated, then the estimation of model fit and *P*-values becomes highly unreliable. This happens because a small number of data points can often be explained almost perfectly by a combination of predictors selected from a relatively large pool of predictors. For instance, if the same 6 main effects and their 15 two-way interactions are fitted to only 30 data points, the resulting minimal models are often excessively significant. As many as 26% of the minimal models cross even the Bonferroni-corrected threshold of $0.05/21 = 0.0024$, such that a much stricter correction to $0.05/286 = 0.00017$ would be required to ensure that only 5% of the minimal models pass that threshold. In other words, running through such an automated assessment of your six predictors and their two-way interactions by step-wise model simplification is expected to give you *P*-values that are as low as you would get from always picking the most significant among an incredible 286 hypothesis tests.

Surely, this is an extreme case where *P*-values are no longer correct (and not adjustable by Bonferroni correction) because they are derived from an over-fitted model. Simulations (Forstmeier & Schielzeth, 2011) revealed that *P*-values begin to become excessively small once there are fewer than three data points per predictor ($N < 3k$ with k being the number of parameters to be estimated). Regarding this result from the other side, the observation that *P*-values were correct (adjustable by Bonferroni correction) as long as there were more than three data points per parameter, does not imply that this sample size is sufficient in all respects. Statisticians often recommend that at least eight data points per estimated parameter should be available (e.g. $N > 8k + 50$; Field, 2005), and they would consider the over-fitting of models described in the previous paragraph a 'statistical crime'. However, when screening the literature in the field of ecology and evolution, Forstmeier & Schielzeth (2011) found that authors rarely described the initial full model that they had fitted. This means that the extent of multiple testing and of possible over-fitting could often not be reconstructed. Out of 50 studies examined, 28 used models with two or more predictors, 6 of which fitted between 6 and 17 effects, and 3 of which violated the rule to not over-fit ($N < 3k$). Moreover, and most strikingly, none of the 28 studies considered any adjustment of *P*-values for multiple testing (e.g. Bonferroni correction).

In some fields, iterative model building of the sort we just described has become less common, but what has replaced it is often not substantially better (Mundry, 2011). The replacement is typically a process by which researchers develop a set of 'plausible models' and evaluate them with measures of overall model fit (e.g. likelihood ratio) or fit accounting for the number of predictors [e.g. Akaike Information Criterion (AIC), or Bayesian Information Criterion (BIC)]. Researchers may then assess parameter estimates or tests of significance for individual predictors only in the 'best' model. Just as with an iterative procedure, it is unreasonable to assess the statistical significance of individual variables in the 'best' model without correction for multiple comparisons. Similarly, assessing the strength of effects in only the 'best' model is also likely to produce an inflated effect.

(*c*) *A priori hypothesis testing versus* HARKing: Does it matter?

The above approach of exploratory data analysis means that a fairly large number of hypotheses get tested in a very short time (i.e. without careful thinking about specific hypotheses considered plausible) and this comes with a high risk of drawing a false-positive conclusion if we only report on the subset of significant predictors. In fact, such exploratory analysis could be seen as an act of generating hypotheses rather than as an act of testing hypotheses, because you only start thinking about the respective hypothesis once you have discovered a significant association. This approach is not wrong *per se*, as long as you are aware and honest about the fact that the hypothesis was derived from the data.

The problem starts where researchers fail to acknowledge this. The psychologist Norbert Kerr called this 'HARKing' (hypothesising after the results are known; Kerr, 1998).

Yet, does it really matter in terms of likelihood of a positive finding being true whether we thought of the hypothesis *a priori* (i.e. before data inspection) and then use the data to test that hypothesis, or whether we came across the hypothesis only after having explored the data and having focused on only significant effects to begin with? Intuitively, we would probably think that *a priori* hypothesis testing is less prone to yield mistakes than 'fishing for significance' and HARKing, but is that intuition correct?

In both cases we would use exactly the same data set (and arrive at the same *P*-values), so for any given hypothesis, the statistical outcome appears exactly the same. Although this is true for any given hypothesis, fishing, HARKing, and hindsight bias often produce hypotheses that researchers never would have deduced from theory. Hindsight bias or the 'knew-it-all-along' effect (Fischhoff, 1975) is the phenomenon that, after having seen the results of data analysis, these results appear logical, inevitable, and in line with what we must have predicted before. Hindsight bias is particularly dangerous because we overestimate the plausibility of our hypothesis (which in fact is a *post hoc* explanation, a hypothesis that was derived from the data, not one that we had *a priori*).

Sometimes it is easy to spot unlikely hypotheses that were derived from the data. When the title of a publication starts with 'Complex patterns of…' and the main finding of the study consists of a difficult interaction between several explanatory variables, then this complex hypothesis may well have been derived from the data.

However, data exploration is not fundamentally a bad thing. In fact when conducted transparently, it is very useful. It may allow you to discover something for which theory has not even been developed yet, or you may actually correctly identify a complex pattern of interactions for which theory is too simplistic. Yet, the main problem with data exploration is that we normally do not keep track of the number of tests that we have conducted or would have been willing to entertain, so there exists no objective way of correcting for the extent of multiple testing (De Groot, 1956/2014). Once a discovery has been made ($P < 0.05$) and a plausible explanation has been found, it is very easy to deceive oneself into thinking that one actually had that hypothesis in mind before starting the exploration, and nothing seems wrong with writing up a publication saying 'here we test the hypothesis that…'.

The failings of this approach were explained long ago by De Groot (1956/2014) and they are strongly linked to points we have already made. In exploratory analyses, we are open to an array of possible relationships and resulting interpretations. As the array of possible detectable relationships expands, the likelihood that we might detect false relationships expands as well. Of course we may well also detect real relationships, but at this stage, we cannot distinguish what is false from what is real. We have generated a suite of hypotheses with our data exploration, and next we (or others in the years to come) need to gather additional data. With the new data, we should conduct only the very limited set of analyses designed to test the hypotheses derived from the exploratory work. Thus in this second round of data collection and analyses, we can operate with a much lower probability of detecting false positives. In other words, we test hypotheses rather than just generate them.

In some fields it is common practice to masquerade exploratory analyses as confirmatory hypothesis testing because exploratory work is often perceived as inferior or old-fashioned. In the distant past, data exploration was presented in the Results section, and its subjective interpretation was given in the Discussion section. Then biologists adopted (or at least pretended to adopt) Popper's idea about hypothesis testing, and in the process started to move their data-derived (*post hoc*) hypotheses to the Introduction so they could pretend they were testing *a priori* hypotheses. Unsurprisingly, when we 'test' a hypothesis with the same data that generated that hypothesis, it tends to be confirmed. In other words, you simply cannot 'cherry-pick' the hypothesis you wanted to test after having seen the outcome of statistical analyses (Fig. 3).

(*d*) *Researcher degrees of freedom: (1) stopping rules*

As promised earlier, we now return to the issue of 'researcher degrees of freedom' (Simmons *et al.*, 2011), which refers to researchers' flexibility in how to collect and how to analyse their data. One striking issue regards stopping rules for data collection. How do you decide that you have enough data? Say you are trying to test whether females of species xy prefer males that sing with a lower-pitched voice. Initially, you do not know how large such an effect might be, so you start by collecting data on 10 females, after which you conduct a simple regression test (pitch predicts female response to song). Now let's say you obtained a trend in the expected direction (slight preference for low-pitch voice), but the effect does not reach significance. You might suspect that the effect is real but small, and that you lacked statistical power to reach significance. You then collect data on another 10 females and then conduct your regression test again with all 20 females. Although the rationale behind such a sampling design seems perfectly understandable, the risk of making a Type I error has just risen from 5% to approximately 7.7 (Simmons *et al.*, 2011). This is because you gave the data two chances of reaching significance. Since the first data set is included in the second, these are not two fully independent chances (which would yield 9.75% false positives; $1 - (0.95 \times 0.95) = 0.0975$), so the combined risk of drawing a false-positive lies somewhere between 5 and 10% (this risk can be estimated from simulations). Thus, when decisions about sample size are not made *a priori*, and data sets are subject to iterative tests for significance as data accumulate, you must correct for multiple testing. The more often you stop data collection to check for significance, the greater your risk of a false positive. It is important to remember here that your decision to collect data on another 10 females was conditional on the first outcome. If you had obtained a statistically significant effect at the

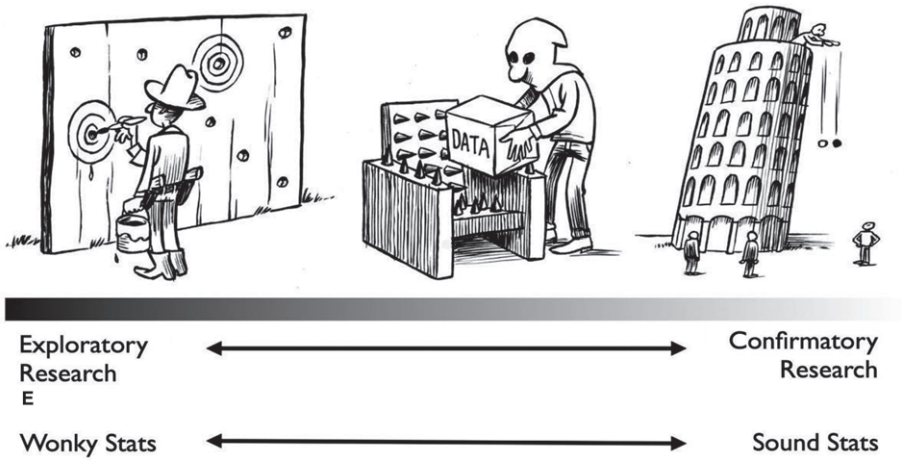

Fig. 3. The graded di stinction between exploratory, hypothesis-generating research and confirmatory, hypothesis-testing research (Wagenmakers *et al.*, 2012). On the right side of the continuum, a purely confirmatory test is conducted. The test is transparent, relevant hypotheses have been explicated beforehand, and a data analysis plan is present. This exemplifies the scenario of hypothesis-testing research. For this type of research – and only for this type of research – statistical tests have their intended meaning. On the left side of the continuum, a purely exploratory test takes place. The 'Texas sharpshooter' first fires at a fence, and then proceeds to draw the targets around the bullet holes. There is no prediction here – there is only postdiction. This scenario exemplifies the scenario of hypothesis-generating research. For this type of research, the resulting statistical tests (invented exclusively for hypothesis-testing research) are misleading, or, in Ben Goldacre's terms, 'wonky'. In between the two extremes lies a continuum where research is conducted that is partially confirmatory, typified by a degree of data massaging – in the figure, the data are 'tortured until they confess'. The statistical results are partially wonky. Unfortunately, it is far too easy to make the mistake of masquerading hypothesis generation as hypothesis testing. Most researchers, including the authors, admit to having done this (John *et al.*, 2012), either because of ignorance of the problem or because of self-deception [see Fischhoff (1975) and Trivers (2011)]. Figure courtesy of Dirk-Jan Hoek.

first try, you would presumably not have collected more data, but rather you would have concluded that the effect seemed to be large because it reached significance with only 10 females. In a scenario in which reaching statistical significance always triggers an end to data gathering, there is never an opportunity to discover whether a larger sample size might eliminate significance.

In a worst-case scenario where you keep testing after every sample until the expected effect reaches significance, you are certain to find the effect eventually, since *P*-values will undergo a random walk (Rouder *et al.*, 2009) and will at some point cross the 5% threshold (unadjusted for multiple testing). Our own (unpublished) simulations with randomly generated numbers show that you can expect to cross the threshold of significance within the first $N = 100$ in about 3 of 10 attempts (hence $\alpha = 0.3$ rather than $\alpha = 0.05$), although if you are willing to continue to sample indefinitely, you will eventually reach statistical significance in every single case (Armitage, McPherson & Rowe, 1969). Hence, continued sampling and a stopping rule based on reaching significance unambiguously elevates Type I error rates and thus we expect this to be one of the many factors leading to false positives in the literature. Fortunately, as researchers are increasingly becoming aware of this problem, it is slowly becoming good practice to specify one's stopping rule for sample size in the methods section of a publication.

In a wider context, the same issue of multiple testing applies to situations where researchers discard one or two initial experiments that were 'unsuccessful' (for instance because of a putative confounding factor that was not yet controlled) and then have full trust in the first experiment that yields the desired result.

(*e*) *Researcher degrees of freedom: (2) flexibility in analysis*

When analysing data, we face a wide variety of rather arbitrary decisions that we have to make, such as: (*i*) should I include covariate *x* in the model as a possible confounding factor, and should *x* be log-transformed or should I subdivide it into categories (and how many)? (*ii*) Should I include or exclude a particular outlier or an influential data point (high leverage)? (*iii*) Should I transform the dependent variable to approximate normality better, and which transformation should I choose? (*iv*) Should I add baseline measures taken before the start of the experiment as a covariate into the model in order to remove some noise in the data? (*v*) Should I control for sex as a fixed effect or also model a sex by treatment interaction term? (*vi*) Should I exclude individuals from the analysis for which the number of observations is low? (*vii*) Should I remove a third treatment category that seems unaffected by the treatment or should I lump it with the control group?

With all these decisions to make, there is again a risk of trying several versions (multiple testing) and of favouring the version that renders the more interesting story (selective reporting). Often, we may subconsciously favour the version

that minimizes the *P*-value for the effect of interest because we convince ourselves that this version must be the correct one or the most powerful one. Since we often believe that an effect of interest exists (and we designed the experiment to reveal the effect), we tend to have greater trust in analyses that confirm our belief. This powerful component of human nature is called confirmation bias, and it has been documented in a wide array of settings (Nickerson, 1998). Obviously, confirmation bias can render our science highly subjective unless we make all these arbitrary decisions *a priori* (if possible) or at least blind to the outcome. By contrast, exploratory analyses that are presented as confirmatory are always a threat to objectivity. Unfortunately, full disclosure of *post-hoc* decision making may often be quite challenging and requires substantial conscientiousness, but increased awareness of the issue is a first step towards mastering this challenge.

In an unpublished manuscript, A. Gelman & E. Loken called this 'the garden of forking paths', which nicely illustrates that there may be a near-endless diversity of combinations of decision variants. Simonsohn, Simmons & Nelson (2015) hence suggested an automated routine of going through all possible combinations of identified decisions in terms of their influence on the effect of interest (the effect at the heart of the 'story' of a publication; see also Steegen *et al.*, 2016). Simonsohn *et al.* (2015) call this routine 'Specification-Curve Analysis' (SCA), and they demonstrate its utility using the example of a recent study (Jung *et al.*, 2014) that led to some controversy about subjectivity in decision making. In that study there were seven decisions to be made, some of which had more than two options to choose from, leading to a total of $3 \times 6 \times 2 \times 2 \times 2 \times 4 \times 3 = 1728$ possible ways of analysis. SCA shows that only 37 out of these 1728 versions (2%) yield significant support for the prediction that Jung *et al.* (2014) evaluated and confirmed in their publication. A particularly problematic aspect of researcher flexibility is the decision to remove outliers after having seen their influence on the *P*-value. Selective removal of outliers has a high potential of generating biased results (Holman *et al.*, 2016), so the removal of data points is generally discouraged. Publications should always explain the reasons behind any attrition (loss of data points between study initiation and data analysis) and should discuss whether the missed samples might have led to biased results. Up to this point we have been dealing with the problem of multiple testing in all kinds of versions, and we have seen that this problem can be addressed by (*i*) limiting the number of tests conducted, and (*ii*) adjusting α-thresholds to keep the false-positive rate at some desired level. In all cases we assumed *P*-values to be calculated correctly. Yet, in the following chapter we will see that *P*-values are often incorrect (often too small), deceiving us into over-confidence in our result.

(3) Incorrect *P*-values

P-values indicate how often chance alone will produce a pattern of at least the strength observed in the experiment. Accordingly, for any given sample size, if $P = 0.05$ we might still be sceptical whether the pattern could have arisen by chance, but if $P = 0.0001$ we will probably be much more confident that we have discovered a true effect. However, this confidence is only justified if the statistical test that yielded the *P*-value was applied appropriately in the first place, but not if the data violated the assumptions that underlie the test. Statistical tests may have many underlying assumptions (e.g. normally distributed residuals), although many of these assumptions can be violated without drastic effects on the *P*-values. One assumption, however, is crucial for *P*-values, and that is the independence of data points. If data points do not represent true independent replicates but are grouped in clusters ('clustered data'; Weissgerber *et al.*, 2016), we speak of pseudoreplication, and this may lead to over-optimistically low *P*-values (Hurlbert, 1984). As we will see below, some kind of structure in the data leading to non-independence is ubiquitous. However, such structure only becomes a problem for testing the significance of a predictor of interest (e.g. treatment effect), if the samples are non-independent with respect to the predictor. The latter is what defines pseudoreplication.

There are many sources of non-independence of data: repeated measures from the same individual, measures from individuals that are closely genetically related to each other, and measures from species that are related through phylogeny are all non-independent of each other. Variation in space, for instance in territory quality, may introduce non-independence of measurements. The occurrence of a disease may vary not only in space, but also in time, just like data on daily weather or minute-by-minute data on whether a bird is singing will show temporal non-independence.

All these dependencies lead to problems in *P*-value estimation, the full extent of which is truly unknown. From own experiences as reviewer or editor of manuscripts we gained the impression that a substantial proportion of submitted manuscripts contain analyses that are clearly incorrect, and that the rate at which referees spot and eliminate these mistakes is not sufficiently high to ensure that the published literature would not contain numerous errors. Surely, awareness of the pseudoreplication issue is well developed in some areas like experimental design (Hurlbert, 1984; Milinski, 1997; Ruxton & Colegrave, 2010) or phylogenetically controlled analysis (Felsenstein, 1985; Freckleton, Harvey & Pagel, 2002). However, in some other fields, non-independence of data has been overlooked for an extended period of time because dependencies may be deceivingly cryptic (Schielzeth & Forstmeier, 2009; Hadfield *et al.*, 2010; Valcu & Kempenaers, 2010) and it seems likely that more such problems will get highlighted and become better known in the future.

Generally we feel that there is insufficient recognition of the extent to which incorrect *P*-values resulting from pseudoreplication have contributed to the current reliability crisis. We therefore provide a practical introduction into some aspects of pseudoreplication, starting from the most basic principle that most readers will already be familiar with and then exploring some less-obvious and more-specialized examples. Those who feel sufficiently versed in statistics could

skip the remainder of Section III.3, while the less experienced may want to go through the examples that we provide.

(*a*) *Pseudoreplication at the individual level*

Imagine an experiment where you want to test whether females lay larger eggs when mated to an attractive male compared to an unattractive male (differential allocation hypothesis; Sheldon, 2000). For that purpose you experimentally enhance or reduce the ornamentation of males of species xy, and you measure the size of the eggs that females lay when paired to such males. You have 6 females, each of which you pair to a different male with enhanced ornamentation, and 6 different females each assigned to a different male with reduced ornamentation, and for each of the 12 females you measure the size of 5 eggs (60 eggs in total; see Fig. 4). The five eggs that come from the same female are obviously not independent of each other (i.e. they are pseudoreplicates with respect to the treatment) and this is problematic, because females are rather consistent in laying eggs of a certain size (Fig. 4).

If this non-independence is ignored, and you test the 30 eggs from 'enhanced' against the 30 eggs from 'reduced', you will get a highly misleading $P = 0.002$ in this case [R-code: glm(egg_mass~treatment)]. Note that this *P*-value would be correct if you had had 30 independent females in each treatment group and if you had measured only one egg from each of them. In the present case, you can either eliminate pseudoreplication at the level of individuals by calculating mean egg size per female and testing the six 'enhanced' means against the six 'reduced' means which yields $P = 0.10$ [R-code: glm(mean_of_egg_mass~treatment)], or you can account statistically for the non-independence by fitting female identity (ID) as a random effect ('random intercepts') in your model [R-code using the lme4 package (Bates *et al.*, 2014): lmer(egg_mass~treatment+(1|female_ID))], which should yield about the same *P*-value as the first option (here $P = 0.07$). Thus, it is important to acknowledge that, in this example, the effective sample size is 6 females rather than 30 eggs per group. Therefore, always make sure to choose the correct unit of analysis (where independence is ensured), or make sure to identify sources of non-independence and to model them correctly as random effects (watch out for repeated measures on the same individual). Cases of such overt pseudoreplication have become rare in the literature, but they still persist in some research areas.

However, there is a risk of making another mistake, less often spotted. After obtaining a non-significant result ($P = 0.07$) from testing the *a priori* hypothesis that females would lay larger eggs for 'enhanced' males, it is tempting to use the data set for further exploratory analysis. Maybe the treatment effect will come out more clearly if we also consider the order in which the five eggs of each female have been laid (laying order).

In our example, egg mass typically increases from the first to the fifth egg (Fig. 5). We do not know the function (the adaptive value) of this increase, but we could speculate that it mitigates competitive conditions for the last-hatching chicks. We also notice that the increase in egg mass over the laying sequence appears to be steeper for the 'enhanced' group (Fig. 5). We therefore test whether the treatment interacts with laying order in its effect on egg mass [R-code using the lme4 package: lmer(egg_mass~treatment* laying_order+(1|female_ID))], and indeed the interaction term seems significant ($P = 0.042$). This specification of the model has been widely used, but it is in fact incorrect and may yield 30% false-positive outcomes for the treatment by laying order interaction term (Schielzeth & Forstmeier, 2009). So where is the mistake?

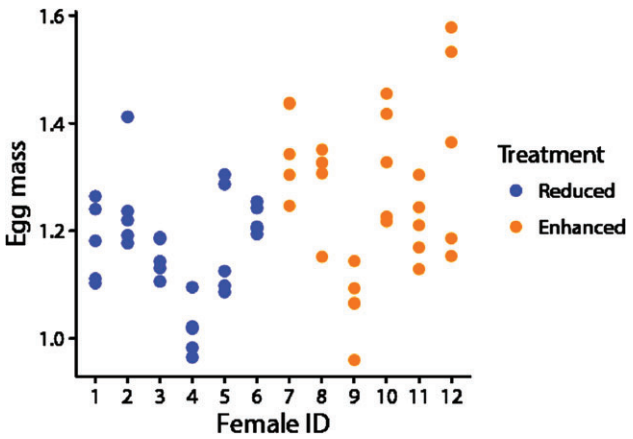

Fig. 4. Pseudoreplication at the individual level: different intercepts. Fictional data on egg mass of 5 eggs from each of 12 females, half of which were assigned to a male with experimentally enhanced ornamentation and half to a male with reduced ornaments. Individual females differ in their mean egg mass (12 different intercepts).

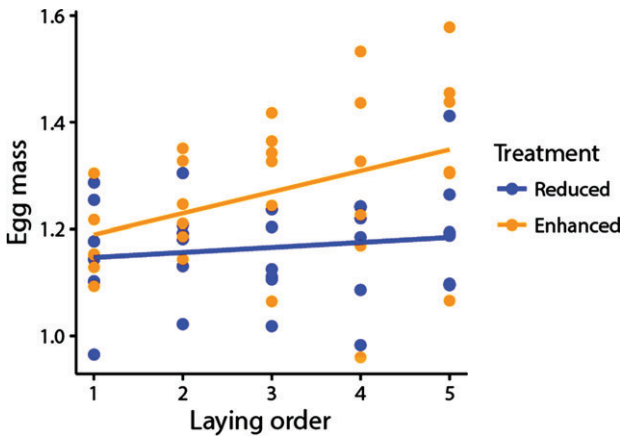

Fig. 5. Pseudoreplication at the individual level: different slopes. Fictional data on egg mass from Fig. 4, but this time plotted against the order in which the five eggs from each female were laid. Egg mass appears to increase more steeply in the 'enhanced' group (compared to the 'reduced' group), but statistical testing requires specification of female-specific slopes (six 'enhanced' *versus* six 'reduced' slopes).

Note that we have shifted our interest from testing for a treatment main effect (Fig. 4) to testing for a treatment by laying-order interaction, i.e. a difference in slopes between treatments (Fig. 5). The former requires modelling of individual-specific intercepts [R-code lme4: (1|female_ID)], to acknowledge correctly that we are actually testing only six *versus* six intercepts. The latter, testing for a difference in slopes, requires modelling of individual-specific slopes [R-code lme4: (laying_order|female_ID)], to acknowledge correctly that we are actually testing only six *versus* six slopes. Again, the mistake is to think that you could use all 30 eggs from 'enhanced' for calculating the 'enhanced' slope (and the other 30 for the 'reduced' slope) as if they were fully independent of each other. In fact, each female has its own slope that you could calculate and then do a *t*-test of six *versus* six slope estimates, and, given the small sample size, this will rarely reach significance. Indeed, when the full model is specified correctly [R-code using lme4: lmer(egg_mass∼treatment* laying_order+(laying_order|female_ID))] the *P*-value for the treatment by laying-order interaction is clearly non-significant ($P = 0.22$).

Again, make it clear to yourself which hypothesis you are testing (a difference in slopes), and what the independent units are (female-specific slopes) for testing that hypothesis. As in the earlier example (Fig. 4) where you had the option of eliminating pseudoreplication by calculating mean egg mass of each female, you here have the same option of calculating a slope for each female and doing the testing on the derived statistic. Yet in reality, not every female will lay exactly five eggs, so the derived statistic (mean or slope) will vary in its precision among females (most uncertain for females that lay only two eggs). In that case, the method of choice is to fit a model with the appropriate random-effects structure that accounts for all non-independence in the data that is relevant for hypothesis testing.

(*b*) *Pseudoreplication due to genetic relatedness*

In the previous section we focussed on repeated measures within individuals that were obviously not independent of each other. In this section we consider only one measurement per individual, but focus on how individuals can be non-independent of each other because of kinship (Hadfield *et al.*, 2010). This is most often a problem in observational studies, and less so in experimental studies, because the latter allow us to e.g. split up a pair of brothers into the two treatment groups (making the confounding structure in the data independent of the predictor of interest).

When working with animals that you breed yourself in captivity, you rapidly begin to realize that individuals are not independent of each other. Not surprisingly, pairs of siblings tend to be more similar to each other when compared to less-related individuals (Burley & Bartels, 1990). For instance, you may find that across all individuals there is a significant positive correlation ($r = 0.68$, $P = 0.021$) between two phenotypic traits, here male body mass and male courtship rate (Fig. 6).

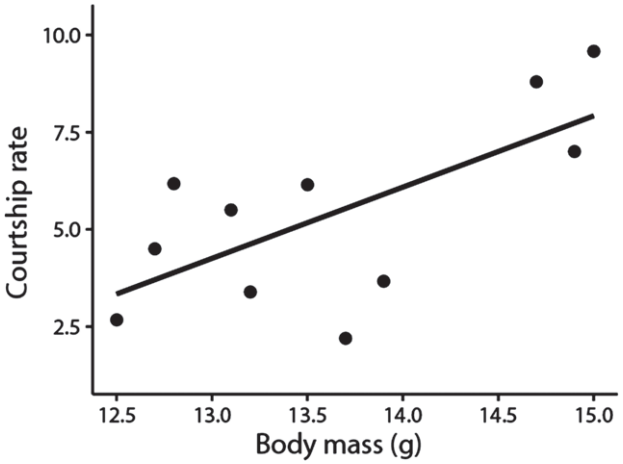

Fig. 6. Pseudoreplication at the family level. Fictional data showing the rate of male courtship ($N = 11$ males) as a function of male body mass ($r = 0.68$, $P = 0.021$). Note that significance may be overestimated if the three males on the right come from the same family that happens to carry alleles for high mass and high courtship rate.

However, the statistical significance of that relationship may have been overestimated if the 11 data points are non-independent. Both phenotypic traits (mass and courtship rate) are partly genetically inherited, and it might be the case that the three males with the highest body mass and highest courtship rate are three brothers. If this is the case, we need to fit family identity as a random effect into the model [R-code lme4: lmer(courtship∼mass+(1|family_ID))] and let's say that the other eight males come from eight independent families. This changes the *P*-value for the effect of mass on courtship rate from $P = 0.021$ to 0.084. This is still a trend, but one that is more likely to have come about by chance, and so we should not have too much confidence that we will observe the same pattern in other males. Some researchers may argue that correcting for pseudoreplication is misguided in this case since it could mask a real relationship among these individuals. If the goal were only to describe the pattern in this population of 11 males, then we would agree. However, if we wanted to predict the likely pattern in other populations or in the species in general, we want to avoid being misled by chance associations driven by relatedness among individuals in our sample (in which case $P = 0.084$ is a more realistic estimate of the probability that the observed pattern arose by chance alone).

In the above example, relatedness may lead to inflated significance because both the dependent variable (courtship rate) and the predictor (body mass) are partly genetically inherited. This confounding effect gets even larger when the predictor is inherited entirely, as the next example will show. Let's say we study male courtship rate in zebra finches (*Taeniopygia guttata*) in relation to alleles at genes that are good candidates for affecting courtship rate (so-called phenotype–genotype associations). We find that a particular allele (ESR1_10) at the oestrogen receptor locus (ESR1)

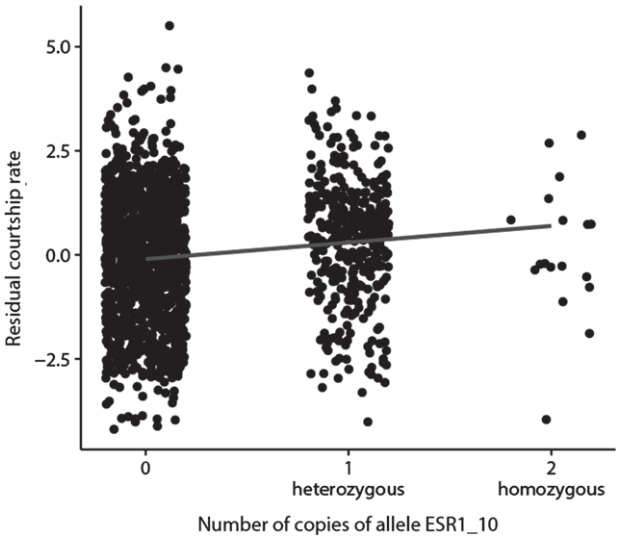

Fig. 7. Average courtship rate (corrected for between-generation differences) of 1556 male zebra finches as a function of the number of ESR1_10 alleles they carry. Jitter was added to the *x*-axis in order to increase the visibility of data points. The regression line ($y = 0.4x - 0.1$) indicates by how much courtship rate increases per gene copy, explaining 1.4% of the total variance.

was associated with increased male courtship (Forstmeier, Mueller & Kempenaers, 2010).

If we assume statistical independence of the 1556 males from our captive zebra finch population (comprising seven generations of birds) and model courtship rate as a function of the genotype as illustrated in Fig. 7 we obtain a remarkably significant *P*-value of $P < 10^{-15}$ [R-code: glm(courtship∼ESR1_10_copies)]. If we fit family identity as a random effect into this model [R-code lme4: lmer(courtship∼ESR1_10_copies+(1|family_ID))], where family_ID groups together all full-brothers that come from the same parents within each generation, the model yields $P < 10^{-9}$, still a remarkably significant effect. However, this coding of families accounts for non-independence of brothers within generations, but ignores that both alleles and behaviour are passed on longitudinally from father to sons, making the corresponding family groups similar in terms of alleles and behaviour. Hence, to account for all genetic relationships, we need to fit the entire seven-generations pedigree as a random effect into a so-called 'animal model' [R-code for the pedigreemm package (Vazquez *et al.*, 2010; Bates & Vazquez, 2014): pedigreemm(courtship∼ESR1_10_copies+(1|animal))]. Soberingly, this analysis yields $P = 0.015$ for the effect of this allele on courtship rate. Maybe this effect is still real, but the exceedingly high confidence we had from the initial analyses was unwarranted. As an aside, another lesson here is that *P*-values are not useful for indicating strength of effect. *P*-values here varied dramatically based on effective sample size, but any effect of these alleles on courtship rate was always weak as indicated by the r^2 value (0.014).

What is most disturbing about the problem of non-independence driven by relatedness is that the problem would be much harder to fix when studying a population of animals in the wild (if relatedness is also high there). If pedigree information is unavailable, we could genotype each individual at say 10000 single nucleotide polymorphism (SNP) markers, run a principal component analysis over these data, and fit the principal components as fixed effects to control for patterns of relatedness in this wild population (Price *et al.*, 2006). If we went through this trouble, we might discover that a promising-looking phenotype–genotype association has entirely evaporated in terms of its statistical significance. This would no doubt be very disappointing, but learning that this pattern is unreliable should save us from wasting money on other expensive follow-up projects that would have been built on an unreliable foundation.

(*c*) *Pseudoreplication due to spatial and temporal autocorrelation*

Above we have considered the case that individuals yield non-independent data points because they are influenced by the same genetic effects (shared alleles). Besides the effects of genetics, individual phenotypes are influenced by numerous environmental factors. Such environmental factors typically vary in space and time, so individuals that are close to each other in space and time will often share the same effects and hence will be more similar to each other (non-independent). Any such shared influences will create spatial and temporal autocorrelation in the data. To examine those, you may want to consider sorting your data either by time or in space and checking the extent to which the preceding measurement predicts the following one (this can be easily done by copying your *y*-variable column into a new column but shifted down by one row, and then quantifying the correlation between the columns). However, remember that other confounding factors (like repeated measures on the same individual) can induce the illusion of temporal autocorrelation if subsequent measures are typically from the same individual. If you find autocorrelation in your data, you may want to consult some of these references for methods of accounting for non-independence (Cliff & Ord, 1981; Valcu & Kempenaers, 2010; Dale & Fortin, 2014).

When designing an experiment, it is always good to consider the possibility of temporal and spatial non-independence, because this will remind you to allocate your treatments carefully (blocking is often better than randomizing). You obviously should not locate all your nutrient-enrichment plots in one field and your control plots in another field. For the same reasons, you should not put the cages holding the 'enhanced' males close to the room window and the 'reduced' males on the corridor side. Although it may not be the case that daylight will affect egg size, this will nevertheless put you into a situation where you lose all power to detect a treatment effect, because you need to control for the distance to the window as a covariate, which will be strongly collinear with your treatment and hence the two potential effects will be difficult to tease apart. Likewise, putting all males of one treatment category into one aviary

and all males of the other category into another aviary, will leave you with $N = 1$ *versus* $N = 1$, because you need to control for the effect of aviary identity as a random effect.

Temporal non-independence of events also often leads to the phenomenon of data being 'overdispersed'. This means that extreme values are more frequently observed than would be expected from chance alone. For instance, subsequent eggs are often more alike, not only in size (Fig. 5) but also with regard to paternity. Studies of female promiscuity that measure the proportion of eggs within a clutch that is sired by an extra-pair male typically observe that extreme outcomes (0 or 100% of extra-pair young) are more frequent than expected by chance (Neuhäuser, Forstmeier & Bretz, 2001). Such overdispersion in the data needs to be accounted for; otherwise this will again result in anti-conservative *P*-values. For this, the sequence of eggs does not have to be known, and using clutch identity (unique code for every clutch) as a random effect will typically help solve the issue. Hence, overdispersion may be easy to account for in cases where we understand the source of non-independence (here clutch identity). Another way of correcting for overdispersion is through the use of quasi-likelihood models (Wedderburn, 1974).

A final mistake related to overdispersion that one can sometimes observe is that measurements of latency (e.g. the number of seconds that a bird takes to return to its nest) are modelled as a Poisson trait (for count data). Rather obviously, subsequent seconds are not statistically independent events, and hence the data will typically be strongly overdispersed. Also, when you compare different options, you will see that *P*-values will strongly depend on whether you counted the time in hours, minutes, seconds, or even milliseconds. An example is shown in Fig. 8, where the latency to return to the nest is analysed as a function of a measure of the bird's exploratory behaviour.

What is striking about this example (adopted and modified from an unpublished study) is that a remarkably shallow regression line compared to the total range of variation is accompanied by a *P*-value of $<10^{-7}$. In this example, each minute gets evaluated as an independent event, and a few very high values on the left side (up to 559 min) cause all the apparent statistical significance. If the same data are modelled (again wrongly) as counts of hours (ranging from 0 to 9), we arrive at $P = 0.078$ although the data look almost the same [R-code: glm(hours∼exploration, family = 'poisson')]. Latencies can often be transformed into a nice normal distribution by taking the logarithm of the number of minutes or seconds [here the choice does not really matter, but note that ln(0) is not defined]. Modelling the natural logarithm of the number of seconds as a Gaussian trait, we obtain $P = 0.26$, which fits the impression of a weak trend given by Fig. 8 [R-code: glm(lnsec∼exploration)].

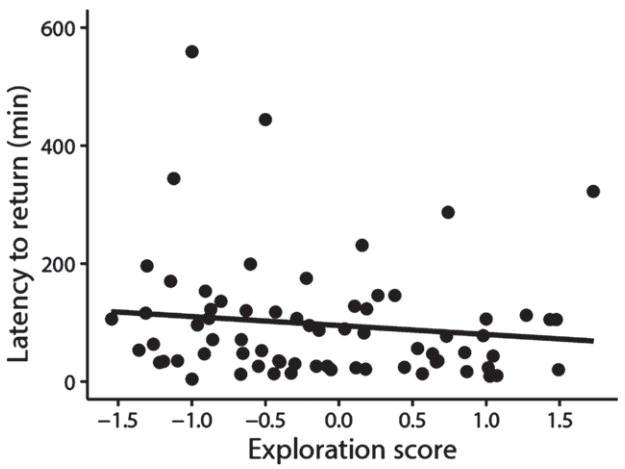

Fig. 8. Fictional data on the latency of 70 birds to return to their nest after disturbance as a function of their exploratory behaviour recorded in another test. The line is based on ordinary least-squares regression on untransformed data.

(*d*) *Pseudoreplication renders* P*-curve analysis invalid*

Simonsohn *et al.* (2014) recently suggested that one could examine the subset of all published *P*-values that reach significance ($P < 0.05$) in order to find out whether a true effect exists or not (referred to as '*P*-curve analysis'). In the presence of a true effect, *P*-values between 0 and 0.01 should be more frequent than *P*-values between 0.04 and 0.05, i.e. there should be an excess of highly significant *P*-values. Hence, right-skewed *P*-curves have been suggested to be evidential for true effects (Jager & Leek, 2014; Simonsohn *et al.*, 2014). However, if genetic relatedness and temporal or spatial autocorrelation are ubiquitous in real data sets, and often lead to pseudoreplication that remains unaccounted for (e.g. because relatedness is unknown), then such pseudoreplication will cause an excess of overly significant *P*-values that renders invalid such interpretation of right-skewed *P*-curves as evidence for a true effect. The assumptions of *P*-curve analyses are almost certainly seriously violated in multiple other ways as well and so unfortunately this briefly promising method for assessing biased reporting cannot fulfil expectations (Gelman & O'Rourke, 2014; Bishop & Thompson, 2016; Bruns & Ioannidis, 2016).

(4) Errors in interpretation of patterns

(*a*) *Overinterpretation of apparent differences*

Humans have a tendency readily to recognize patterns, even where none exist. This may be partly enhanced by binary thinking in terms of effect (if $P < 0.05$) *versus* no effect (if $P > 0.05$). Accordingly, one can also find this as a common mistake in the scientific literature: the title of a paper may claim that 'sexes differ in their response to a treatment', but the study only found that an effect was significant in males and non-significant in females. This does not mean *per se* that the sexes are actually different. Whether the difference itself reaches significance has to be assessed by testing the sex by treatment effect interaction term (Gelman & Stern, 2006). Only if the *P*-value for that interaction passes the threshold of $P < 0.05$ can we conclude that the sexes differ significantly in that treatment effect on whatever the dependent variable was.

Likewise, there is often a tendency to jump prematurely to the conclusion that the findings of two studies are different. Are they significantly different? Not very intuitively, a parameter estimate from a replication study has a probability of about one in six (16.6%) to fall outside the 95% confidence interval of the estimate from the initial study (Cumming, Williams & Fidler, 2004). This may come as a surprise, because one may think that the 95% confidence interval should contain 95% of the replication results (Cumming *et al.*, 2004). However, the 95% confidence interval is defined in a way that it contains the (typically unknown) true value of the parameter with a probability of 95%. And while the true value is a fixed number, both the estimate from the first study and the estimate from the second study come with uncertainty. This means that either the first or the second study could have yielded an unlikely (unusually extreme) outcome, so the probability that they agree is lower than the probability of one estimate agreeing with the fixed true value. Again, a formal test for the study by effect interaction term will inform you correctly about the probability of obtaining such a difference between two studies by chance alone. So make sure you are not over-interpreting a difference that may not be real.

(*b*) *Misinterpretation of measurement error*

There is one final statistical phenomenon that we would like to highlight: 'regression to the mean' (Barnett, van der Pols & Dobson, 2005). Although it is not related to any of the examples above, it is a sufficiently common trap and has led to errors in a wide range of scientific disciplines (Kelly & Price, 2005; Danchin, Wajnberg & Wagner, 2014). Moreover, since the regression to the mean will consistently produce a spurious but often significant effect, and since we typically publish when encountering something significant, one can readily find erroneous interpretations of this artefact in the literature.

'Regression to the mean' is a phenomenon that results from measurement error. Say we measure a group of individuals once (e.g. we measure, with some error, the attractiveness of individuals), and then divide them into two groups according to the first measurement, namely those that lie above the mean (attractive half) and those that lie below the mean (unattractive half). If we then measure the individuals from the two groups a second time, we can predict that the two group averages will deviate less from the population mean than in the first measure (hence 'regression toward the mean'; i.e. the attractive group will become less attractive, while the unattractive group will become more attractive). Figure 9 illustrates the origin of this effect.

Regression to the mean leads to an apparent systematic change in the phenotype of the individuals (on average, the orange dots in Fig. 9 decreased and the blue dots increased their trait values from first to second measurement). This change has often been misinterpreted as resulting from an experimental treatment that was also applied between the first and the second measurement. When we know the expected amount of measurement error that is inherent to each measure (i.e. 1 − repeatability), we can make predictions about the expected magnitude of regression toward the mean, and we can test whether the experimental treatment had any additional effects beyond this statistical artefact (Barnett *et al.*, 2005). However, in practice one should avoid such situations whenever possible (Danchin *et al.*, 2014). Hence, the rule

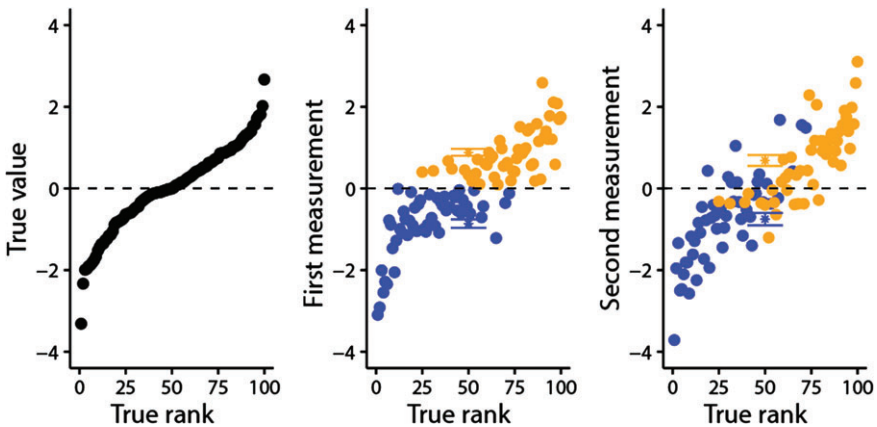

Fig. 9. The panel on the left shows the true trait values of 100 individuals sorted by their rank in trait values. In practice, such true trait values are unknown, and we can only measure trait values with some measurement error (central panel). If we then assign individuals into categories ('below average' in blue and 'above average' in orange) based on our first measurement, we make some misassignments with respect to their true ranks (e.g. some with true rank >50 get assigned to the 'below average' group). A second measurement on the same individuals will again approximate the true values with equal amount of error, but most of the previously misassigned individuals and some of the correctly assigned ones will this time fall on the other side of the population average. As a consequence, the means for the two groups (blue and orange asterisks) will move closer together (and closer to the population average). Also note how the standard errors around the two group means (indicated by horizontal bars) increase from the first to the second measurement because values can now vary over a wider range (no longer restricted by the 'definition' of having to lie above or below the average).

should be 'never assign individuals to different treatments according to their phenotype!' If you cannot come up with a better experimental design, you should at least be aware of the phenomenon, i.e. you should expect that the more aggressive individuals will become less aggressive when measured again, and that the previously preferred option in a choice test will become less preferred next time.

(5) Cognitive biases

Somewhat surprisingly, it appears that the human brain has not evolved to maximize the objectivity of its judgements (Haselton, Nettle & Murray, 2005). Accordingly, psychologists have described a near-endless list of cognitive biases that influence our perception, reasoning and memory. In Table 2 we have compiled a selection of biases which should also have an impact on the judgements made by scientists. Of these, we have already discussed the hindsight bias in Section II.2*c*, which makes it sometimes difficult to recall whether a hypothesis was derived from the data or whether the test was planned *a priori*. We further have touched on confirmation bias in Section II.2*e* when discussing how wishful thinking may influence our arbitrary decisions on how to analyse our data. Another form of confirmation bias is worth mentioning, namely that preconceptions may influence our observations ('observer bias'). In other words, if an observer expects a treatment to produce a certain measureable effect, the observer's measurements may be unconsciously biased towards detecting that effect. This bias can be minimized by 'blinding' observers to the hypotheses being tested or to the treatment categories of the individuals being measured. However, blinding is rare. For example, in a collection of 79 studies of nest-mate recognition in ants, just 29% of the studies were conducted blind. This rarity of blinding appears to have seriously impacted observations since non-blind studies were much less likely (21%) to report aggression among nest-mates than blind ones (73%), leading to a twofold overestimation of effect size (van Wilgenburg & Elgar, 2013). In 83 pairs of evolutionary biology studies matched for type of experiment, non-blind studies had substantially larger effect sizes than blind studies (mean ± S.E. difference in Hedges' $g = 0.55 \pm 0.25$), and the non-blind study had a higher effect size than its matched blinded experiment in significantly more cases (Holman *et al.*, 2015). Comparisons with much larger samples lend considerable support to these observations. In 7644 papers identified *via* automated text mining (from 4511 journals in the Open Access collection of *PubMed*), the proportion of significant *P*-values in a paper was significantly lower in blind than in non-blind papers (Holman *et al.*, 2015). Among a sample of 492 papers from the disciplines of ecology, evolution, and behaviour published in high-impact-factor journals in 2012, 248 presented studies 'that could have been influenced by observer bias'. However, only 13% of these studies appeared to have gathered data through a blind process (Kardish *et al.*, 2015).

If we recognize our cognitive biases as fundamental to our nature rather than as character flaws to be ashamed of, we can structure our scientific endeavours in ways to minimize their effects. We blind observers not because observers are

Table 2. A collection of cognitive biases that may hinder objectivity of researchers. Names and explanations were adopted from Wikipedia (www.wikipedia.org) and inspired by a compilation of 175 cognitive biases by Buster Benson (https://betterhumans.coach.me/cognitive-bias-cheat-sheet-55a472476b18)

Bias	Explanation
Confirmation bias	The tendency to search for, interpret, favour, and recall information in a way that confirms one's pre-existing beliefs or hypotheses, while giving disproportionately less consideration to alternative possibilities
Selective perception	The tendency not to notice and more quickly forget stimuli that cause emotional discomfort and contradict our prior beliefs
Bias blind spot	The cognitive bias of recognizing the impact of biases on the judgement of others, while failing to see the impact of biases on one's own judgment
Confabulation	The production of fabricated, distorted or misinterpreted memories about oneself or the world, without the conscious intention to deceive. This may help us in making sense of what we see
Clustering illusion	The tendency to erroneously consider the inevitable 'streaks' or 'clusters' arising in small samples from random distributions to be non-random
Illusion of validity	A cognitive bias in which a person overestimates his or her ability to interpret and predict accurately the outcome when analysing a set of data, in particular when the data analysed show a very consistent pattern – that is, when the data 'tell' a coherent story
Belief bias	The tendency to judge the strength of arguments based on the plausibility of their conclusion rather than how strongly they support that conclusion. This is an error in reasoning, such as accepting an invalid argument because it supports a conclusion that is plausible
Hindsight bias	The inclination, after an event has occurred, to see the event as having been predictable, despite there having been little or no objective basis for predicting it
Overconfidence effect	A bias in which a person's subjective confidence in his or her judgments is reliably greater than the objective accuracy of those judgments
Appeal to novelty	A fallacy in which one prematurely claims that an idea or proposal is correct or superior, exclusively because it is new and modern

dishonest, but because we know that we all have a tendency to see what we expect to see. We preregister analysis plans only because we know that even people with the purest conscious motives are more likely to choose the method that produces the story that they most believe.

III. SOLUTIONS

(1) Need for replication and rigorous assessment of context dependence

In face of the problems that we have outlined above (multiple testing including researcher degrees of freedom, pseudoreplication, selective reporting, and HARKing), it is clear that we should be fastidiously sceptical consumers of published scientific results. Given publication bias in favour of positive results and given the rather soft criteria for reaching significance, it is currently possible to find positive 'evidence' in the scientific literature for almost any possible phenomenon. If you recognize this, you presumably will also recognize that the extreme pursuit of novelty (by high-impact journals) and researchers' pursuit of impact (imposed by employers and funding agencies) will contribute to an ever-increasing body of false-positive claims that hampers scientific progress (Ware & Munafo, 2015).

Hence, we need to promote scepticism of spectacular but highly unlikely claims and turn attention to sorting out all the false-positives from the true positives. How can this be done? As we have seen, we can use a variety of clues to identify findings that are less likely to be true, but what we really need is a rigorous method of assessment in the form of well-controlled and standardized attempts to closely replicate previous studies (Nakagawa & Parker, 2015). Further, institutions need to favour the publication of the results of replication independent of their outcome. To see the utility of unbiased replication attempts, we can look to the recent coordinated effort to replicate 100 findings published in top journals in the field of psychology (Open Science Collaboration, 2015). This large-scale initiative found that about 40% of the findings appear to hold up (reminding us of Fig. 1F), while most of the remainder were contradicted or not supported (but see Etz & Vandekerckhove, 2016). The high statistical power of most of the replications lend strength to the conclusion that many of the original studies were either the result of error or were more dependent on subtle differences in context than had been assumed.

(*a*) *Obstacles to replication*

In face of the request for novelty, researchers often address a commonly asked question in a new species or with new methods. However, in such quasi-replications (Palmer, 2000), if results differ from the original, we are left to speculate about why the outcomes differed and we will rarely be able to identify the true reason for the difference in outcomes, because quasi-replicates differ in so many aspects. Close replication, by contrast, minimizes differences among studies and facilitates the identification of plausible hypotheses to explain divergent results. Unfortunately, close replications are rare in many disciplines (Palmer, 2000; Kelly, 2006; Drotar, 2010; Nakagawa & Parker, 2015). There are two interrelated explanations for this. First, many researchers have not yet come to appreciate the important role of replication in developing robust scientific inference, and second, the institutions that influence scientists' choices do not reward close replication (Nosek, Spies & Motyl, 2012).

Funding agencies and journal editors focus on novelty. This is particularly hard to justify on the part of funders since failing to invest in replication means failing to seek robust answers to questions they already have made a commitment to answering. If the answer truly was worth paying for, then the replication should also be worth paying for (Nakagawa & Parker, 2015). Promoting the funding of replication studies would be relatively straightforward. Most obviously, agencies could set aside funds for important and well-justified replications. Agencies could also incentivize replication by preferentially funding novel studies when those studies rest on well-replicated foundations (Parker, 2013). They could also preferentially fund researchers whose prior work has often been successfully replicated.

In the case of journals, pursuit of novelty may be harder to curb, but there are paths to reducing the tyranny of this pursuit. Journals seek novelty in part because of the competition for impact factors. Studies which report surprising (i.e. unlikely) findings are often highly cited and thus contribute to the stature of the journal. Thus, 'the more surprising, the better'. This effect may be exacerbated by the for-profit publishing industry. Fortunately, replications can also be heavily cited. Recent attempts to replicate classic studies in psychology have received citations at a much higher rate than the average study in the journal in question. In 2014, the journal *Social Psychology* published an issue (issue 3, May) devoted to replications of previously published studies. As of 15 March 2016, the mean number of citations from those 15 replications (of 15 different earlier studies) was 7.1 (median = 4, with no articles having gone uncited). By the same date in 2016, the average article from the previous two issues (1 and 2 from 2014), including no replications, had received 1.2 citations (median = 1, with 5 of 12 articles remaining uncited). Of course this may be in part due to the current novelty of replication research (ironically). However, robust, well-conducted replications of important work will presumably attract considerable attention in the future, especially as awareness grows about the importance of replication in assessing validity of prior work. We expect that as more journals explicitly invite replications (as some are beginning to do), more researchers will come to recognize their utility, and thus researchers will more often seek to cite replications because of the strong inferences they facilitate.

Even without institutional obstacles, there are important social obstacles to navigate. An attempt to replicate closely someone else's finding may be perceived as a personal attack on the original researcher. The very act of replication implies

insufficient confidence in the original findings, and in cases of failure to confirm the original finding, the researcher who published the original study may fear for his or her reputation (although we expect this phenomenon to be less common as replications become more frequent and failure to get confirmed is recognized as normal). Journals almost invariably ask the author of the previous study to review the replication manuscript since he or she is the expert and is directly concerned. This reviewer will often be predisposed to be negative, sometimes trying to save his or her own results by questioning the quality of the replication (e.g. making the case that an incompetent person will often fail to get the correct result; Bissell, 2013). Thus it may often be difficult to publish a replication, especially when that replication contradicts earlier work, and this is a strong disincentive to replicate.

(*b*) *Overcoming the obstacles*

A partial solution to this dilemma could come from researchers replicating their own findings. This eliminates the quality issue as well as issues related to dissimilarity in materials or methods. A simple and cheap way of getting this started was suggested by one of our colleagues, Jarrod Hadfield (Hadfield, 2015). He proposed that researchers running long-term studies could publish addenda to their previous publications, declaring in a one-page publication that their original finding did or did not hold up in the data of the following years (after the publication), and comparing the effect sizes between the original data and the newer data. This would be a quick way of producing another publication, and it would be enormously helpful for the scientific field. This may also relax the feeling of stigma when something does not hold up to future evaluation. Admitting a failure to replicate could actually be perceived as a signal of a researcher's integrity and be praised as a contribution to the scientific community. For grant applications, funding agencies could even specifically ask for visible signs of such integrity rather than exclusively focussing on metrics of productivity and impact.

Apart from publishing addenda, how should we go about conducting replication studies? First of all, the study should be preregistered (see Section III.3) in order to solve two issues: (*i*) preregistration of analysis plans takes out any researcher degrees of freedom that would risk biasing the observed effect size in the direction desired by the researcher (either confirmation of the previous finding or clear refutation of it), and (*ii*) preregistered studies that do not make it to the stage of publication will still be accessible at a public repository, documenting the attempt and hopefully also the reason for failure. Besides being preregistered, replication studies should attempt to match the previous study as closely as possible in methods and materials and should aim for a larger sample size. Incentives to preregister should be particularly strong for replication studies since a study and analysis plan effectively already exist, and preregistration will clearly signal to reviewers and editors that the presentation of results has not been altered in an attempt to achieve a particular outcome.

A particularly compelling option for publishing replications is through a process known as registered reports, a format advocated by Chris Chambers (2013). Registered reports involve preregistration, but with a registered report, the researcher first submits the study and analysis plan to a journal for review, potential revision of methods plans, and preliminary acceptance prior to conducting the study. Thus a proposed replication could be reviewed, and if judged meritorious, provisionally accepted independent of results. This would give the scientist who published the original study the opportunity to recommend changes to methods of the replication before it was initiated, and thus increase the quality of the replication while also reducing the opportunity for a critique, spurious or genuine, of the quality of replication.

(*c*) *Interpretation of differences in findings*

When a replication fails to confirm the original result, this is often interpreted as context dependence (e.g. 'this was a wetter year', 'this location contained more conifers', or 'these animals were raised on a higher-protein diet'). After all, we know that ecology and behaviour are highly complex and we expect variability. However, in this situation context dependence is simply an untested *post-hoc* hypothesis. We cannot claim that divergent results stem from context dependence without explicit testing with new data. As explained in Section II.4*a*, it may be that the difference in effect sizes observed in the two studies is no larger than what one would expect from chance alone (sampling noise). Meta-analysts (researchers who summarize effect sizes across numerous studies) are very familiar with this idea, and they quantify the extent of disagreement between studies as 'heterogeneity' in effect sizes. Since each observed effect size is accompanied by a measure of uncertainty (for instance a standard error or 95% confidence interval, both of which depend on sample size), one can test statistically whether there is significant heterogeneity in effect sizes. Such tests are frequently significant, but does this observation provide strong evidence for context dependence? Unfortunately not!

For tests of heterogeneity to provide insight into context dependence, we need to minimize other sources of heterogeneity. One source of heterogeneity is publication bias in favour of stronger effects, often facilitated by use of researcher degrees of freedom to reach significance more often than expected by chance. In an extreme example, two studies could yield non-significant trends in opposite directions (a small difference due to sampling noise), but those differences could get amplified by 'researcher degrees of freedom' and selective reporting, because each team of researchers (in good faith of doing the right thing) feels obliged to emphasize the outcome of their study by selecting the conditions where trends approach or reach statistical significance. When publication bias is common, effect sizes often vary as a function of sample size because as sample size declines, deriving a statistically significant effect requires larger effect sizes (Gelman & Weakliem, 2009). This too can generate estimates of significant heterogeneity among studies in the absence of context dependence. Thus an important step towards using tests for heterogeneity as reasonable indicators of context dependence

is minimizing sources of bias, for instance through preregistered studies. Heterogeneity can also arise due to differences in study methods that are unrelated to hypothesized contextual differences. If we are truly interested in context dependence and its sources, then we should design replication studies explicitly to investigate context dependence. This means systematically evaluating environmental variables that we hypothesize may be driving context dependence using 'replication batteries', in which conditions hypothesized to drive differences in results are manipulated while attempting to hold other variables constant (Kelly, 2006). *Post-hoc* hypotheses about context dependence are valid, but they remain nothing more than hypotheses before studies have been designed and implemented specifically to evaluate them.

(*d*) *Is the world more complex or less complex than we think?*

The tendency of many researchers to interpret all apparent differences as important (see Section II.4*a*) and to attribute these differences to context dependence by default has a remarkable effect on the development of our world view. Such world views become increasingly complex, emphasizing the importance of context dependence which results in hard-to-interpret interaction terms. By contrast, the sceptic who emphasizes the large amount of sampling noise in most sets of data which further may get inflated by researcher flexibility, may often hold a nihilistic world view where most or all effects are spurious. This is an interesting debate which we only will be able to resolve by promoting transparency and by replicating studies as rigorously as possible.

(2) Collecting evidence for the null and the elimination of zombie hypotheses

Given the many false-positive findings in the literature, it is the foremost goal of rigorous replication studies to validate or reject previous findings. This will often mean that evidence we collect contradicts the biological hypothesis. But can this evidence lead to rejection of our biological hypothesis? After all, we can never rule out the possibility that this hypothesis might apply in some other context and that some unknown, uncontrolled difference between our replication and the original study led to our failure to replicate. In practice, however, we think we can at least approximate rejection of the original hypothesis. The key is multiple replications and some sort of meta-analytical framework. For instance, when reporting a result, we may calculate a 95% confidence interval around our estimate, and then highlight that our study shows an effect that is significantly smaller than this or that quantity. We can calculate a weighted average of the two results, and as we accumulate more independent replications, we gain confidence in our average, and if this average approximates zero, we become more confident that the hypothesis in question is wrong, or at least of extremely narrow applicability (Seguin & Forstmeier, 2012; Nakagawa & Parker, 2015).

Another excellent tool for drawing conclusions from a series of replications is Bayesian statistics which allow us to pitch two competing hypotheses (H0 and H1) against each other and to evaluate which of them is better supported by the data (Dienes, 2016). The Bayes factor (BF) can be used to quantify how many times more likely the observed data are if the hypothesis H1 is true rather than if H0 is true. A Bayes factor of 1 means that the data are equally likely under both hypotheses, so the data contribute no information towards resolving the question of which hypothesis may be true. Depending a bit on conventions, a Bayes factor larger than 3 is typically considered as substantial or moderate evidence for H1, while a Bayes factor smaller than 1/3 represents substantial or moderate evidence for the null hypothesis H0, and these thresholds are approximately comparable to the threshold of $\alpha = 0.05$ in significance testing (Dienes, 2016). For the purpose of contrasting a specified hypothesis H1 (usually defined by the effect size reported in a previous study that we want to replicate) against the null hypothesis H0, Bayesian statistics hence allow us to assess whether the new data from the replication study support either H1 or H0. Of course Bayesian statistics do not guarantee that we will resolve the issue (if $1/3 < BF < 3$). This lack of clarity may come, for instance, if there is some truth to the published finding, but the true effect size lies half-way between the one that is published and the null (overestimation by a factor of about two would make $BF = 1$ a likely outcome).

In fact it is well known that published effect sizes tend to be overestimates of true effects. It is frequently observed that the first publications on a given topic report larger effect sizes than later follow-up studies, leading to a general decline in effect sizes over time (Jennions & Møller, 2002; Barto & Rillig, 2012; Koricheva, Jennions & Lau, 2013). Equally problematic is the observation that sample size and effect size are typically negatively correlated in meta-analyses meaning that only the studies with the largest sample size will yield trustworthy effect-size estimates (Levine, Asada & Carpenter, 2009). Meta-analysts examine this phenomenon in so-called funnel plots where effect sizes of studies are plotted in relation to sample size (Pillemer & Light, 1984). Funnel plots can be used to detect publication bias in meta-analyses (Egger *et al.*, 1997), but such tests should be regarded with caution (Ioannidis & Trikalinos, 2007). Modest amounts of publication bias, that may not be apparent from funnel plots, can render the conclusion of a meta-analysis invalid (Scargle, 1999; Ferguson & Heene, 2012).

Besides many true effects being overestimated, it is conceivable that some fields of research could exist for extended periods of time in the complete absence of any true effects of theoretical relevance. More than 40 years ago, Greenwald (1975) complained that systematic "prejudice against the null hypothesis" can lead to a dysfunctional system of research and publication that allows untrue hypotheses to persist undefeated, similar to what was recently proposed for a substantial body of sexual selection research (Prum, 2010). More recently, and along the same lines, Ferguson & Heene (2012) argued that our aversion to the null will result in 'a vast graveyard of undead theories'. We feel that it is high time to overcome this aversion, and to remind ourselves that researchers are supposed to be the unbiased referee in

a game between H1 and H0, and that falsification of untrue hypotheses lies at the heart of making scientific progress.

(3) Making science more objective

The weight of all these obstacles to objective science could leave you frustrated and depressed. Scientists are often unaware of many of the ways that science is not maximally objective and the ways that scientific practices often serve only the short-term interest of the scientist who is under pressure to produce success stories in order to attract the next grant. Fortunately, unscientific practices like fishing for significance, HARKing, and many others are on their way out, as a growing community becomes more aware of the risks and better able to recognize the signs of bad practices. Further, as discussions of these issues become more common, we hope that more researchers will realize that sticking to protocols that promote objectivity is the best strategy in the long run. For instance, anyone who conducts a series of studies in the same system will benefit from drawing robust conclusions in their foundational work. Maximizing objectivity, for instance through preregistering your studies, should also bolster your reputation. Then, if one of your findings is contradicted by later work you need not worry about your reputation, and maybe more important, you can feel good about the fact that you interpreted the data in the most objective way. In this context, a recent commentary by Markowetz (2015) is an interesting read. He lists five selfish reasons why you should work reproducibly.

We have already touched on a couple of promising ways to make science more reliable, and we add more details below.

(a) *Why should I preregister my next study?*

As noted above, preregistration of study plans solves the issues of (*i*) HARKing, because you registered your hypotheses in advance, (*ii*) researcher degrees of freedom, because you registered your data-analysis strategy in advance, and (*iii*) publication bias, because the added rigour makes nearly every finding worth publishing (or otherwise the reason for failure to publish gets documented in a public space). What might hold you back from preregistering your next study?

1 I have checked the requirements, and it looks like a substantial amount of work.

Preregistering your study may take you a couple of days, but in the long run it will benefit you tremendously by forcing you to think through your study plans very carefully. Likely you will discover some weaknesses in your questions, study design or analysis plan and you still have time to fix or amend these issues before starting data collection. Also, the preparatory work will make the data analysis easier since you will already have a detailed plan, and it will make writing your paper much easier, since you will already have written your Methods section.

2 My colleagues are not preregistering their work, so why should I?

If you are thinking of preregistering your study now, it is not unlikely that you will be among the first in your field to do so. Would you like to be able to say that you were among the first to embrace this new tool that ensures objectivity? Give it a try and you will likely discover that preregistering is emotionally rewarding like the submission of a manuscript. It also lends importance to your project.

3 I am worried that someone will steal my project idea.

No reason to worry. You can embargo your plans, and they will only become publicly visible later.

4 I need more flexibility in study design.

Preregistration does not limit the freedom of the researcher; it only documents the ideas and plans at any given time, making the process maximally transparent. You always have the possibility of modifying your study plans, and the exact time of modification and reasons for modification will be documented, probably still long before final data analysis when researcher degrees of freedom would come into play. The original study plan will always remain visible with its date of registration, but making failed aspects of a plan visible to others might also save them from repeating the same mistake.

5 What if I make an unexpected discovery?

Having preregistered your study does not prevent you from publishing any analysis you believe is interesting or informative. All that preregistration does is clarify what tests were formulated *a priori* and what tests were not. For instance, you may subdivide your publication into a part that covers the original analysis plan (the rigorous *a priori* testing part) and a second part that explores the data *post hoc* and yields unexpected discoveries.

If you have other questions, or want to start registering, check out the website of the Center for Open Science (https://cos.io/and specifically https://cos.io/prereg/). The Center for Open Science is currently sponsoring a 'Preregistration Challenge' in which they will award US$1000 to the first 1000 researchers to publish preregistered studies. An alternative site that offers a maximally convenient and hassle-free opportunity to preregister your study is provided by AsPredicted (https://aspredicted.org/).

(b) *Badges make good scientific practice visible*

The Open Science Framework (https://osf.io/) has also started an initiative to make good scientific practice visible by awarding badges to studies that meet certain criteria, currently including preregistration, the availability of archived data, and the availability of detailed materials.

Journals decide if they want to award badges to publications that meet the criteria, and a few journals (mostly from the field of psychology) have already started doing so. Authors, when they submit their paper, apply for the badge by declaring that the study complies with the criteria. Editors or referees may check whether this is true but they may also leave the responsibility with the authors for making correct declarations (thereby minimizing the additional workload for journals). There is already evidence that awarding badges is effective in promoting the sharing of data (Kidwell *et al.*, 2016). Badges might also facilitate evaluation of bias. For instance, badges could make it possible to identify preregistered studies and thus to compare effect sizes meta-analytically between preregistered and non-preregistered studies. If you want to publish a preregistered experiment, it may well make sense to contact the editor-in-chief of the journal prior to submission to ask whether they would be ready to give you a badge in case of acceptance. Currently it seems that journal editors are waiting to see whether they start receiving such requests before deciding to join the list of journals that award badges (see https://osf.io/tvyxz/wiki/5.%20Adoptions%20and%20Endorsements/).

(*c*) *Blinding during data collection and analysis*

To rule out cognitive biases (Section II.5) such as the observer effect during data collection or confirmation bias during data analysis, it is generally a good idea to blind the researcher (MacCoun & Perlmutter, 2015).

During data collection, blinding ourselves to treatment groups provides an important protection against any intrinsic subconscious biases that we may have (van Wilgenburg & Elgar, 2013; Holman *et al.*, 2015; MacCoun & Perlmutter, 2015). In all cases where data collection is not entirely objective and free of observer effects, it is almost impossible not to end up with bias. Despite the importance of observer effects in many fields of science, strategies of observer blinding are implemented in fewer studies than one would hope (van Wilgenburg & Elgar, 2013; Holman *et al.*, 2015; Kardish *et al.*, 2015).

During data analysis, blinding the researcher from the effect of arbitrary decisions on statistical significance of the hypothesis test is an important tool that ensures objectivity (MacCoun & Perlmutter, in press). Hence, you should try to take your choices of analysis variants before seeing their effects on *P*-values. If this is not possible, you could ask someone else to make these choices blindly (without regard to outcome) for you, always going for the option that sounds more reasonable based on criteria other than significance or effect size.

(*d*) *Objective reporting of non-registered studies*

If you have not preregistered your hypotheses and analysis plan, how can you reach comparable levels of objectivity in your publication? First, you should explicitly distinguish your *a priori* hypotheses (typically just a few, namely the ones you designed the study for) from your exploratory data analysis. Second, you should avoid selective reporting. For any question or field of questions within your study, you should attempt to consider all possibly relevant dependent variables and predictors (see Fig. 2). If this makes the manuscript too long, you can always put large tables of results in an electronic supplementary file. You can then report averaged effect sizes in the paper itself. Third, you should avoid reporting estimates that are biased towards significance by non-blind choice of 'researcher degrees of freedom'. If you cannot use blinding as described above, you may want to consider using specification-curve analysis (SCA) (Simonsohn *et al.*, 2015) to go through all combinations of analysis variants, and to average effect sizes across all combinations. Currently, U. Simonsohn and co-workers are planning to create an R-package that would make SCA easy to carry out. A less-ambitious, but still noteworthy option has been suggested by the same set of authors (Simmons, Nelson & Simonsohn, 2012) who advocate 'a 21 word solution' of the problem in your Methods section. Specifically, your Methods should say: 'We report how we determined our sample size, all data exclusions (if any), all manipulations, and all measures in the study.' This should take out a range of researcher degrees of freedom, and should reduce the bias in reported effects (see also http://www.researchtransparency.org/). Note that it also covers the issue of specifying a stopping rule for sample size.

Finally, when attempting to publish your manuscript, you should emphasize its goal of yielding maximally objective and unbiased estimates of effect sizes, as opposed to fishing, HARKing and overselling. Remember that most effect sizes are small and hence single studies usually lack the power to detect them. Hence, any parameter estimate is worth publishing, but only if it has been derived in an unbiased way.

(*e*) *Concluding recommendations for funding agencies*

In the future, what will scientists say when they look back on our current organization of the scientific undertaking? We think there are good reasons for calling this system inefficient and wasteful.

The key problem is that we are expecting too much from every single empirical study (despite knowing that most effect sizes are small and hence power is very limited), meaning that we set up the unrealistic expectation that each study should yield a clear-cut conclusion by itself. This leads to a situation where junior scientists complain when their laborious efforts of data collection have not yielded a significant finding, meaning that their work cannot be published. In response senior scientists help with advice on alternative data analyses designed to squeeze out something significant (see the torture of data in Fig. 9). And there are more consequences of our unrealistic expectations.

We end up with a large amount of wasted effort because non-significant parameter estimates end up unpublished in the so-called 'file-drawer'. And, the studies that make it to the publication stage often yield parameter estimates that are biased upwards or are simply false positive, and these

estimates therefore paint a distorted picture of the reality that we set out to study. How absurd is a system in which we measure an effect of interest with meticulous accuracy, but then subject our measure to a self-imposed censorship by only reporting it if it exceeded a certain strength?

It appears that this practice is currently ubiquitous across a wide swathe of scientific disciplines (John *et al.*, 2012), despite the fact that it is fundamentally anti-scientific. We believe that this practice could be stopped most effectively by adequate measures from funding bodies. In an ideal world, all measures of effect size would be reported (not necessarily in peer-reviewed journals) and the respective raw data would be made openly available (see also Morey *et al.*, 2016). Further, as preregistration became the norm, exploratory studies would become more transparent and studies without preregistration would come to be viewed as more provisional. If funding bodies rewarded preregistration and unbiased reporting practices along with intellectual merit rather than rewarding only success in attracting citations, then we would rapidly have a transition from a fairly dysfunctional to a much more objective science.

Such a change in incentives would also be good news for the above-mentioned junior scientists who would worry about the rigour and merit of their experiments rather than the outcome. They could move forward knowing that well-designed tests of interesting ideas would make all their parameter estimates valuable and publishable.

IV. CONCLUSIONS

(1) False-positive findings can easily arise when statistical methods are applied incorrectly or when *P*-values are interpreted without sufficient understanding of the multiple-testing problem (false-positive report probability). Incorrect *P*-values can arise from the over-fitting of models or from a failure to control for pseudoreplication, autocorrelation, or overdispersion. It is also essential to understand the consequences of multiple testing that arise from conditional stopping rules, from researcher flexibility when choosing an analysis strategy *post hoc*, or from multiple testing during the process of model selection.

(2) Psychological biases may also lead to false-positive results. Researchers may be systematically biased against the null hypothesis because positive findings are more appealing than null results, and this bias may get amplified by the selective interest of journals in discoveries. This incentive is problematic because it can motivate a widespread but unhelpful scientific practice: namely, extensive data exploration in search for patterns that reach nominal significance, followed by selective reporting of the most interesting (significant) results, combined with depicting data exploration as confirmatory testing of *a priori* hypotheses. Researchers may often be unaware that such practice is problematic, because hindsight bias can make many chance findings appear plausible and in line with theory. Finally, confirmation bias during data collection by non-blinded observers may also contribute to biased results. Because of these influences, 'data do not speak for themselves', but need to be judged within the context of the procedures of data collection, analysis, and presentation.

(3) Preregistration of hypotheses, research methods and complete analysis plans solves many of these issues. It prevents both HARKing and subjective choice of analysis methods that is conditional on significance because hypotheses and analysis plans have been specified in advance. It also mitigates the problem of publication bias. Labelling preregistered studies with badges may allow us to quantify how much these biases contribute to overall effect-size estimates.

(4) Non-preregistered studies should implement a strategy of comprehensive and unbiased reporting that is not conditional on significance. Researcher blinding during analysis or specification-curve analysis are helpful techniques that promote objectivity.

(5) Seeking novelty and discovery may be emotionally rewarding, but in light of the currently low thresholds for reaching nominal significance, isolated, unreplicated reports of findings should be regarded as preliminary until confirmed by rigorous replication studies. The term 'evidence' should be used more cautiously (when there is consensus from confirmatory tests) and the expression 'as predicted' should maybe be limited to predictions that have been documented or to those that strictly follow from theory. The crucial second step from exploratory to confirmatory research should be encouraged by funding bodies supporting rigorous replication studies and by citation practices of researchers who might want to prefer citing the rigorous confirmatory over the initial exploratory study.

(6) A research system in which results are much more likely to get reported if they reach statistical significance violates scientific objectivity and is highly inefficient if our interest lies in the quantification of effect sizes because unbiased effect-size estimates are difficult to obtain in such a system. Hence, researchers should recognize the value of unbiased reporting and funding bodies should reward such practice during the review process. The latter will have to think of ways of assessing researcher performance in terms of scientific rigour and integrity, because the current assessment in terms of productivity and impact causes unwanted natural selection pressure in favour of bad science (Smaldino & McElreath, 2016).

V. GLOSSARY

Alpha probability = the accepted risk of drawing a false-positive conclusion in a single statistical test, which in most fields is arbitrarily set to $\alpha = 5\%$.

A priori = typically before gathering data, but potentially just before analysis or before seeing the data.

Attrition = reduction in sample size between study initiation and data analysis, which might lead to a bias in the results (e.g. when outliers are selectively removed).

Bayesian statistics = a statistical method that quantifies uncertainty about parameters and models using the laws of probability theory.

Bayes factor = a measure of predictive performance for two competing models or hypotheses.

Beta probability = the accepted risk of drawing a false-negative conclusion in a single statistical test (e.g. $\beta = 20\%$ when the statistical power equals 80%).

Bias = a systematic deviation from a true or representative value (note how this differs from sampling noise which causes a random deviation, with equal probability of being too high or too low).

Bonferroni correction = adjustment of α that allows us to limit the risk of drawing one or more false-positive conclusions from a whole series of tests.

Close (or exact) replication = an attempt to repeat an earlier study with maximally similar methods.

Clustered data = non-independence of data points.

Collinearity = two or more predictors that are correlated with each other, making it difficult to disentangle their respective effects on the dependent variable.

Confirmatory testing = a planned test that seeks additional evidence for a hypothesis (derived from theory or from previous observations).

Exploratory analysis = a broad search for patterns in a given data set with statistical or graphical methods.

False-negative finding = concluding an absence of effect despite the opposite being true (failure to detect an existing effect; = Type II error).

False-positive finding = concluding that an effect exists while in fact it does not (= Type I error).

False-positive report probability (FPRP) = the probability that a statistically significant finding is not true ($\mathrm{FPRP} = (\alpha(1-\pi)/[\alpha(1-\pi)+(1-\beta)\pi]$, with $\alpha =$ Type I error probability, $\beta =$ Type II error probability, $\pi =$ the proportion of tested hypotheses that are true).

File-drawer problem = studies with null-results (no significant effect) often do not get published and remain hidden in the file-drawers of the researchers.

Fishing for significance = a range of strategies that can be employed to increase the chance of obtaining a statistically significant result.

HARKing = hypothesising after the results are known (see Hindsight bias).

Heterogeneity in effect sizes = the degree to which estimates of effects differ from one another (e.g. across a range of studies). There is a range of statistical descriptors of heterogeneity (Q, T^2, I^2) that come with different properties and interpretation.

Hindsight bias = also known as 'knew-it-all-along' bias, this is the tendency to underestimate the extent to which outcomes were caused by noise, after these outcomes have been observed. It can be a self-deceiving tendency to believe, after seeing the data, that the result had been predicted *a priori* when there was in fact no *a priori* prediction.

Hypothesis testing = statistical analysis of data that usually serves to reject a hypothesis.

Interaction term = two or more factors that interact with each other rather than having effects that simply add up (e.g. lifespan may be affected by smoking and gender, but if the effect of smoking is larger in one sex than the other, then the two factors interact in their effects on lifespan).

Leverage = a data point that is an outlier with regard to the dependent variable, which hence has a strong effect on the position of a fitted regression line (such influential data points are said to have high leverage).

Multiple hypotheses testing = the testing of several hypotheses at once (which leads to a high probability of finding at least one significant effect).

Outlier = a data point with an extreme value that has no other data points nearby.

Overfitting = estimating too many parameters simultaneously from a limited number of data points, which results in unreliable parameter estimates and *P*-values.

Pi (π) = symbol used for the proportion of hypotheses that are in fact true.

P-hacking = another term for 'fishing for significance' (see above).

P-value = probability that chance alone will produce an effect (e.g. a correlation, a difference) as strong as or stronger than the one observed in the data.

Post hoc = after analysis or after seeing the data.

Power (statistical power) = the probability that an existing effect (of given size) will be detected (i.e. will reach statistical significance) in a data set (of given size). Power is defined as $1-\beta$, the probability of failing to detect the effect.

Preregistration = submitting a document to a repository in which one outlines the hypotheses, methods and analysis strategies of a planned study before conducting the study. This prevents *post-hoc* modification of hypotheses (HARKing) and researcher flexibility in analysis and thus reduces the risk of unreported multiple hypothesis testing.

Pseudoreplication = independent data points represent proper replicates, while non-independent data points are referred to as pseudoreplicates. Such dependent data points do not contribute as much information as independent data points would. Most statistical tests assume that data points are independent, and violating this assumption leads to *P*-values that are too small.

Quasi-replication = replicating a study in a wider sense with a different approach (e.g. different methods or different species). In contrast to close replications, this leaves a lot of room for interpreting differences in findings.

Researcher degrees of freedom = flexibility of the researcher, who can choose how to analyse the data, giving him/her the opportunity to select whatever yields the desired outcome.

Sampling noise = random fluctuations in outcomes under an identical data-generating process. Sampling noise

arises from the fact that when sampling at random from a population, we could have collected a different, but equally random, sample leading to different estimates.

Type I error = concluding that an effect exists while in fact it does not (= false-positive finding).

Type II error = concluding an absence of effect despite the opposite being true (failure to detect an existing effect; = false-negative finding).

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