432 Class 27 Slides

github.com/THOMASELOVE/432-2018

2018-04-24

```
library(tidyverse)
```

Roger Peng's description of a successful data analysis

> *A data analysis is successful if the audience to which it is presented accepts the results.*

- "What is a Successful Data Analysis?" *simplystatistics.org* (2018-04-17).

So what makes a data analysis more believable / more acceptable?

Today's Agenda

- Replicable Research and the Crisis in Science
  - ASA Statement on P values
  - Is changing the p value cutoff the right strategy?
  - Second-generation p values: A next step?
- Retrospective Power and why most smart folks avoid it
  - Type S and Type M error: Saying something more useful

Problems with *P* Values

1. *P* values are inherently unstable
2. The *p* value, or statistical significance, does not measure the size of an effect or the importance of a result
3. Scientific conclusions should not be based only on whether a *p* value passes a specific threshold
4. Proper inference requires full reporting and transparency
5. By itself, a *p* value does not provide a good measure of evidence regarding a model or hypothesis

Link

Solutions to the *P* Value Problems

1. Estimation of the Size of the Effect
2. Precision of the Estimate (Confidence Intervals)
3. Inference About the Target Population
4. Determination of Whether the Results Are Compatible With a Clinically Meaningful Effect
5. Replication and Steady Accumulation of Knowledge

Link

Importance of Meta-Analytic Thinking

In JAMA Otolaryngology: Head & Neck Surgery, we look to publish original investigations where the investigators planned the study with sufficient sample size to have adequate power to detect a clinically meaningful effect and report the results with effect sizes and CIs. Authors should interpret the effect sizes in relation to previous research and use CIs to help determine whether the results are compatible with clinically meaningful effects. And finally, we acknowledge that no single study can define truth and that the advancement of medical knowledge and patient care depends on the steady accumulation of reliable clinical information.

Link

The Value of a *p*-Valueless Paper

Jason T. Connor (2004) *American J of Gastroenterology* 99(9): 1638-40.

Abstract: As is common in current bio-medical research, about 85% of original contributions in *The American Journal of Gastroenterology* in 2004 have reported *p*-values. However, none are reported in this issue's article by Abraham et al. who, instead, rely exclusively on effect size estimates and associated confidence intervals to summarize their findings. **Authors using confidence intervals communicate much more information in a clear and efficient manner than those using *p*-values. This strategy also prevents readers from drawing erroneous conclusions caused by common misunderstandings about *p*-values**. I outline how standard, two-sided confidence intervals can be used to measure whether two treatments differ or test whether they are clinically equivalent.

Link

Editorial from JAMA Cardiology 2016-10-12

Editor's Note

Do Not Over (*P*) Value Your Research Article

Laine E. Thomas, PhD; Michael J. Pencina, PhD

P value is by far the most prevalent statistic in the medical literature but also one attracting considerable controversy. Recently, the American Statistical Association[1] released a policy statement on *P* values, noting that misunderstanding and misuse of *P* values is an important contributing factor to the common problem of scientific conclusions that fail to be reproducible. Furthermore, reliance on *P* values may distract from the good scientific principles that are needed for high-quality research. Mark et al[2] delve deeper into the history and interpretation of the *P* value in this issue of *JAMA Cardiology*. Herein, we take the opportunity to state a few principles to help guide authors in the use and reporting of *P* values in the journal.

Related article

When the limitations surrounding *P* values are emphasized, a common question is, "What should we do instead?" Ron Wasserstein of the American Statistical Association explained: "In the post p<0.05 era, scientific argumentation is not based on whether a p-value is small enough or not. Attention is paid to effect sizes and confidence intervals. Evidence is thought of as being continuous rather than some sort of dichotomy.... Instead, journals [should evaluate] papers based on clear and detailed description of the study design, execution, and analysis, having conclusions that are based on valid statistical interpretations and scientific arguments, and reported transparently and thoroughly enough to be rigorously scrutinized by others."[3]

We suggest that researchers submitting manuscripts to *JAMA Cardiology* should also consider the following:

1. Data that are descriptive of the sample (ie, indicating imbalances between observed groups but not making inference to a population) should not be associated with *P* values. Appropriate language, in this case, would describe numerical differences and sample summary statistics and focus on differences of clinical importance.
2. In addition to summary statistics and confidence intervals, standardized differences (rather than *P* values) are a preferred way to exhibit imbalances between groups.
3. *P* values are most meaningful in the context of clear, a priori hypotheses that support the main conclusions of a manuscript.
4. Reporting stand-alone *P* values is discouraged, and preference should be given to presentation and interpretation of effect sizes and their uncertainty (confidence intervals) in the scientific context and in light of other evidence. Crossing a threshold (eg, $P < .05$) by itself constitutes only weak evidence.
5. Researchers should define and interpret effect measures that are clinically relevant. For example, clinical importance is often difficult to establish on the odds ratio scale but is clearer on the risk ratio or absolute risk difference scale.

In summary, following Mark et al,[2] we encourage researchers to focus on interpreting clinical research data in terms of treatment "effect" magnitude and precision, using *P* value only as one of many complementary tools in the statistical toolbox.

Mark, Lee, Harrell JAMA Cardiol 2016-10-12

Abstract

P values and hypothesis testing methods are frequently misused in clinical research. Much of this misuse appears to be owing to the widespread, mistaken belief that they provide simple, reliable, and objective triage tools for separating the true and important from the untrue or unimportant. The primary focus in interpreting therapeutic clinical research data should be on the treatment ("oomph") effect, a metaphorical force that moves patients given an effective treatment to a different clinical state relative to their control counterparts. This effect is assessed using 2 complementary types of statistical measures calculated from the data, namely, effect magnitude or size and precision of the effect size. In a randomized trial, effect size is often summarized using constructs, such as odds ratios, hazard ratios, relative risks, or adverse event rate differences. How large a treatment effect has to be to be consequential is a matter for clinical judgment. The precision of the effect size (conceptually related to the amount of spread in the data) is usually addressed with confidence intervals. *P* values (significance tests) were first proposed as an informal heuristic to help assess how "unexpected" the observed effect size was if the true state of nature was no effect or no difference. Hypothesis testing was a modification of the significance test approach that envisioned controlling the false-positive rate of study results over many (hypothetical) repetitions of the experiment of interest. Both can be helpful but, by themselves, provide only a tunnel vision perspective on study results that ignores the clinical effects the study was conducted to measure.

Link

p-Hacking

Hack Your Way To Scientific Glory (fivethirtyeight)

Hack Your Way To Scientific Glory

You're a social scientist with a hunch: **The U.S. economy is affected by whether Republicans or Democrats are in office.** Try to show that a connection exists, using real data going back to 1948. For your results to be publishable in an academic journal, you'll need to prove that they are "statistically significant" by achieving a low enough p-value.

1 CHOOSE A POLITICAL PARTY

Republicans | Democrats

2 DEFINE TERMS

Which politicians do you want to include?

- [ ] Presidents
- [x] Governors
- [x] Senators
- [ ] Representatives

How do you want to measure economic performance?

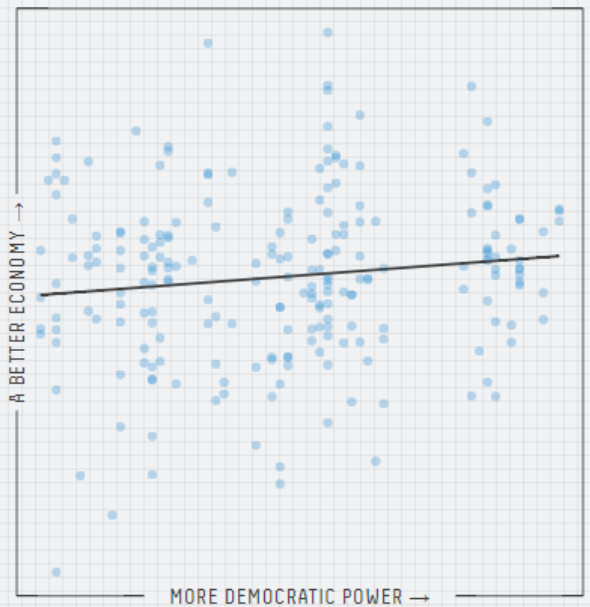
- [ ] Employment
- [x] Inflation
- [x] GDP
- [x] Stock prices

Other options

- [x] **Factor in power**
  Weight more powerful positions more heavily
- [x] **Exclude recessions**
  Don't include economic recessions

3 IS THERE A RELATIONSHIP?

Given how you've defined your terms, does the economy do better, worse or about the same when more Democrats are in power? Each dot below represents one month of data.



4 IS YOUR RESULT SIGNIFICANT?

If there were no connection between the economy and politics, what is the probability that you'd get results at least as strong as yours? That probability is your p-value, and by convention, you need a **p-value of 0.05 or less** to get published.

Result: Almost

Your **0.06** p-value is close to the 0.05 threshold. Try tweaking your variables to see if you can push it over the line!

If you're interested in reading real (and more rigorous) studies on the connection between politics and the economy, see the work of Larry Bartels and Alan Blinder and Mark Watson.

Data from The @unitedstates Project, National Governors Association, Bureau of Labor Statistics, Federal Reserve Bank of St. Louis and Yahoo Finance.

"Researcher Degrees of Freedom", 1

> *[I]t is unacceptably easy to publish statistically significant evidence consistent with any hypothesis.*
>
> *The culprit is a construct we refer to as* ***researcher degrees of freedom****. In the course of collecting and analyzing data, researchers have many decisions to make: Should more data be collected? Should some observations be excluded? Which conditions should be combined and which ones compared? Which control variables should be considered? Should specific measures be combined or transformed or both?*

Simmons et al. *link*

"Researcher Degrees of Freedom", 2

> *. . . It is rare, and sometimes impractical, for researchers to make all these decisions beforehand. Rather, it is common (and accepted practice) for researchers to explore various analytic alternatives, to search for a combination that yields statistical significance, and to then report only what worked. The problem, of course, is that the likelihood of at least one (of many) analyses producing a falsely positive finding at the 5% level is necessarily greater than 5%.*

For more, see

- Gelman's blog 2012 – 11 – 01 "Researcher Degrees of Freedom",
- Paper by *Simmons* and others, defining the term.

And this is really hard to deal with. . .

The garden of forking paths: Why multiple comparisons can be a problem, even when there is no "fishing expedition" or p-hacking and the research hypothesis was posited ahead of time

> *Researcher degrees of freedom can lead to a multiple comparisons problem, even in settings where researchers perform only a single analysis on their data. The problem is there can be a large number of potential comparisons when the details of data analysis are highly contingent on data, without the researcher having to perform any conscious procedure of fishing or examining multiple p-values. We discuss in the context of several examples of published papers where data-analysis decisions were theoretically-motivated based on previous literature, but where the details of data selection and analysis were not pre-specified and, as a result, were contingent on data.*

- *Link* to the paper from Gelman and Loken

Do Confidence Intervals get us out of this mess?

Confidence Intervals - do they solve our problem?

Chelsea Parlett Pelleriti
@ChelseaParlett

Follow

Hey Stats folk, what's your 280 character definition of a confidence interval? 🤔

4:30 PM - 13 Mar 2018

Confidence Intervals - do they solve our problem?

Thomas Leeper
@thosjleeper

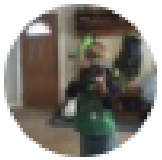
Follow

Replying to @ChelseaParlett

An interval drawn such that, were repeated, equal-sized samples of units drawn from the population of units using an identical sampling procedure and the same estimator was applied to each sample, 100*(1-α)% of those intervals would contain the population parameter of interest.

4:58 PM - 13 Mar 2018

Confidence Intervals - do they solve our problem?



Joran Elias
@joranelias

Follow

A confidence interval is a meaure of uncertainty such that all definitions of it elicit corrections from Bayesians.

(Didn't need all 280.)

Confidence Intervals - do they solve our problem?

Jenny Bryan
@JennyBryan

Following

Pedantry about the definition of a confidence interval ... why is this the hill statisticians choose to die on? Every time you feel the urge, go convert a table to a figure. It is likely to do more good.

Confidence Intervals - do they solve our problem?

Frank Harrell @f2harrell · 28 Dec 2017

Tables and figures are important but so is this. We need to get this right. Too many faulty conclusions being drawn with frequentist statistical analysis. If one is going to be a frequentist one should make exactly correct interpretations.

2 10

Jenny Bryan
@JennyBryan

Following

Replying to @f2harrell

I just feel like the people we're often trying to reach aren't making informed comparisons of frequentist vs Bayesian methods, they're still struggling with decision making under uncertainty

1:02 PM - 28 Dec 2017

Using Bayesian Ideas: Confidence Intervals

> *My current favorite (hypothetical) example is an epidemiology study of some small effect where the point estimate of the odds ratio is 3.0 with a 95% conf interval of [1.1, 8.2].*
>
> *As a 95% conf interval, this is fine (assuming the underlying assumptions regarding sampling, causal identification, etc. are valid).*

(but on some level you need to deal with the fact that. . .)

> *. . . real-world odds ratios are much more likely to be near 1.1 than to be near 8.2.*

See Gelman 2014-12-11.

Uncertainty intervals?

I've (Gelman) become increasingly uncomfortable with the term "confidence interval" for several reasons:

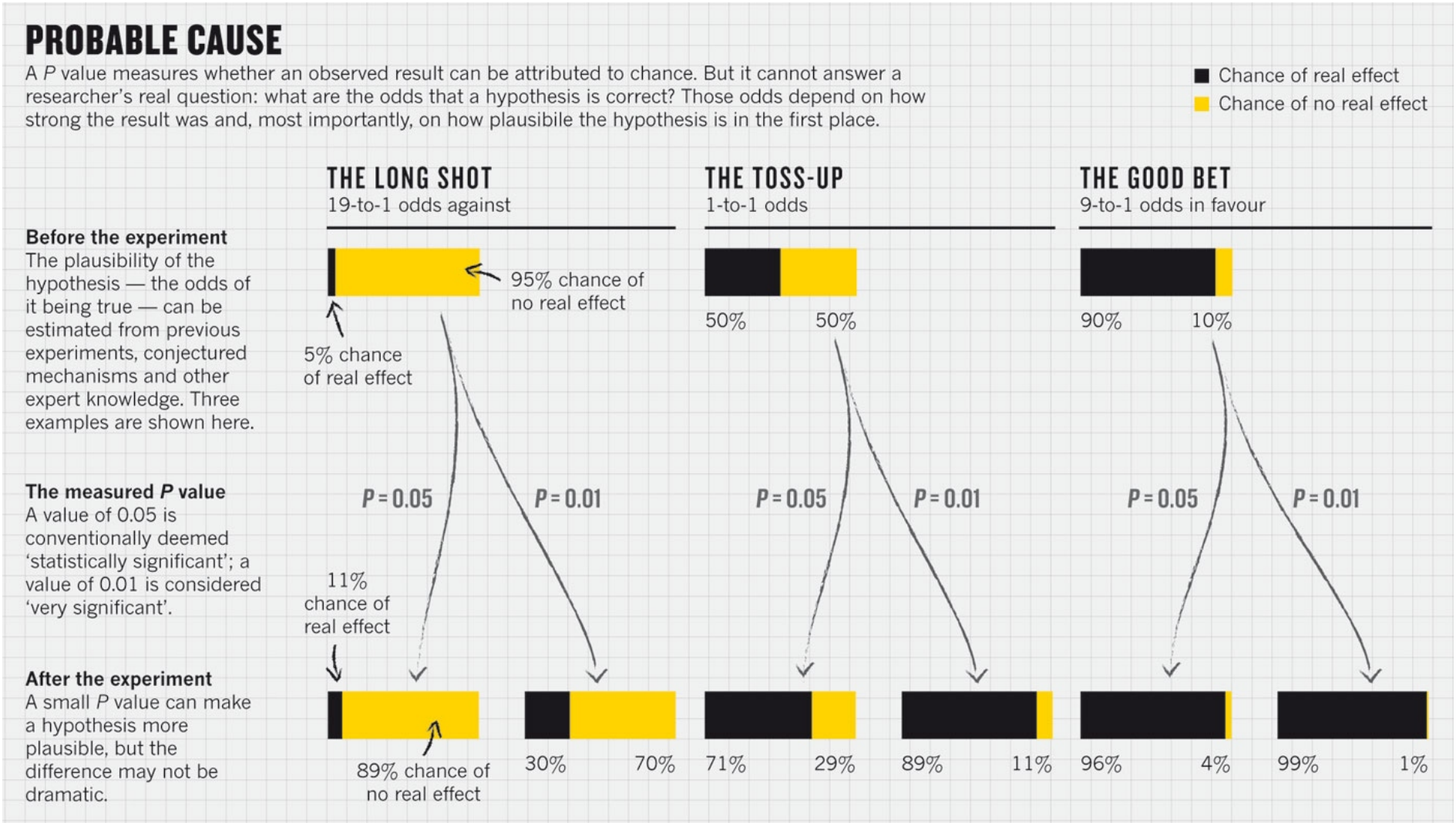
- The well-known difficulties in interpretation (officially the confidence statement can be interpreted only on average, but people typically implicitly give the Bayesian interpretation to each case.)
- The ambiguity between confidence intervals and predictive intervals.
- The awkwardness of explaining that confidence intervals are big in noisy situations where you have less confidence, and confidence intervals are small when you have more confidence.

So here's my proposal. Let's use the term "uncertainty interval" instead. The uncertainty interval tells you how much uncertainty you have.

See Gelman 2010-12-21.

Dividing Data Comparisons into Categories based on p values

Regina Nuzzo in Nature on Statistical Errors



Gelman on *p* values, 1

> *The common practice of dividing data comparisons into categories based on significance levels is terrible, but it happens all the time. . . . so it's worth examining the prevalence of this error.*

Consider, for example, this division:

- "really significant" for $p < .01$,
- "significant" for $p < .05$,
- "marginally significant" for $p < .1$, and
- "not at all significant" otherwise.

Now consider some typical *p*-values in these ranges: say, $p = .005$, $p = .03$, $p = .08$, and $p = .2$.

Translate these two-sided *p*-values back into z-scores. . .

Gelman 2016-10-15

Gelman on *p* values, 2

Description	really sig.	sig.	marginally sig.	not at all sig.
p value	0.005	0.03	0.08	0.20
Z score	2.8	2.2	1.8	1.3

The seemingly yawning gap in p-values comparing the not at all significant *p*-value of .2 to the really significant *p*-value of .005, is only a z score of 1.5.

If you had two independent experiments with z-scores of 2.8 and 1.3 and with equal standard errors and you wanted to compare them, you'd get a difference of 1.5 with a standard error of 1.4, which is completely consistent with noise.

Gelman on *p* values, 3

From a **statistical** point of view, the trouble with using the p-value as a data summary is that the p-value can only be interpreted in the context of the null hypothesis of zero effect, and (much of the time), nobody's interested in the null hypothesis.

Indeed, once you see comparisons between large, marginal, and small effects, the null hypothesis is irrelevant, as you want to be comparing effect sizes.

From a **psychological** point of view, the trouble with using the p-value as a data summary is that this is a kind of deterministic thinking, an attempt to convert real uncertainty into firm statements that are just not possible (or, as we would say now, just not replicable).

The key point: The difference between statistically significant and NOT statistically significant is not, generally, statistically significant.

Some Noisy Recent Suggestions

Benjamin et al 2017 Redefine Statistical Significance

We propose to change the default P-value threshold for statistical significance for claims of new discoveries from 0.05 to 0.005.

Motivations:

- links to Bayes Factor interpretation
- 0.005 is stringent enough to "break" the current system - makes it very difficult for researchers to reach threshold with noisy, useless studies.

Visit the main *article*. Visit an explanatory piece in *Science*.

Lakens et al. Justify Your Alpha

"In response to recommendations to redefine statistical significance to $p \leq .005$, we propose that researchers should transparently report and justify all choices they make when designing a study, including the alpha level." Visit *link*.

Abandon Statistical Significance

Gelman blog 2017 – 09 – 26 on "Abandon Statistical Significance"

"Measurement error and variation are concerns even if your estimate is more than 2 standard errors from zero. Indeed, if variation or measurement error are high, then you learn almost nothing from an estimate even if it happens to be 'statistically significant.' "

Read the whole paper *here*

JAMA 2018-04-10 (just 2 weeks ago!)

VIEWPOINT

John P. A. Ioannidis, MD, DSc
Stanford Prevention Research Center, Meta-Research Innovation Center at Stanford, Departments of Medicine, Health Research and Policy, Biomedical Data Science, and Statistics, Stanford University, Stanford, California.

The Proposal to Lower *P* Value Thresholds to .005

P values and accompanying methods of statistical significance testing are creating challenges in biomedical science and other disciplines. The vast majority (96%) of articles that report *P* values in the abstract, full text, or both include some values of .05 or less.[1] However, many of the claims that these reports highlight are likely false.[2] Recognizing the major importance of the statistical significance conundrum, the American Statistical Association (ASA) published[3] a statement on *P* values in 2016. The status quo is widely believed to be problematic, but how exactly to fix the problem is far more contentious. The contributors to the ASA statement also wrote 20 independent, accompanying commentaries focusing on different aspects and prioritizing different solutions. Another large coalition of 72 methodologists recently proposed[4] a specific, simple move: lowering the routine *P* value threshold for claiming statistical significance from .05 to .005 for new discoveries. The proposal met with strong endorsement in some circles and concerns in others.

P values are misinterpreted, overtrusted, and misused. The language of the ASA statement enables the dis-

fully considered how low a *P* value should be for a research finding to have a sufficiently high chance of being true. For example, adoption of genome-wide significance thresholds ($P < 5 \times 10^{-8}$) in population genomics has made discovered associations highly replicable and these associations also appear consistently when tested in new populations. The human genome is very complex, but the extent of multiplicity of significance testing involved is known, the analyses are systematic and transparent, and a requirement for $P < 5 \times 10^{-8}$ can be cogently arrived at.

However, for most other types of biomedical research, the multiplicity involved is unclear and the analyses are nonsystematic and nontransparent. For most observational exploratory research that lacks preregistered protocols and analysis plans, it is unclear how many analyses were performed and what various analytic paths were explored. Hidden multiplicity, nonsystematic exploration, and selective reporting may affect even experimental research and randomized trials. Even though it is now more common to have a preexisting protocol and statistical analysis plan and preregistration of

Blume et al. PLoS ONE (2018) 13(3): e0188299

RESEARCH ARTICLE

Second-generation *p*-values: Improved rigor, reproducibility, & transparency in statistical analyses

Jeffrey D. Blume[1]*, Lucy D'Agostino McGowan[2], William D. Dupont[3], Robert A. Greevy, Jr.[1]

Second-generation p values

Verifying that a statistically significant result is scientifically meaningful is not only good scientific practice, it is a natural way to control the Type I error rate. Here we introduce a novel extension of the p-value—a second-generation p-value (p_δ)–that formally accounts for scientific relevance and leverages this natural Type I Error control. The approach relies on a pre-specified interval null hypothesis that represents the collection of effect sizes that are scientifically uninteresting or are practically null. The second-generation p-value is the proportion of data-supported hypotheses that are also null hypotheses. As such, second-generation p-values indicate when the data are compatible with null hypotheses ($p_\delta = 1$), or with alternative hypotheses ($p_\delta = 0$), or when the data are inconclusive ($0 < p_\delta < 1$). Moreover, second-generation p-values provide a proper scientific adjustment for multiple comparisons and reduce false discovery rates. This is an advance for environments rich in data, where traditional p-value adjustments are needlessly punitive. Second-generation p-values promote transparency, rigor and reproducibility of scientific results by *a priori* specifying which candidate hypotheses are practically meaningful and by providing a more reliable statistical summary of when the data are compatible with alternative or null hypotheses.

Nature P values are just the tip of the iceberg!

COMMENT

P values are just the tip of the iceberg

Ridding science of shoddy statistics will require scrutiny of every step, not merely the last one, say **Jeffrey T. Leek** and **Roger D. Peng**.

Evaluation through Retrospective Design

Gelman, 2016-03-11

Reviewing "The Association Between Men's Sexist Attitudes and Facial Hair" PubMed 26510427 (*Arch Sex Behavior* May 2016)

Headline Finding: A sample of ~500 men from America and India shows a significant relationship between sexist views and the presence of facial hair.

Excerpt 1:

> *Since a linear relationship has been found between facial hair thickness and perceived masculinity . . . we explored the relationship between facial hair thickness and sexism. . . . Pearson's correlation found no significant relationships between facial hair thickness and hostile or benevolent sexism, education, age, sexual orientation, or relationship status.*

Facial Hair and Sexist Attitudes

Excerpt 2:

> *We conducted pairwise comparisons between clean-shaven men and each facial hair style on hostile and benevolent sexism scores. . . . For the purpose of further analyses, participants were classified as either clean-shaven or having facial hair based on their self- reported facial hair style . . . There was a significant Facial Hair Status by Sexism Type interaction . . .*

- So their headline finding appeared only because, after their first analysis failed, they shook and shook the data until they found something statistically significant.

Facial Hair and Sexist Attitudes

Excerpt 2:

> *We conducted pairwise comparisons between clean-shaven men and each facial hair style on hostile and benevolent sexism scores. . . . For the purpose of further analyses, participants were classified as either clean-shaven or having facial hair based on their self- reported facial hair style . . . There was a significant Facial Hair Status by Sexism Type interaction . . .*

- So their headline finding appeared only because, after their first analysis failed, they shook and shook the data until they found something statistically significant.
- All credit to the researchers for admitting that they did this, but poor practice of them to present their result in the abstract to their paper without making this clear, and too bad that the journal got suckered into publishing this.

How should we react to this?

Gelman:

- Statisticians such as myself should recognize that the point of criticizing a study is, in general, to shed light on statistical errors, maybe with the hope of reforming future statistical education.
- Researchers and policymakers should not just trust what they read in published journals.

Assessing Type S (Sign) and Type M (Magnitude) Errors

- Gelman and Carlin *Psychological Science* 2014 9(6): 641-651.

Thinking About Power

Specifying effect sizes for power calculations

1. **Empirical**: assuming an effect size equal to the estimate from a previous study or from the data at hand (if performed retrospectively).
    - generally based on small samples
    - when preliminary results look interesting, they are more likely biased towards unrealistically large effects
2. **On the basis of goals**: assuming an effect size deemed to be substantively important or more specifically the minimum effect that would be substantively important.
    - Can also lead to specifying effect sizes that are larger than what is likely to be the true effect.

- Both lead to performing studies that are too small or misinterpretation of findings after completion.

Gelman and Carlin

- The idea of a **design analysis** is to improve the design and evaluation of research, when you want to summarize your inference through concepts related to statistical significance.
- Type 1 and Type 2 errors are tricky concepts and aren't easy to describe before data are collected, and are very difficult to use well after data are collected.
- These problems are made worse when you have
  - Noisy studies, where the signal may be overwhelmed,
  - Small Sample Sizes
  - No pre-registered (prior to data gathering) specifications for analysis
- Top statisticians avoid "post hoc power analysis"...
  - Why? It's usually crummy.

Why not post hoc power analysis?

So you collected data and analyzed the results. Now you want to do an after data gathering (post hoc) power analysis.

1. What will you use as your "true" effect size?
    - Often, point estimate from data - yuck - results very misleading - power is generally seriously overestimated when computed on the basis of statistically significant results.
    - Much better (but rarer) to identify plausible effect sizes based on external information rather than on your sparkling new result.
2. What are you trying to do? (too often)
    - get researcher off the hook (I didn't get $p < 0.05$ because I had low power - an alibi to explain away non-significant findings) or
    - encourage overconfidence in the finding.

Gelman and Carlin: Broader Design Ideas

- A broader notion of design, though, can be useful before and after data are gathered.

Gelman and Carlin recommend design calculations to estimate

1. Type S (sign) error - the probability of an estimate being in the wrong direction, and
2. Type M (magnitude) error, or exaggeration ratio - the factor by which the magnitude of an effect might be overestimated.

- These can (and should) have value **both** before data collection/analysis and afterwards (especially when an apparently strong and significant effect is found.)
- The big challenge remains identifying plausible effect sizes based on external information. Crucial to base our design analysis on an external estimate.

The Building Blocks

You perform a study that yields estimate d with standard error s. Think of d as an estimated mean difference, for example.

- Looks significant if $|d/s| > 2$, which roughly corresponds to $p < 0.05$. Inconclusive otherwise.

The Building Blocks

You perform a study that yields estimate d with standard error s. Think of d as an estimated mean difference, for example.

- Looks significant if $|d/s| > 2$, which roughly corresponds to $p < 0.05$. Inconclusive otherwise.
- Now, consider a true effect size D (the value that d would take if you had an enormous sample)

The Building Blocks

You perform a study that yields estimate d with standard error s. Think of d as an estimated mean difference, for example.

- Looks significant if $|d/s| > 2$, which roughly corresponds to $p < 0.05$. Inconclusive otherwise.
- Now, consider a true effect size D (the value that d would take if you had an enormous sample)
- D is hypothesized based on *external* information (Other available data, Literature review, Modeling as appropriate, etc.)

The Building Blocks

You perform a study that yields estimate d with standard error s. Think of d as an estimated mean difference, for example.

- Looks significant if $|d/s| > 2$, which roughly corresponds to $p < 0.05$. Inconclusive otherwise.
- Now, consider a true effect size D (the value that d would take if you had an enormous sample)
- D is hypothesized based on *external* information (Other available data, Literature review, Modeling as appropriate, etc.)
- Define d^{rep} as the estimate that would be observed in a hypothetical replication study with a design identical to our original study.

Design Analysis (Gelman and Carlin)

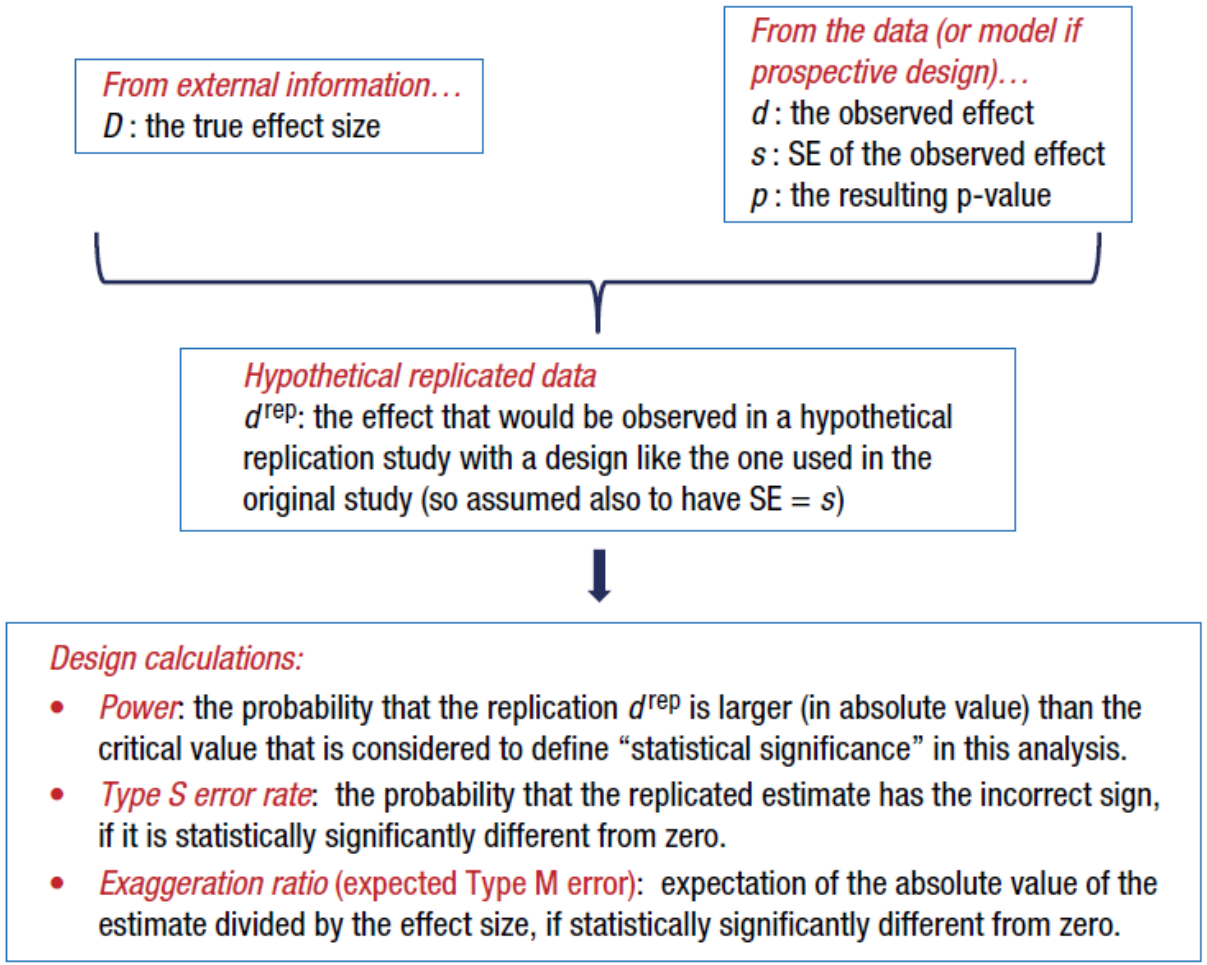


Figure 1. Diagram of our recommended approach to design analysis. It will typically make sense to consider different plausible values of D, the assumed true effect size.

Retrodesign function (shown on next slide)

Inputs to the function:

- `D`, the hypothesized true effect size (actually called `A` in the function)
- `s`, the standard error of the estimate
- `alpha`, the statistical significance threshold (default 0.05)
- `df`, the degrees of freedom (default assumption: infinite)

Output:

- the power
- the Type S error rate
- the exaggeration ratio

Retrodesign function (Gelman and Carlin)

```
retrodesign <- function(A, s, alpha=.05, df=Inf,
                        n.sims=10000){
    z <- qt(1-alpha/2, df)
    p.hi <- 1 - pt(z-A/s, df)
    p.lo <- pt(-z-A/s, df)
    power <- p.hi + p.lo
    typeS <- p.lo/power
    estimate <- A + s*rt(n.sims,df)
    significant <- abs(estimate) > s*z
    exaggeration <- mean(abs(estimate)[significant])/A
    return(list(power=power, typeS=typeS,
                exaggeration=exaggeration))
}
```

What if we have a beautiful, unbiased study?

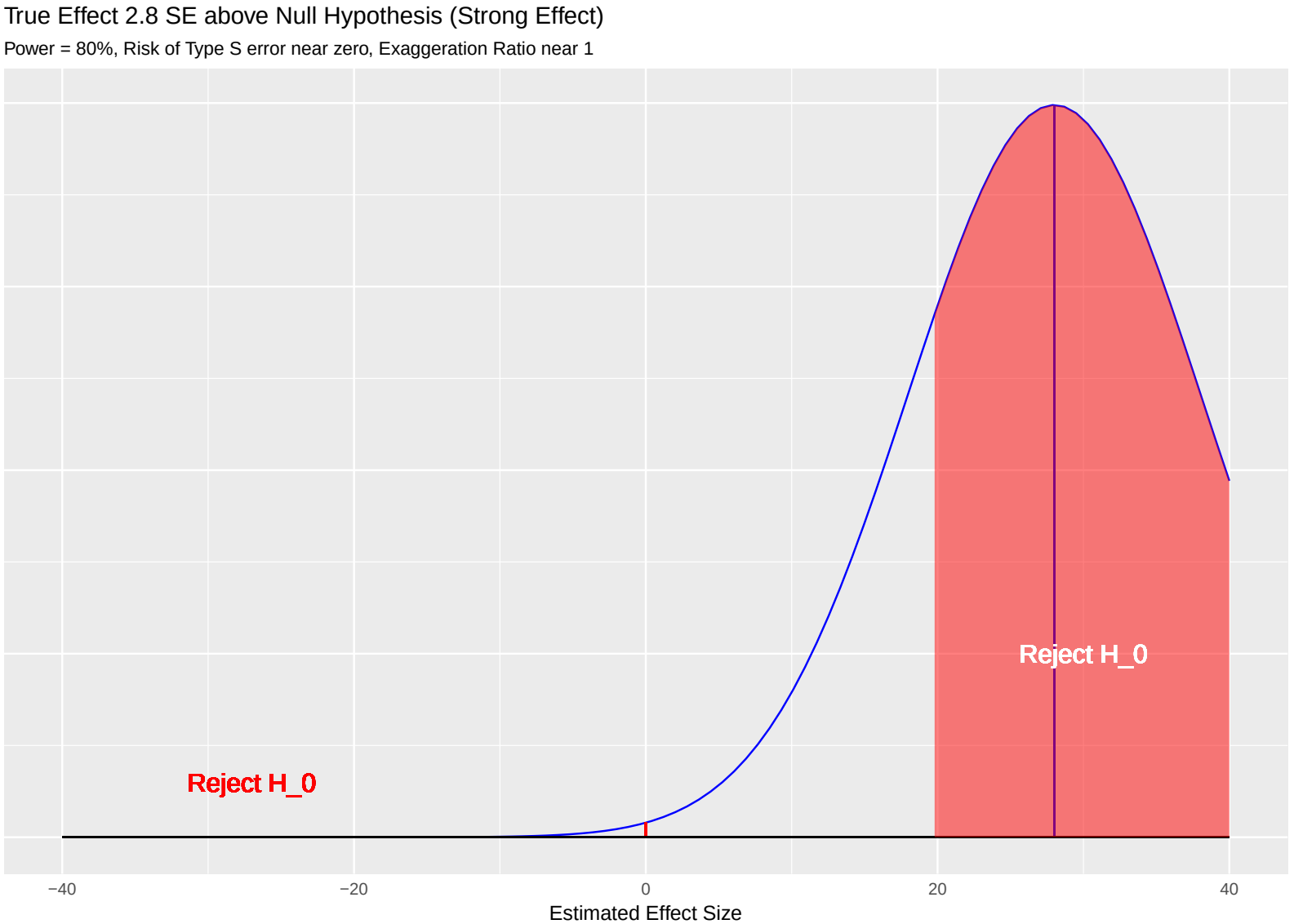
Suppose the true effect that is 2.8 standard errors away from zero, in a study built to have 80% power for that effect with 95% confidence.

```
set.seed(201803161)
retrodesign(A = 28, s = 10, alpha = 0.05)
```

```
$power
[1] 0.7995569

$typeS
[1] 1.210843e-06

$exaggeration
[1] 1.12875
```

- With the power this high (80%), we have a type S error rate of 1.2 x 10^{-6} and an expected exaggeration factor of 1.13.
- Nothing to worry about with either direction of a statistically

80% power; large effect (2.8 SE above H_0)



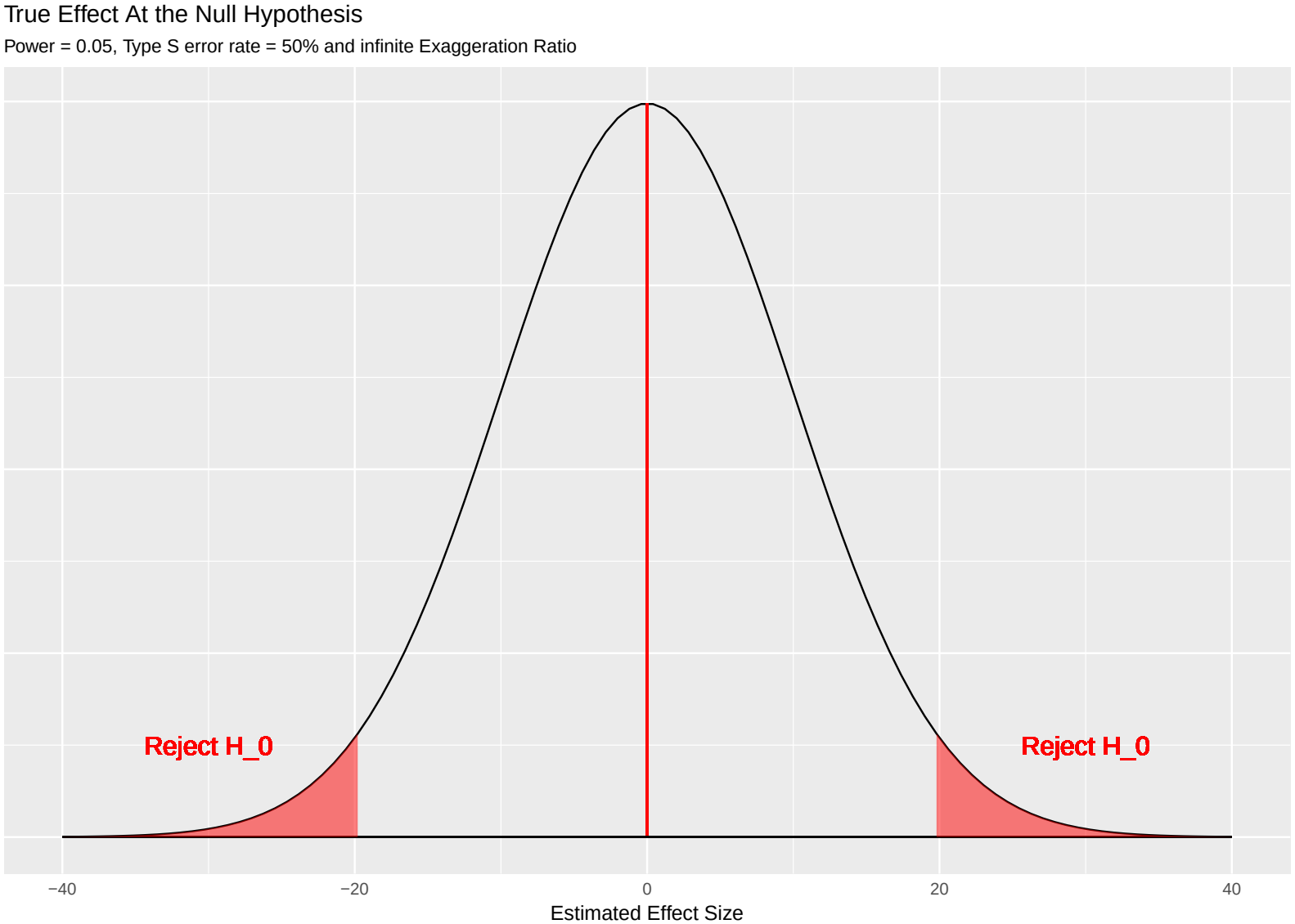
retrodesign for Zero Effect

```
set.seed(201803162)
retrodesign(A = 0, s = 10)
```

```
$power
[1] 0.05

$typeS
[1] 0.5

$exaggeration
[1] Inf
```

- Power = 0.5, Pr(Type S error) = 0.5, Exaggeration Ratio is infinite.

Power, Type S and Type M Errors: Zero Effect

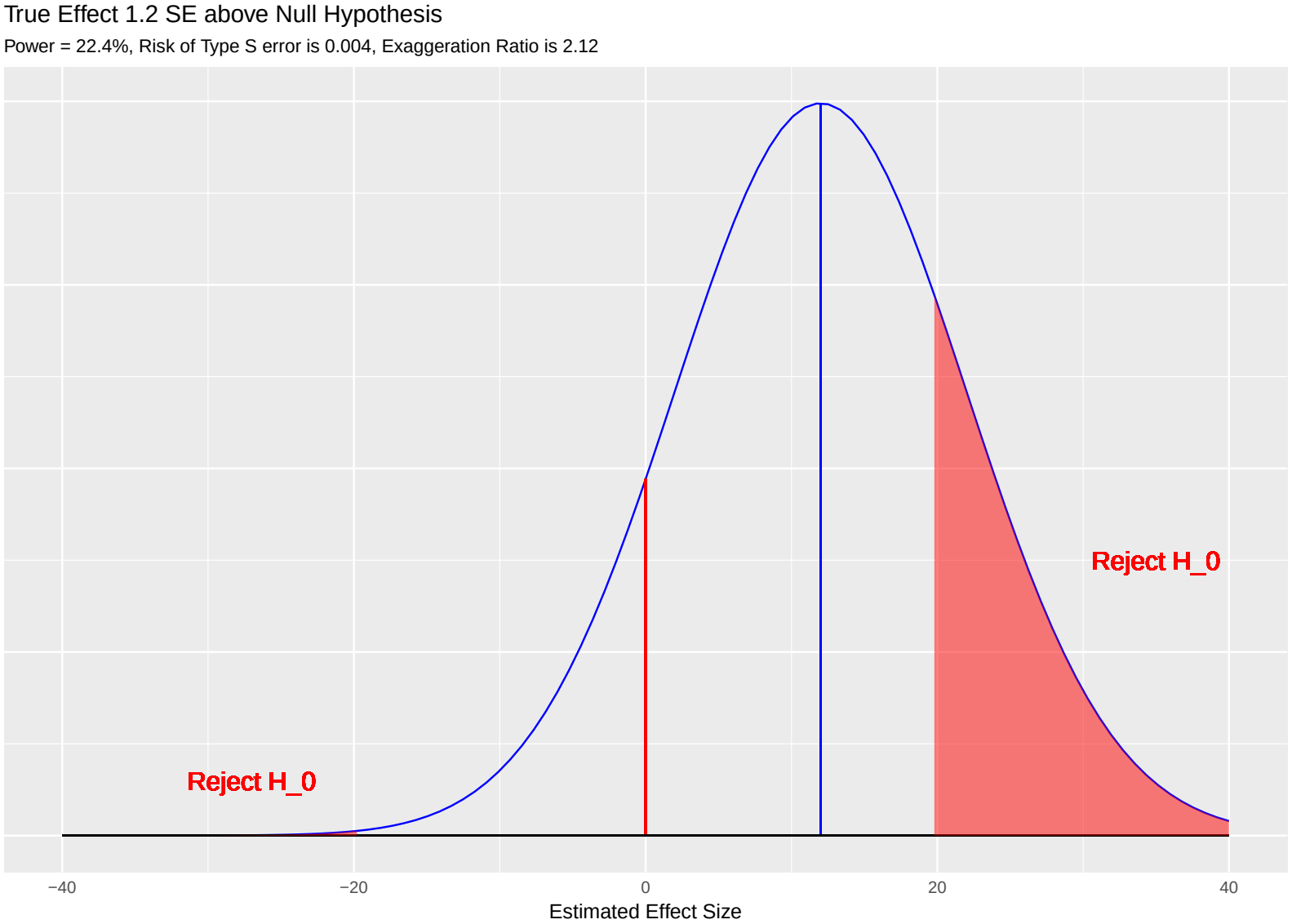


Retrodesign for a true effect 1.2 SE above H_0

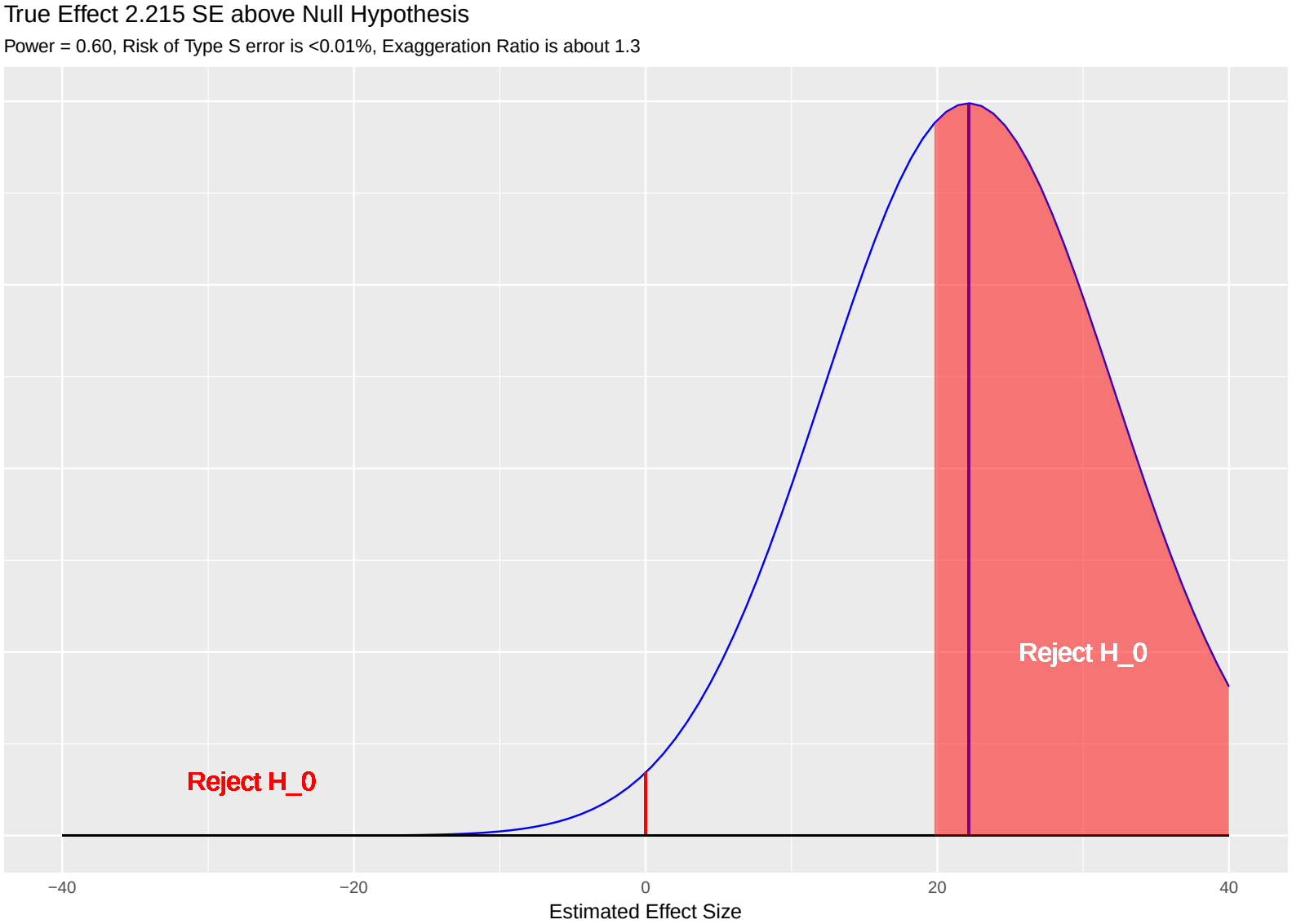
```
set.seed(201803163)
retrodesign(A = 12, s = 10)
```

```
$power
[1] 0.224427

$typeS
[1] 0.003515367

$exaggeration
[1] 2.117846
```

What 22.4% power looks like. . .



What 60% Power Looks Like



Gelman & Carlin, Figure 2

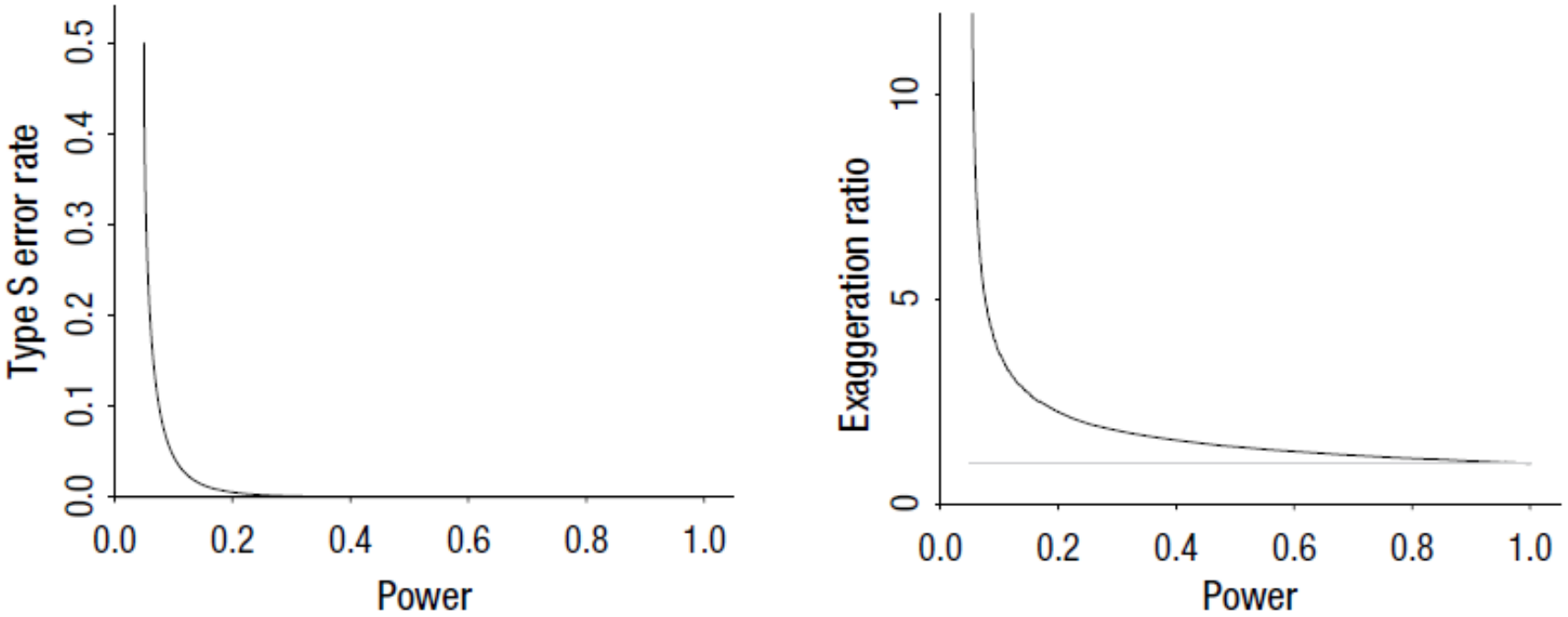


Figure 2. Type S error rate and exaggeration ratio as a function of statistical power for unbiased estimates that are normally distributed. If the estimate is unbiased, the power must be between 0.05 and 1.0, the Type S error rate must be less than 0.5, and the exaggeration ratio must be greater than 1. For studies with high power, the Type S error rate and the exaggeration ratio are low. But when power gets much below 0.5, the exaggeration ratio becomes high (that is, statistically significant estimates tend to be much larger in magnitude than true effect sizes). And when power goes below 0.1, the Type S error rate becomes high (that is, statistically significant estimates are likely to be the wrong sign).

Example: Beauty and Sex Ratios

Kanazawa study of 2972 respondents from the National Longitudinal Study of Adolescent Health

- Each subject was assigned an attractiveness rating on a 1-5 scale and then, years later, had at least one child.
- Of the first-born children with parents in the most attractive category, 56% were girls, compared with 48% girls in the other groups.
- So the estimated difference was 8 percentage points with a reported $p = 0.015$
- Kanazawa stopped there, but Gelman and Carlin don't.

Beauty and Sex Ratios

We need to postulate an effect size, which will not be 8 percentage points. Instead, Gelman and colleagues hypothesized a range of true effect sizes using the scientific literature.

> *There is a large literature on variation in the sex ratio of human births, and the effects that have been found have been on the order of 1 percentage point (for example, the probability of a girl birth shifting from 48.5 percent to 49.5 percent). Variation attributable to factors such as race, parental age, birth order, maternal weight, partnership status and season of birth is estimated at from less than 0.3 percentage points to about 2 percentage points, with larger changes (as high as 3 percentage points) arising under economic conditions of poverty and famine. (There are) reliable findings that male fetuses (and also male babies and adults) are more likely than females to die under adverse conditions.*

So, what is a reasonable effect size?

- Small observed differences in sex ratios in a multitude of studies of other issues (much more like 1 percentage point, tops)
- Noisiness of the subjective attractiveness rating (1-5) used in this particular study

So, Gelman and colleagues hypothesized three potential effect sizes (0.1, 0.3 and 1.0 percentage points) and under each effect size, considered what might happen in a study with sample size equal to Kanazawa's study.

How big is the standard error?

- From the reported estimate of 8 percentage points and p value of 0.015, the standard error of the difference is 3.29 percentage points.
  - If p value = 0.015 (two-sided), then Z score = `qnorm(p = 0.015/2, lower.tail=FALSE)` = 2.432
  - Z = estimate/SE, and if estimate = 8 and Z = 2.432, then SE = 8/2.432 = 3.29

Retrodesign Results: Option 1

- Assume true difference D = 0.1 percentage point (probability of girl births differing by 0.1 percentage points, comparing attractive with unattractive parents).
- Standard error assumed to be 3.29, and $\alpha = 0.05$

```
set.seed(201803164)
retrodesign(A = 0.1, s = 3.29, alpha = 0.05)
```

```
$power
[1] 0.05010584

$typeS
[1] 0.4645306

$exaggeration
[1] 76.93614
```

Option 1 Conclusions

Assuming the true difference is 0.1 means that probability of girl births differs by 0.1 percentage points, comparing attractive with unattractive parents.

If the estimate is statistically significant, then:

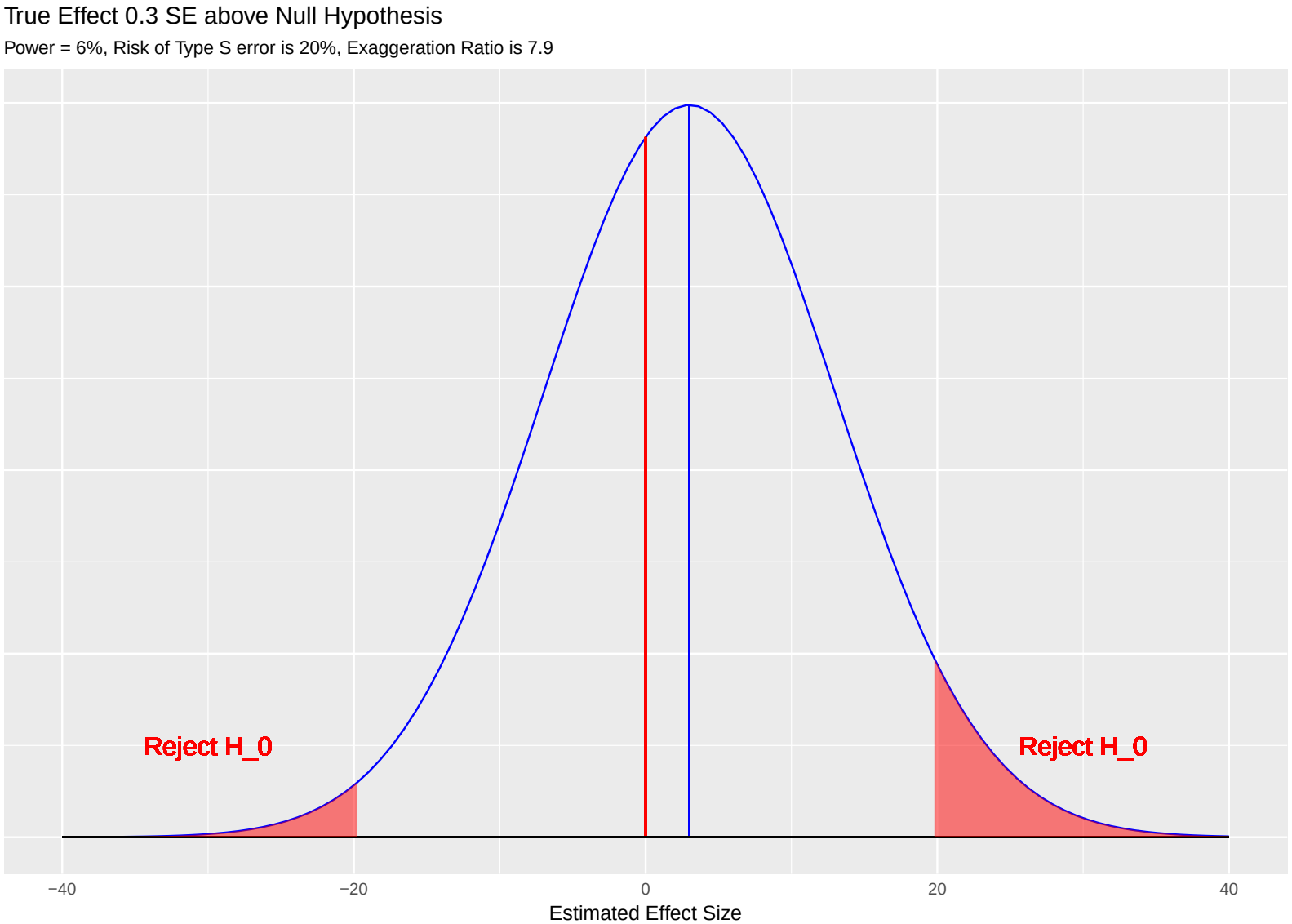
1. There is a 46% chance it will have the wrong sign (from the Type S error rate).
2. The power is 5% and the Type S error rate of 46%. Multiplying those gives a 2.3% probability that we will find a statistically significant result in the wrong direction.
3. We thus have a power - 2.3% = 2.7% probability of showing statistical significance in the correct direction.
4. In expectation, a statistically significant result will be 78 times too high (the exaggeration ratio).

Retrodesign Results: Options 2 and 3

Assumption	Power	Type S	Exaggeration Ratio
D = 0.1	0.05	0.46	78
D = 0.3	0.05	0.39	25
D = 1.0	0.06	0.19	7.8

- Under a true difference of 1.0 percentage point, there would be
  - a 4.9% chance of the result being statistically significantly positive and a 1.1% chance of a statistically significantly negative result.
  - A statistically significant finding in this case has a 19% chance of appearing with the wrong sign, and
  - the magnitude of the true effect would be overestimated by an expected factor of 8.

What 6% power looks like. . .



Gelman's Chief Criticism: 6% Power = D.O.A.

Their effect size is tiny and their measurement error is huge. My best analogy is that they are trying to use a bathroom scale to weigh a feather . . . and the feather is resting loosely in the pouch of a kangaroo that is vigorously jumping up and down.

What to do?

In advance, **and** after the fact, think hard about what a plausible effect size might be.

Then. . .

- Analyze *all* your data.
- Present *all* your comparisons, not just a select few.
  - A big table, or even a graph, is what you want.
- Make your data public.
  - If the topic is worth studying, you should want others to be able to make rapid progress.

But I do studies with 80% power?

Based on some reasonable assumptions regarding main effects and interactions (specifically that the interactions are half the size of the main effects), you need **16 times** the sample size to estimate an interaction that you need to estimate a main effect.

> *And this implies a major, major problem with the usual plan of designing a study with a focus on the main effect, maybe even preregistering, and then looking to see what shows up in the interactions.*
>
> *Or, even worse, designing a study, not finding the anticipated main effect, and then using the interactions to bail you out. The problem is not just that this sort of analysis is "exploratory"; it's that these data are a lot noisier than you realize, so what you think of as interesting exploratory findings could be just a bunch of noise.*

- Gelman 2018-03-15

What I Think I Think Now

- Null hypothesis significance testing is much harder than I thought.
  - The null hypothesis is almost never a real thing.
  - Rather than rejiggering the cutoff, I would mostly abandon the p value as a summary
  - Replication is far more useful than I thought it was.
- Some hills aren't worth dying on.
  - Think about uncertainty intervals more than confidence or credible intervals
  - Retrospective calculations about Type S (sign) and Type M (magnitude) errors can help me illustrate ideas.
- Which method to use is far less important than finding better data
  - The biggest mistake I make regularly is throwing away useful data
  - I'm not the only one with this problem.
- The best thing I do most days is communicate more clearly.
  - When stuck in a design, I think about how to get better data.
  - When stuck in an analysis, I try to turn a table into a graph.
- I have A LOT to learn.

Next Time?

- Matching in Observational Studies to estimate Causal Effects
- Quiz 2