Replication Has Limited Power to Detect Bad Science

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Replication seems a sensible way to assess whether a scientific result is right. The intuition is clear: if a result is right, you should get a similar answer when repeating the work; if it it's wrong, your answer should be quite different. Statisticians have devised numerous statistical tests for deciding whether a replication passes or fails thus validating of refuting the original result. I simulate many of these tests across a range of conditions. For exact replications, simple significance testing works fine as a validation test, but no test works well when replicas diverge from the original studies. Much of the replication literature focuses, perhaps unwittingly, on methods for testing whether the studies are similar; these tests work quite poorly under all conditions analyzed here.

Introduction

The basic replication rationale goes something like this: (1) many published papers are wrong; (2) this is a serious problem the community must fix; and (3) systematic replication is an effective solution. (In recent months, I've seen an uptick in pre-registration as another solution. That's a topic for another day.) In this post, I focus on the third point and ask: viewed as a statistical test, how well does replication work; how well does it tell the difference between valid and invalid results?

I consider a basic replication scheme in which each original study is repeated once.

Various authors have proposed tests for deciding whether a replication succeeds or fails. These include significance testing of the replica study, seeing whether the observed effect size of one study falls in the confidence or prediction interval of the other, checking whether the confidence or prediction intervals of the two studies overlap, significance testing of the studies combined via meta-analysis, and comparing the observed effect size of the replica study with a "small telescope" threshold derived from the smallest true effect size the original study could have plausibly detected.

I simulate these rules (and more) across many replication conditions and compute false positive and false negative rates across a range of conditions. The simulations vary the samples size from 10 to 1000 and true effect size from 0 to 1; in total, I simulate <<12,100>> conditions each with 10^4 simulated replications, for a grand total of more than <<100 million>> simulated instances.

A replication is *exact* if the two studies are sampling the same population and *near-exact* if the populations differ slightly. This is an obvious replication scenario. You have a study that you think may be a false positive; to check it out, you repeat the study, typically with a larger sample size, taking care to ensure that the replica closely matches the original.

A replication is *inexact* if the two studies are sampling very different populations. This scenario seems disconnected from the goal of validating an existing study. Since the populations are different, there's no reason to expect the studies to get similar answers and little basis for declaring a study invalid if the replication fails. What motivates this scenario, I think, is *generalizability* not validity. You have a study that demonstrates an interesting effect in a limited setting and want to know whether it generalizes to other settings.

Significance testing of the replica works fine as a validation test for exact and near-exact replications, but error rates increase rapidly as the populations diverge. All other tests have excessive error rates under all conditions I analyzed. All tests have unacceptable error rates when used to check whether the replications are similar.

Literature

These are the main papers and blog posts that led to this work.

- The Science paper by the Open Science Collaboration "Estimating the reproducibility of psychological science", accessible here **if you have a Science account**, the Comment by Gilbert et al, the authors' response, Uri Simonsohn's blog post commenting on the paper and response, and Daniel Lakens's post on the response
- The Many Labs paper by Klein and many others, the many published comments, and Uri's post
- Uri's Small Telescopes paper, and posts on methods for evaluating replications, the 90x75x50 heuristic for setting replication sample sizes, accepting the NULL, the difficulty of accurately estimating effect size, the difficulty of evaluating replications, and significant results overestimate effect size
- Daniel Lakens's posts on capture percentages and cost/benefit analysis of replications
- Lebel et al's A Guide to Evaluate Replications
- Anderson and Maxwell's paper on replication goals and the Replication Network blog post commenting on the paper
- Papers on prediction intervals by Patil, Peng, and Leek and Stanley and Spence
- Sabeti's counterpoint in the Boston Globe
- Several articles from the Sackler Colloquium on Improving the Reproducibility of Scientific Research published in PNAS, notably Fanelli's opinion piece and Shiffrin, Börner, and Stigler's big picture view

The Simulation

The software first simulates *studys* across a range of conditions, then combines pairs of studies into *pairwise replications*, applies rules (called *measures*) for deciding which pairwise replications pass, summarizes the results as counts and pass rates, and finally computes true and false positive and negative rates for measures and conditions of interest.

The studies are simple two group comparisons parameterized by sample size n and population effect size d_{pop} ($d_{pop} \geq 0$). For each study, I generate two groups of random numbers, each of size n. One group, *group0*, comes from a standard normal distribution with $mean = 0$; the other, *group1*, is standard normal with mean $d_{pop} \geq 0$. I then calculate basic statistics of interest, most notably the *standardized observed effect size* d_{sdz}, aka *Cohen's d*, as the mean of *group1* minus the mean of *group0* divided by the pooled standard deviation of the two groups. The software simulates many studies (default 10^4) for each combination of n and d_{pop}.

When I need to be pedantic, I use the terms *study instance* for each individual study and *study set* for the ensemble of study instances for a given combination of n and d_{pop}.

The program varies n from 10 to 1000 and d_{pop} from 0 to 1. When analyzing results, I interpolate to get values that weren't simulated directly.

To generate pairwise replications, I consider all (ordered) pairs of study sets. For each pair, the software permutes the instances of each study, then combines the instances row-by-row to get *pairwise replication instances*. It's convenient to think of the first study of the pair as the *original* and the second as the *replica*.

A *pairwise replication set* is the ensemble of pairwise replication instances for a given pair of study sets. Four variables parameterize each pairwise replication set: $n1$, $n2$, $d1pop$, $d2_{pop}$. These are, naturally enough, the sample and population effect sizes for the two study sets.

After forming the pairwise replications, I apply *measures*, i.e., rules for deciding which replications pass. Each measure takes a pairwise replication set as input and returns a vector of boolean values telling which instances pass or fail. The result is a boolean matrix whose rows represent instances and columns represent measures.

This post focuses on eight measures that seem most important.

- *sig2* - the second study of the pair has a significant p-value
- *sigm* - the fixed effect meta-analyis of the studies has a significant p-value

- *d1.c2* (resp. *d2.c1*) - $d1_{sdz}$ (resp. $d2_{sdz}$), the standardized observed effect size (aka Cohen's d) of the first (resp. second) study is in the confidence interval of the second (resp. first) study; my implementation of confidence intervals is based on Uri Simonsohn's code supporting his post We cannot afford to study effect size in the lab
- *d1.p2* (resp. *d2.p1*) - $d1_{sdz}$ (resp. $d2_{sdz}$) is in the prediction interval of the second (resp. first) study; my implementation of prediction intervals adapts code from David Stanley's predictionInterval package
- *c1.c2* (resp. *p1.p2*) - the confidence (rep. prediction) intervals of the two studies overlap

All measures assume that the first study is significant (*sig1* in my notation) and the observed effect sizes of the two studies have the same sign (both positive or both negative).

I briefly examine Uri Simonsohn's *small telescopes* method from his paper and post - *d2.scp1* in my notation. My implementation is based on Uri's code supporting that post.

Small telescopes, unlike the others, assumes that *sig2* holds. For this reason, it needs a separate analysis.

The software sumarizes the results by counting the number of positive results for each measure, taking into account the assumptions in the preceding paragraph, and then converts the counts into pass rates. The final step is to convert pass rates into true positive, false positive, true negative, and false negative rates. This requires a definition of *true* and *false* instances, which in turn requires an explicit statement as to which replication instances represent replications that should succeed vs. ones that should fail.

Correctness Criteria

I found no concise, rigorous definition of replication correctness anywhere. Many authors rely on same variant of "A replication should succeed if my method or methods say so". It's impossible to define error rates with such circular definitions.

Replication researchers study two aspects of correctness.

1. The most basic concern is that the original study is a false positive.
2. The other concern is that the observed effect sizes of the two studies are inconsistent with each other. This might mean that the population effect sizes are different or that one result is an outlier.

The first concern seems sensible (at least, as sensible as any other use of the null hypothesis testing framework). The second concern baffles me: if the two studies are sampling different populations or one is an outlier, why does this invalidate the first study?

I'm tempted to ignore the second concern, but most of the proposed replication methods address it. Sadly, I'm stuck with it for purposes of this post.

Here are the precise technical definitions I use in the code.

1. *non-zero* - a replication instance is *true* if $d1_{pop} \neq 0$, i.e., the population effect size for the first study is non-zero
2. *same-effect* - a replication instance is *true* with *tolerance* δ if $abs(d1_{pop} - d2_{pop}) \leq \delta$, i.e., the two population effect sizes differ by at most δ

Note that these criteria depend only on the population effect sizes.

Nomenclature

I've already introduced most of the nomenclature. Here is a concise reprise.

For studies

- *study instance* is a single simulated study
- n is the sample size
- d_{pop} is the population effect size

- d_{sdz} is the standardized observed effect size (aka Cohen's d)
- *study set* is the set of study instances for a given n and d_{pop}

For pairwise replications, I add the letters *1*, *2* to mean parameters or statistics from the first or second study of the pair respectively.

- *pairwise replication instance* (or simply *replication instance*) is an ordered pair of study instances
- *s1* and *s2* refer to the first and second study of the pair; *sm* means the fixed-effect meta-analysis of the two studies
- $n1$, $d1_{pop}$, $d1_{sdz}$ are the sample size, population effect size, and Cohen's d for the first study
- $n2$, $d2_{pop}$, $d2_{sdz}$ are the sample size, population effect size, and Cohen's d for the second study
- dm_{sdz} is Cohen's d from the meta-analysis
- *pairwise replication set* (or simply *replication set*) is the set of replication instances for a given $n1$, $n2$, $d1pop$, and $d2_{pop}$
- A replication instance or set is *exact* if the two studies are sampling the same population; for our simulated replications, this means $d1_{pop} = d2_{pop}$
- The terms *true* and *false* refer to the answers given by a correctness criterion when applied to replication instances: *true instance* is an instance for which the criterion returns true; *false instance* is one for which the criterion returns false
- The terms *positive* and *negative* refer to the results of applying measures to replication instances: *positive instance* is an instance for which the measure returns true; *negative instance* is one for which the measure return false
- The terms *true positive*, *false positive*, *true negative*, and *false negative* combine the notions of true vs. false and positive vs. negative instance. For a given correctness criterion and measure
  - *true positive instance* is a replication instance for which the correctness criterion and measure both return true
  - *false positive instance* is an instance for which the correctness criterion is false but the measure returns true
  - *true negative instance* is an instance for which the correctness criterion and measure both return false
  - *false negative instance* is an instance for which the correctness criterion is true but the measure returns false

For correctness criteria

- *non-zero* is *true* if $d1_{pop} = 0$
- *same-effect* is *true* if $d1_{pop} = d2_{pop}$; with tolerance δ, *same-effect* is *true* if $abs(d1_{pop} - d2_{pop}) \leq \delta$

For *non-zero*

- a *false positive* occurs when $d1_{pop} = 0$, but the measure returns true
- a *false negative* occurs when $d1_{pop} \neq 0$, but the measure returns false

For *same-effect* with tolerance δ

- a *false positive* occurs when $abs(d1_{pop} - d2_{pop}) > \delta$, but the measure returns true
- a *false negative* occurs when $abs(d1_{pop} - d2_{pop}) \leq \delta$, but the measure returns false

To simplify the presentation

- *s1* (the first study of the replication instance) represents the original study and *s2* (the second study) represents the replica
- error rates are relative to *sig1*; e.g, an error rate of 5% means 5% of the replications satisfying *sig1* exhibit the error

Graph Types

The parameter space is vast, because it's possible to vary each of the four paramters ($n1$, $n2$, $d1pop$, $d2_{pop}$) across a considerable range. It's challenging to present the data in a comprehensive, yet concise and intelligible, manner. I use several kinds of graphs.

1. line graphs - simple and intuitive, I think, but not good at showing data that varies across many parameters
2. heatmaps - still reasonably intuitive and somewhat better at depicting multiple parameters
3. rate-vs-rate scatter plots - able to display error rates across large swaths of parameter space but with much less parameter resolution and perhaps less intuitive clarity
4. aggregate line graphs - shows the same data as rate-vs-rate scatter plots but for fewer measures and with better resolution

Results

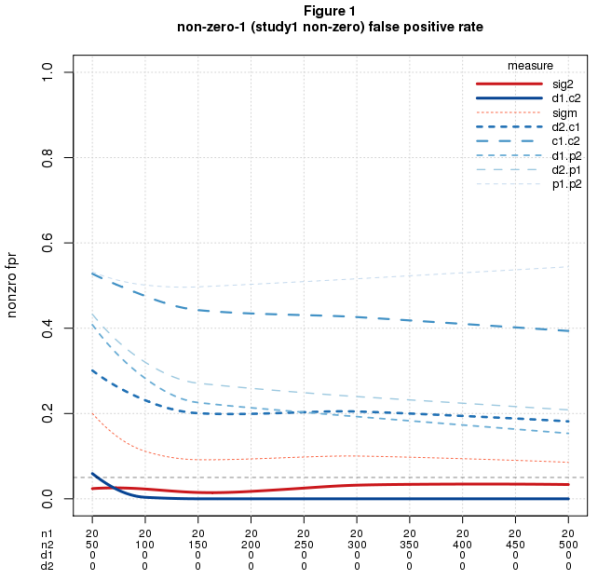
Replication used for validation

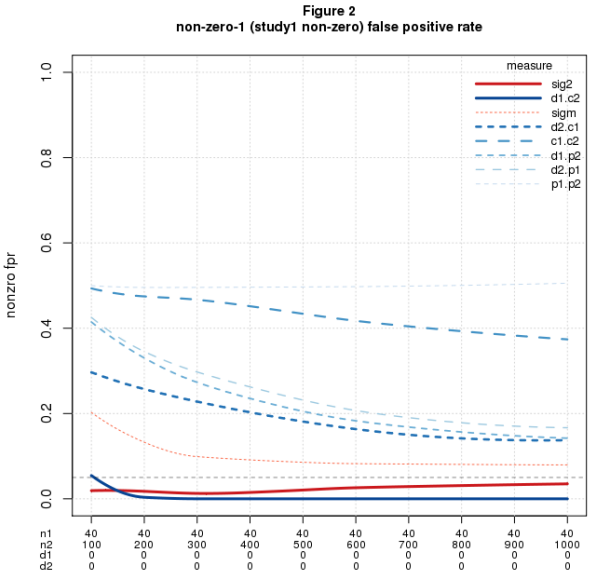
When replication is used to validate a study, *non-zero* is the correctness criterion that matters. I first present results for exact replications, then inexact, and finally near-exact.

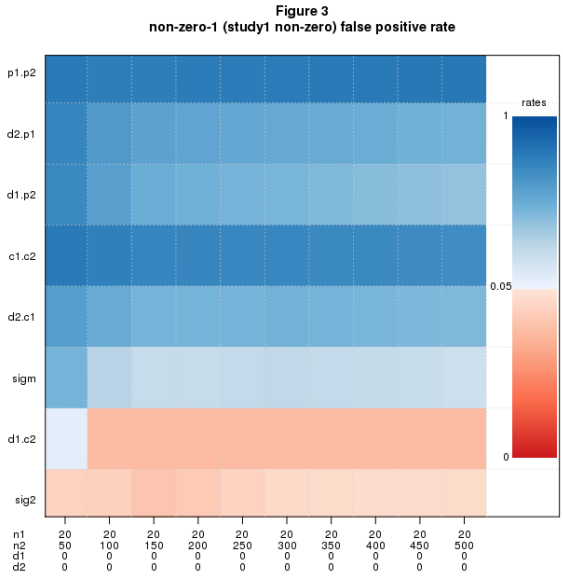
Exact replications

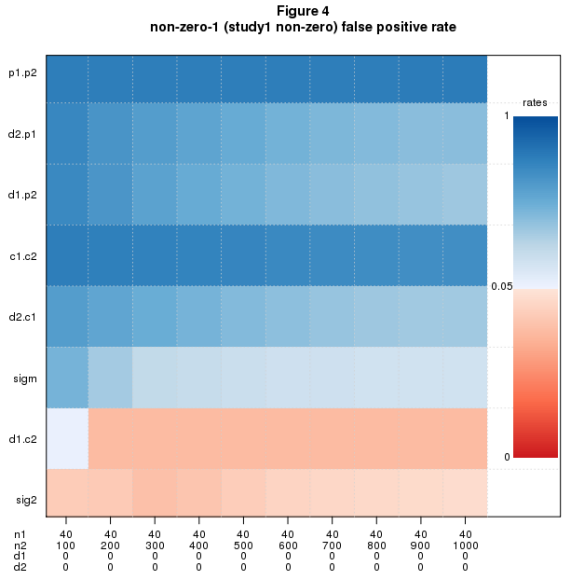
Figures 1-4 show false positive rates for two values of $n1$ (20 and 40) and a range of values for $n2$. The smallest $n2$ in each case satisfies the recommendation in Uri's post on the 90x75x50 heuristic that $n2 = 2.5 \times n1$ is big enough. The x-axis shows all four parameters using $d1$, $d2$ as shorthand for $d1_{pop}$, $d2_{pop}$ to conserve space. $d1_{pop} = d2_{pop} = 0$ throughout because this is the only way to get false positives for *non-zero* with exact replications.

The first two figures are line graphs with the false positive rate along the y-axis; these graphs use color and other line properties to distinguish the measures. The latter two are heatmaps with measures along the y-axis; these plots use color (shades of red and blue) to depict the the false positive rate; the switch from red to blue is set at the conventionally accepted threshold of 0.05 for false positives.



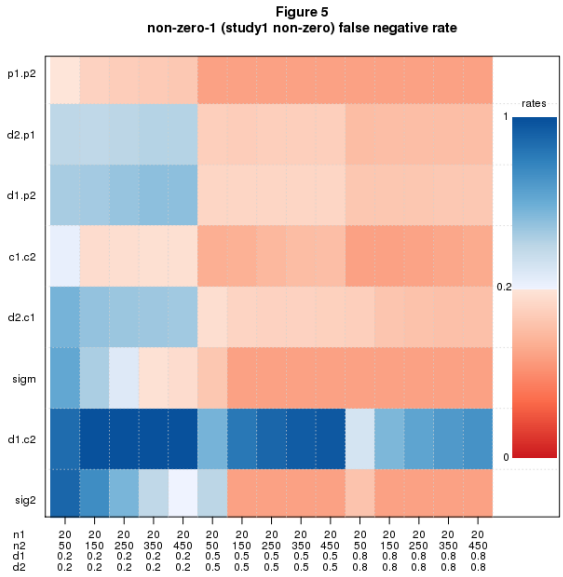


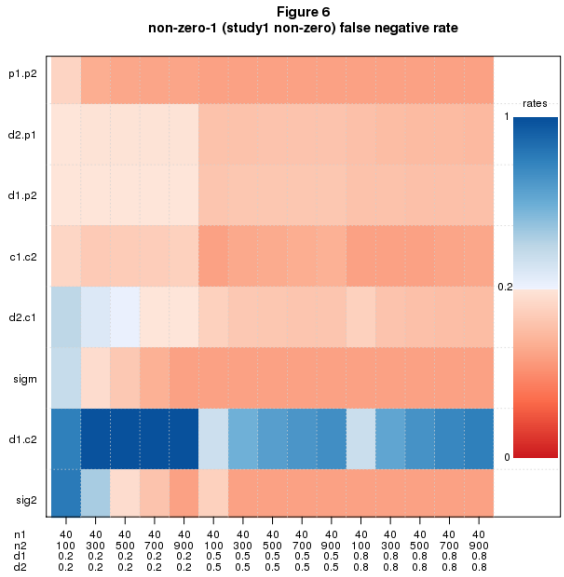




The only measures with acceptable false positive rates across most of the parameter range are *sig2* and *d1.c2*.

Plotting false negatives is more tiresome, because we can also vary $d1_{pop}$ (and simultaneously $d2_{pop}$, of course). Figures 5-6 are heatmaps of false negative rates for the same range of $n1$, $n2$ (but with a coarser grid of $n2$ values) and for $d1_{pop} = d2_{pop}$ varying over $\{0.2, 0.5, 0.8\}$. Each heatmap shows all three values of d_{pop}; the dark vertical lines visually split each plot into separate "panels" for each d_{pop}. The red-to-blue transition is set at the conventionally accepted threshold of 0.20 for false negatives.

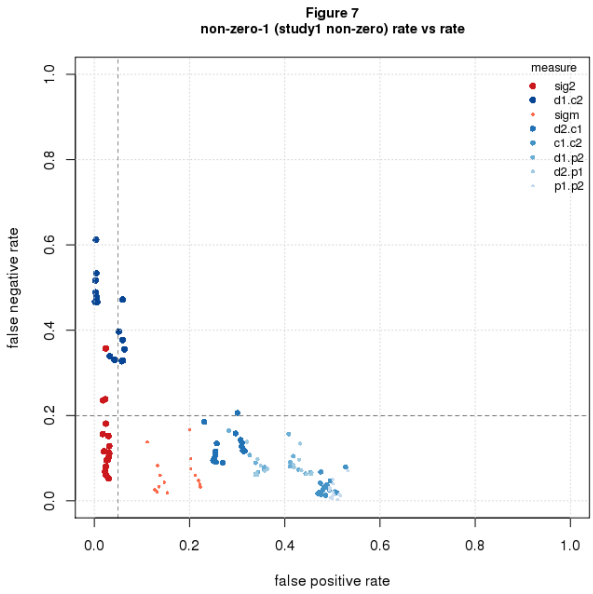




As one would expect, performance improves as sample and effect sizes grow. The heatmaps for the larger sizes show a lot of red, telling us that many measures have acceptable false negative rates under these conditions.

For a measure to be usable, both error rates must be acceptable. Let's compare the heatmaps for false positive and false negatives - figures 3-4 and 5-6. The only measure that is mostly red across all four figures is *sig2*; *d1.c2*, which looked good for false positives, is consistently bad for false negatives.

So far so good, but I've only shown data for a few values of $n1$. To see more conditions, I use a *rate-vs-rate* graph, inspired by *receiver operating characteristic (ROC)* curves, to plot false negative vs. false positive rates for a large range of conditions. See figure 7. The data in this figure extends the cases shown above: $n1$ varies from 20-160 in steps of 20, $n2$ is 2.5 or 5 $\times n1$, $d1_{pop}$ and $d2_{pop}$ range from 0 to 1 in steps of 0.1 with the constraint $d1_{pop} = d2_{pop}$. Each point shows the mean false negative vs. mean false positive rate for these conditions grouped by $n1, n2$, which are the only observable parameters. The dashed lines demark the conventionally acceptable error rates: 0.05 for false positives and 0.2 for false negatives; the bottom left hand corner is the region where both error rates are acceptable.



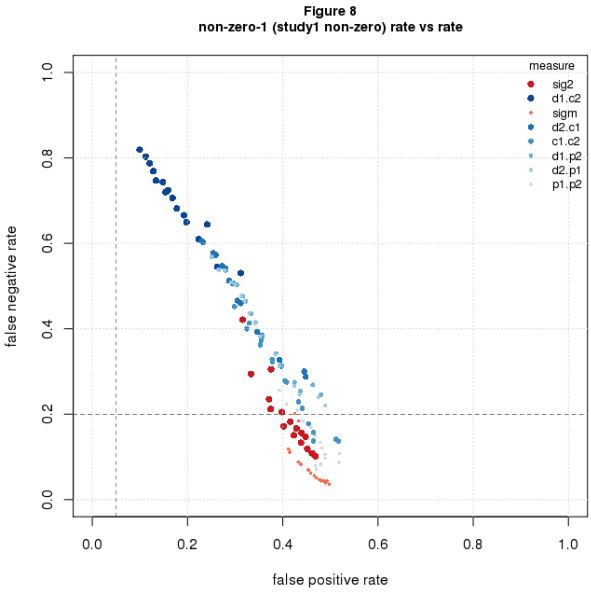
The graph is ugly but the message clear: *sig2* is the only measure with points falling in the acceptable range.

Boiling it down: for exact replications, *sig2* is the only game in town. Its false positive rate is the significance level divided by 2 (the factor of 2 because it's one-sided). The false negative rate is $1 - power$ (the correlation of these statistics across the entire dataset is 0.99, data not shown).

Inexact replications

For inexact replications there are more cases to consider since $d1_{pop}$ and $d2_{pop}$ can vary independently. I'll jump straight to rate-vs-rate graphs to cover the ground succinctly using the same values of $n1$ and $n2$ as above, namely, $n1$ varies from 20-160 in steps of 20, and $n2$ is 2.5 or 5 $\times n1$.

Figures 8 shows the results: error rates are dreary in all conditions.

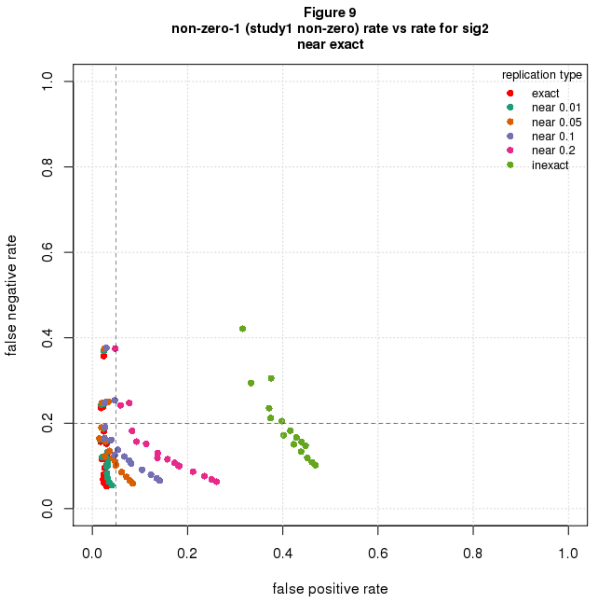


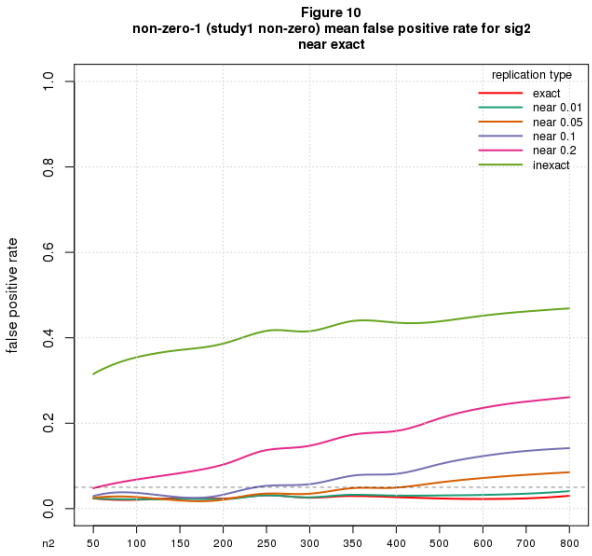
Near exact replications

It seems odd that *sig2* works fine for *non-zero* in exact replications but so poorly in inexact ones. What if we try *near exact replications*, ones where $d1_{pop}$ and $d2_{pop}$ differ slightly? Figure 9 shows the results for nearness ranging from *exact* to fully *inexact* with steps in between. The figure is a rate-vs-rate graph that shows a single measure (*sig2*) across the various nearness values.

The results are discouraging. It doesn't take much separation to exceed acceptable error rates. When $d1_{pop}$ and $d2_{pop}$ differ by as little as 0.05, abut half the points lie beyond the acceptable 0.05 false positive rate; by time we get to 0.2, all points are bad.

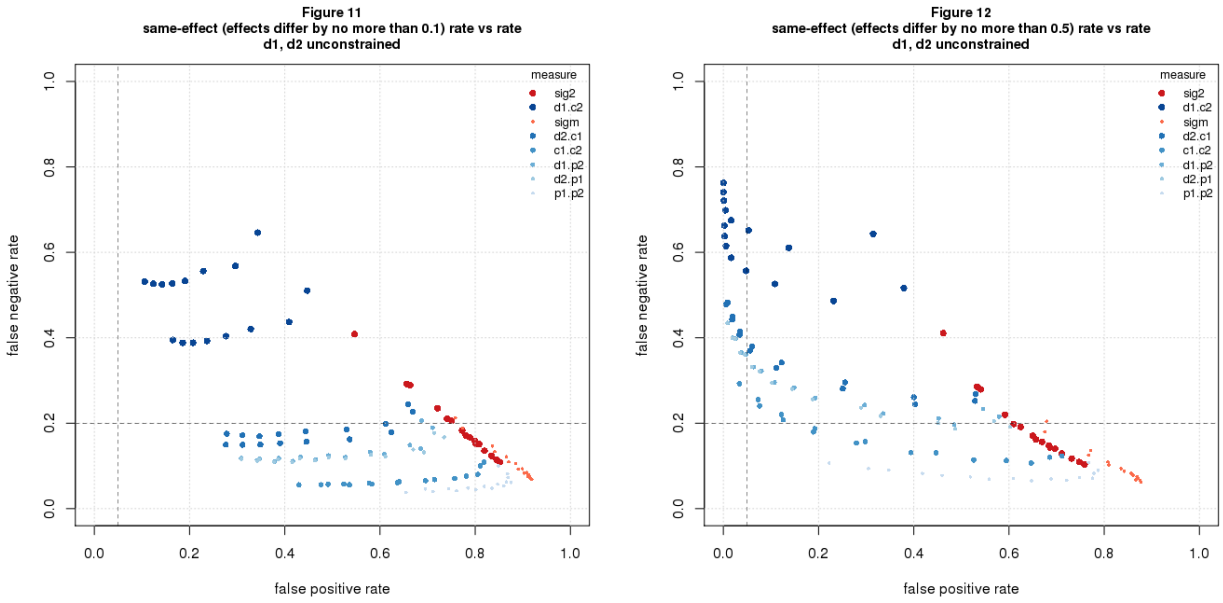
What's going on is a consequence of power. The data in the rate-vs-rate graphs vary $n1$ from 20 to 160 and $n2$ from 50 to 800. With $d2_{pop} = 0.05$, *sig2* has 12% power at $n2 = 500$ and 17% at $n2 = 800$. This is anemic from the usual power standpoint but is plenty to drive *sig2*'s false positive rate beyond 0.05. Figure 11 illustrates the point by graphing *sig2*'s mean false positive rate grouped by $n2$ vs. $n2$. False positive rate is fine across the whole graph for *exact* and until $n2 > 400$ or so for $nearness = 0.05$, but quickly exceeds the acceptable error threshold for larger separations.

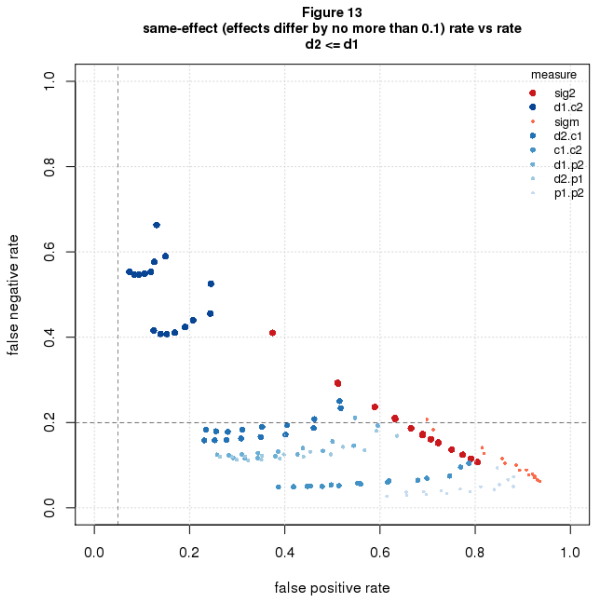


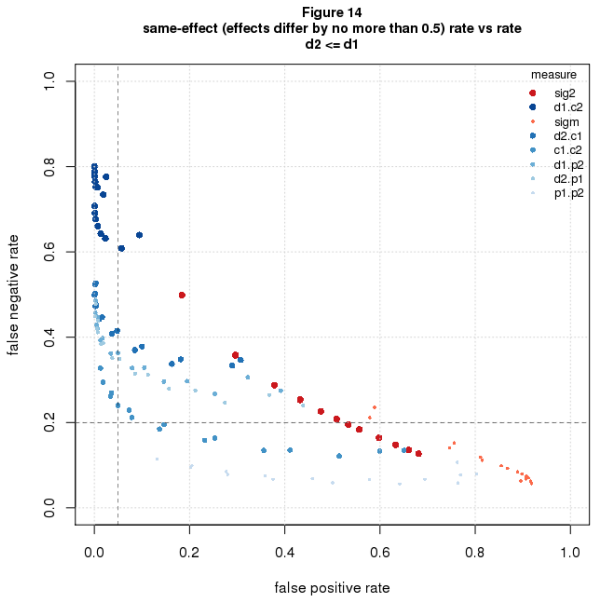


Replication used to check effect size

I now turn to the second correctness criterion, *same-effect*, which tests whether the population effect sizes of the replica and original studies are similar. Figures 11-14 show rate-vs-rate graphs for two values of δ (0.1 or 0.5), and for fully inexact replications (figures 11-12) and assuming $d2_{pop} \leq d1_{pop}$ (figures 13-14). The rationale for showing $\delta = 0.1$ is that this is the largest nearness value with any acceptable points in the *non-zero* analysis; the rationale for $\delta = 0.5$ is this is the difference between *small* and *large* effect sizes in *Cohen's d* terminology. Assuming $d2_{pop} \leq d1_{pop}$ reflects the view that investigators, consciously or not, tend to do original studies with populations that best exhibit the phenomenon of interest







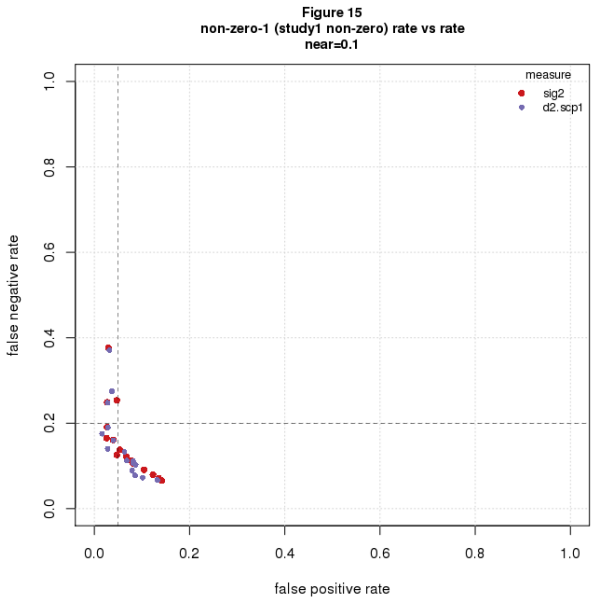
The results are bad in all cases. Error rates are better for $\delta = 0.5$ and with $d2_{pop} \leq d1_{pop}$, but not enough.

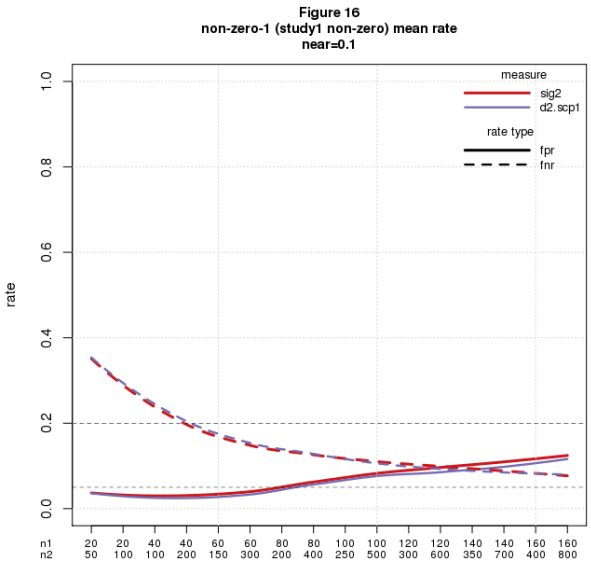
Small telescopes

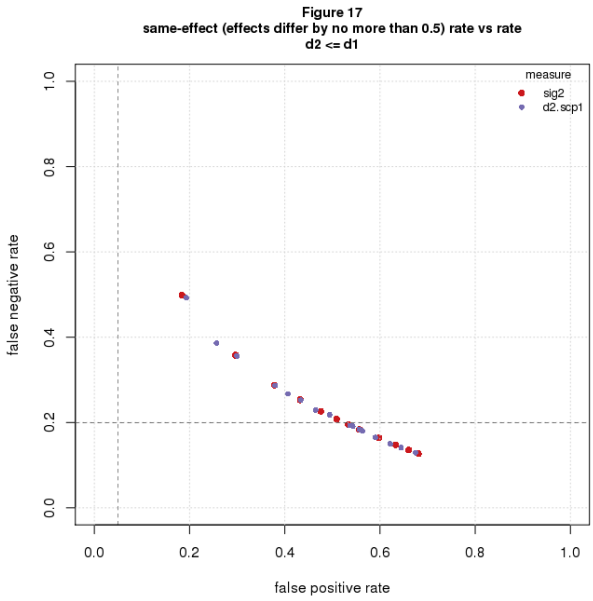
Uri Simonsohn's *small telescopes* method combines both correctness criteria in a single test. It requires

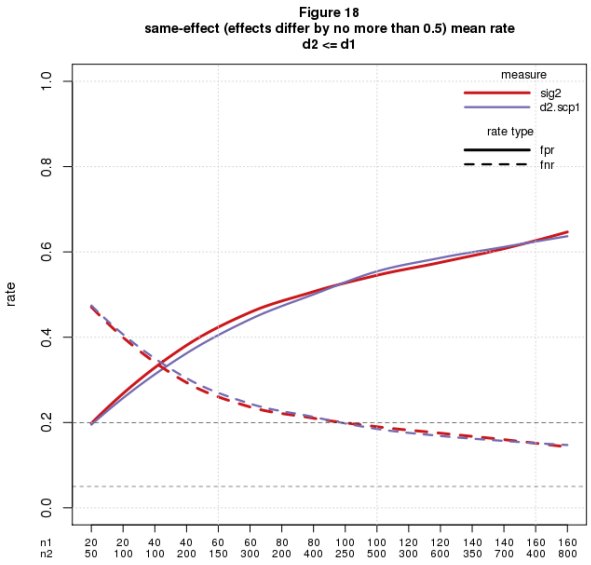
1. *sig2* is true (presumably to test *non-zero*) and
2. $d2_{sdz}$, the replica's observed effect size, exceeds a threshold deemed to be the smallest effect size likely to be observed if *same-effect* is true.

Figures 15-18 compare *sig2* and *small telescopes* (*d2.scp1* in my notation) for the two correctness criteria. The figures reuse conditions from previous sections: for *non-zero*, I use nearness of 0.1; for *same-effect*, I use $\delta = 0.5$ and with $d2_{pop} \leq d1_{pop}$. Figures 15 and 17 are by now familiar rate-vs-rate graphs; figures 16 and 18 show the same data as aggregate line graphs.









The differences are very small: *small telescopes* has almost no effect over and above *sig2*.

Discussion

Replication is a poor statistical test. It works as a validation test only when the original and replica studies are sampling nearly identical populations. Methods for testing whether the populations are similar work poorly under all conditions I analyzed.

These dismal results are really not surprising once we examine replication in a statistical testing framework. When used for validation, we're drawing inferences about the original study from properties of the replica; it stands to reason this will only work if the two studies are very similar. When used to compare the two populations, we're trying to accurately estimate the two population effect sizes, a problem known to require very large samples - $n > 3000$ by Uri Simonsohn's calculations.

I see several ways my results might be wrong. Perhaps I defined the wrong correctness criteria, or set the error thresholds too low, or analyzed the wrong conditions. I assumed throughout that all population effect sizes were equally likely within the range I studied; perhaps a more nuanced distribution would improve the results. The ever-present danger of software bugs also lurks. If you see a mistake, please let me know and I'll try to fix.

If correct, these results suggest that the replication movement needs to change goals or methods. If the goal remains validation, it's essential that each replica closely match the original study. This bodes ill for large, systematic replication efforts, which typically prioritize uniformity over fidelity to run lots of studies at reasonable cost.

An alternative is to switch gears and focus on generalizability. This would change the mindset of replication researchers more than the actual work. Instead of trying to refute a study, you assume the study is correct within the limited setting of the original investigation and try to extend it to other settings. The scientific challenge becomes defining good "other settings" - presumably there are many sensible choices – and selecting original studies that are a good fit for each. This seems a worthy problem in its own right that will move the field forward no matter how many original studies successfully generalize.

I concluded a previous blog with a paragraph that remains germane:

> Good science drives the field forward; bad science is ephemeral. I know it's aggravating to see so much dreck get published, but it's even more aggravating to see good statisticians and data scientists agonizing over the ordure and spending so much effort trying to root out bad science. We will do more good by helping good scientists do good science than by trying to slow down the bad ones.