Mistakes of Significance

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A collection of R scripts and documents exploring mistakes made by significance testing. The content at present are

- blog post When You Select Significant Findings, You're Selecting Inflated Estimates whose main point is that significance testing is a biased procedure that overestimates effect size; also available on my website here
- blog post Your P-Values are Too Small! And So Are Your Confidence Intervals! which explores the impact of heterogeneous effect sizes on p-values and confidence intervals; also available on my website here
- supplementary material for the blog posts TBD

THE SOFTWARE IS A WORK IN PROGRESS. THE CODE IS ROUGH and SOFTWARE DOCUMENTATION NONEXISTENT. PLEASE GET IN TOUCH IF YOU NEED HELP

Installation and Usage

The software is **not a package** and cannot be installed by `devtools::install_github` or related. Sorry. The simplest way to get the software is to download or clone the entire repo.

The code mostly uses base R capabilities but has a few dependencies: `RColorBrewer`, `akima`, `knitr`, and `pryr`. Since it's not a package, you have to manually install these packages if you don't already have them.

The recommended way to run the program is to `source` the file `R/run.R` into your R session; `R/run.R` will source the rest. Once loaded, you can run the program by executing the statement `run()` as shown below.

```
## This code block assumes your working directory is the root of the distribution

source('R/run.R');
run();
```

This runs the program in a demo-like mode that quickly generates the data and produces the figures and table that appear in this README document. The default computation runs three kinds of simulations totaling 47,000 instances, generates 10 other small data files, and produces 8 figures and one table. The data generation takes about 11 seconds on my small Linux server; the figures and table take about 20 seconds, much of which is spent rendering the plots over a remote X11 connection.

The code that generates the data is in `R/dat_readme.R`; the code that creates the figures and table is in `R/doc_readme.R`.

You can run each part separately by running one or more of the statements below.

```
## This code block assumes your working directory is the root of the distribution
## and you've already sourced R/run.R into your session

init(doc='readme');           # you MUST specify doc to run the program in pieces
dodat();                      # generate data
dodoc();                      # generate figures and tables
dodoc(save.out=F);            # generate figures and tables without saving them
dodoc(figscreen=F);           # generate and save figures without plotting to screen. much faster!
```

The program can also generate the data and outputs for the documents associated with the project. To generate these, execute `run()` with a suitable `doc` argument as shown below.

```
## This code block assumes your working directory is the root of the distribution.

source('R/run.R');
run(doc='ovrfx');              # run code for blog post on significant effect size inflation
```

The `doc` arguments for each document are

document	doc argument
When You Select Significant Findings, You're Selecting Inflated Estimates	`ovrfx`
Your P-Values are Too Small! And So Are Your Confidence Intervals!	`ovrht`
README	`readme`
Supplementary Material for README	`readmesupp`
supplementary material for blog posts TBD	TBD

Nomenclature

in code	in text	meaning
`n`	n	sample size
`d.pop`	d_{pop}	population effect size
`d.sdz`	d_{sdz}	standardized observed effect size, aka Cohen's d
`d.het`	d_{het}	mean of heterogeneous population distribution
`sd.het`	sd_{het}	standard deviation of heterogeneous population distribution
`d`	d	variously means either d_{pop}, d_{sdz}, or d_{het}; hopefully clear from context
`meand.simu`	$meand_{simu}$	mean significant observed effect size computed from simulated data
`meand.theo`	$meand_{theo}$	mean significant observed effect size computed analytically
`pval.simu`	$pval_{simu}$	p-value computed from simulated data
`pval.theo`	$pval_{theo}$	p-value computed analytically

The program performs three types of simulations.

1. *fixd*. Fixes d_{pop} to a few values of interest, sets n to a range of values, and simulates many studies for each d_{pop} and n.
2. *rand*. Randomly selects a large number of d_{pop}s, sets n to a range of values, and simulates one study for each d_{pop} and n.
3. *hetd*. Sets d_{het} and sd_{het} to a few values of interest, and selects a large number of d_{pop}s from normal distributions with mean d_{het} and standard deviation sd_{het}. Then sets n to a range of values, and simulates one study for each d_{pop} and n.

The program implements two data generation models:

1. *fixed effect (fix)* which imagines we're repeating a study an infinite number of times, drawing a different sample each time from a population with a fixed true effect size
2. *heterogeneous effect (het)* which assumes that each time we do the study, we're sampling from a different population with a different true effect size

Figures and Tables

The default mode produces figures that illustrate the kinds of graphs the program can produce.

1. d vs. d scatter plot colored by p-value; by default d_{pop} vs. d_{sdz}
2. histogram typically of d_{sdz} colored by p-value
3. probability distribution vs. d_{sdz} colored by p-value; can compute probability density or cumulative probability internally, or you can pass the distribution into the function
4. multiple line plot; my adaptation of R's `matplot`

The first figure shows a d vs. d scatter plot of *rand* simulated data for $n = 20$. The second uses the same data but zooms in to the critical region where p-values switch from nonsignificant to significant.

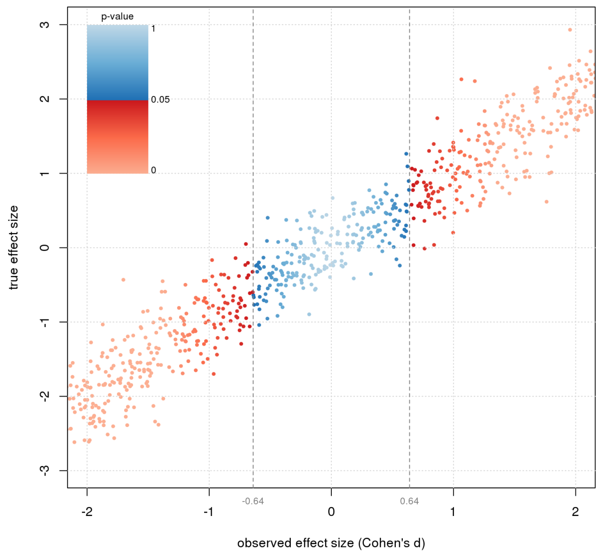


Figure 1a
Scatter plot d.pop vs d.sdz. n=20

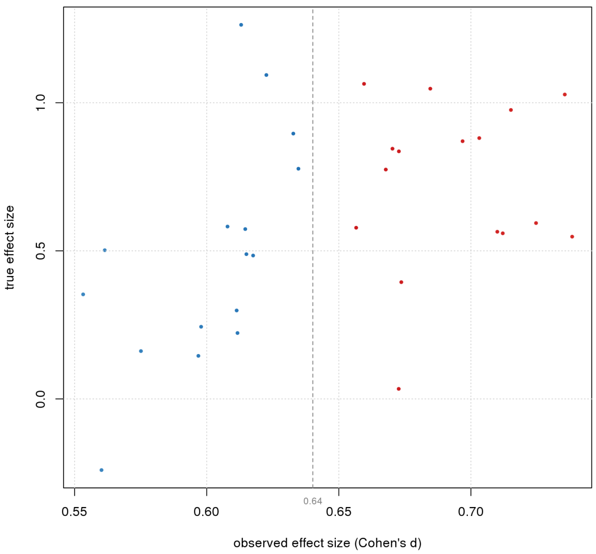


Figure 1b
Scatter plot. d.pop vs d.sdz showing sharp boundary at 0.64. n=20

Next are two histograms of *fixd* simulated data with different values for d_{pop} and n.

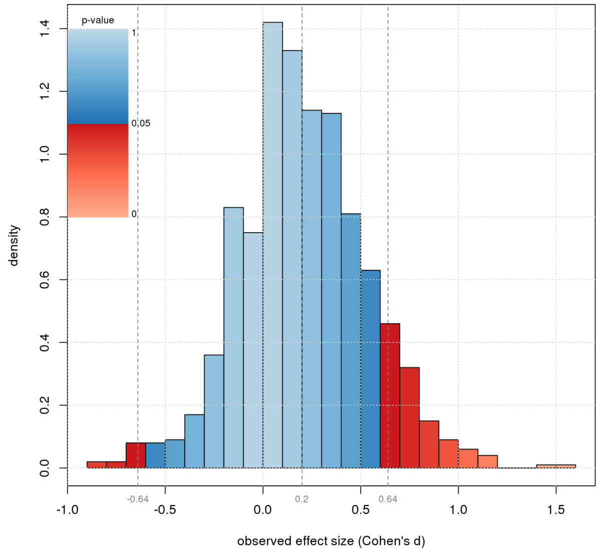


Figure 2a
Histogram of observed effect size. d.pop=0.2, n=20

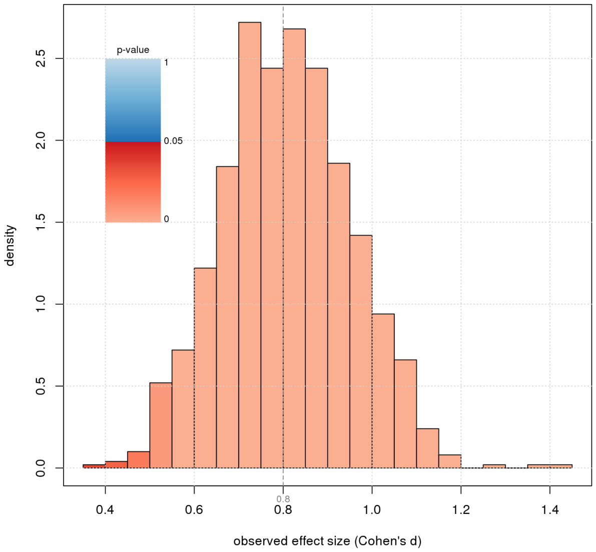


Figure 2b
Histogram of observed effect size. d.pop=0.8, n=100

The next two are sampling distributions for the *het* model with different values for d_{het}, sd_{het}, and n. The first shows probability density, the second cumulative probability.

Figure 3a
het distribution (density). d.het=0, sd.het=0, n=20

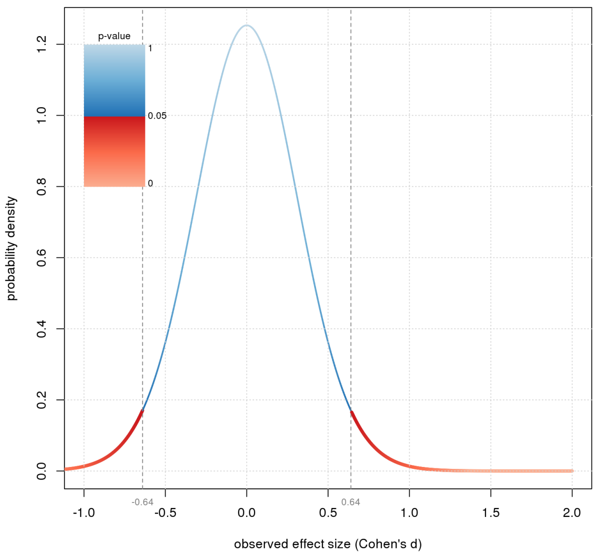
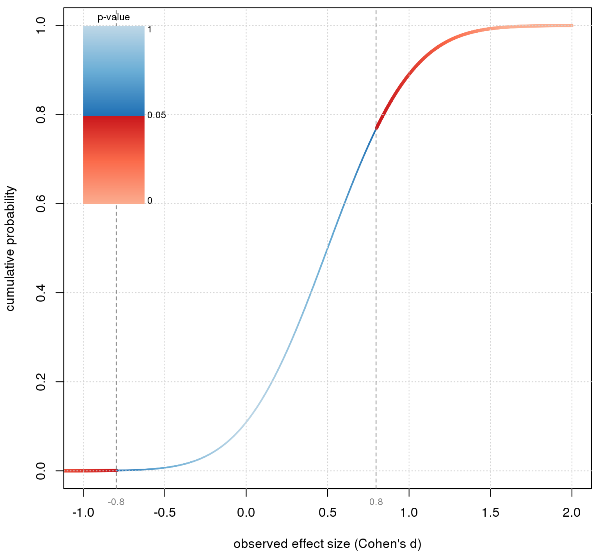


Figure 3b
het distribution (cumulative). d.het=0.5, sd.het=0.4, n=400



The final block are line plots. The first shows mean significant observed effect size inflation for the *fix* model. The second shows p-value inflation for the *het* model. The first has raw data; the second applies a smoothing function. Both figures depict simulated and analytic results to illustrate the concordance.

Figure 4a
Line plot of mean significant observed effect size inflation (raw)

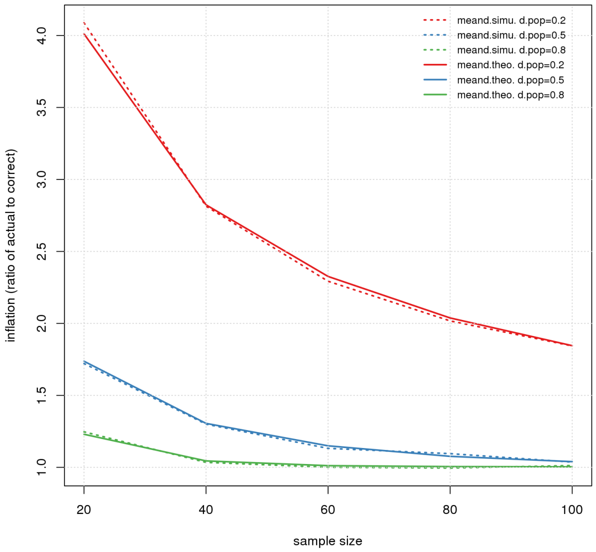
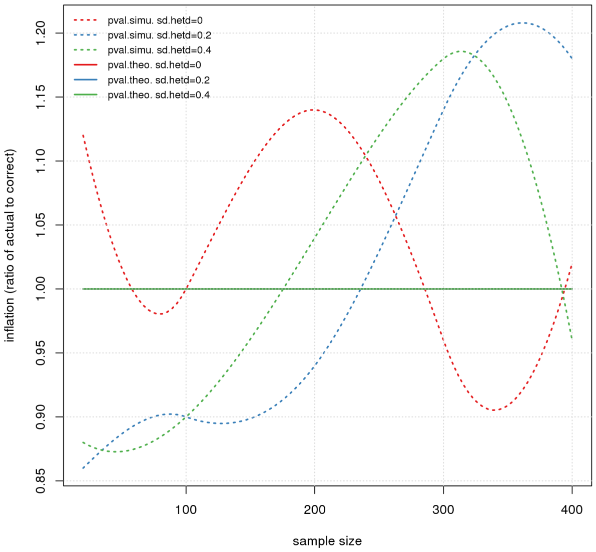


Figure 4b
Line plot of pval inflation (smooth=aspline)



Finally, here is a table of supporting data.

what	d.crit	md20_0.2	md20_0.5	md20_0.8	ov20_0.2	ov20_0.5	ov20_0.8	nov_0.2	nov_0.5	nov_0
meand.fixd	0.64	0.81	0.85	0.99	4.04	1.70	1.24	175.57	45.72	18.
meand.d2t	0.64	0.79	0.86	0.98	3.97	1.72	1.22	166.70	46.64	16.

Comments Please!

Please post comments on Twitter or Facebook, or contact me by email natg@shore.net.

Please report bugs, other software problems, and feature requests using the GitHub Issue Tracker. I will be notified, and you'll be apprised of progress. As already noted, the software is still rough and software documentation nonexistent.

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