

Details of calculations of actual power of replications *DataColada[4]*

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The calculations work as follows. We set the parameters for the original study, sample size: n_{ori} , and its assumed power, $power_{ori}$. (In the blogpost I use $n=20$ throughout for the original, and $power=50$ and then 35%, sample size of the original matters very little).

With n_{ori} and $power_{ori}$ we figure out the true effect size d_{true} . That is, we ask, what d_{true} leads to the $power_{ori}$ given n_{ori} .

With true effect size and sample size in hand, we get the distribution of estimated effect sizes the original study is drawing at random from.

We truncate that distribution at the value associated with $p=.05$, so we assume that any effect too small to be $p<.05$ is not published and hence nobody tries to replicate it.

Knowing the claimed level of power of the replicator, we can map this distribution of possible effect sizes obtained in the original study onto a distribution of possible sample sizes the replicator will run. Because we know d_{true} this distribution of sample sizes of the replication is mapped onto a distribution of true power for the replication. The mean of those levels of power is what the figures in the blog post show.

There are only two relevant assumptions in the calculations.

- 1) The original and the replication are studying the same true effect
- 2) Nonsignificant original findings are not published, or at least, do not get replication attempts.

These two assumptions are also made when replicators power their replications based on observed effect size, so they seem uncontroversial for our purposes.

See R code for more specific details.