Supplementary material 2: Converting within-subjects sample size into between-subjects sample size

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A statistical limitation that arises when we approximate standard error from sample size alone is that we ignore the statistical design of the studies we intend to compare, which is usually important for accurately estimating the standard error (Borenstein et al. 2009, chap. 8). As one example, a paired samples t-test has better precision for the difference score that is calculated between the two measurements than an independent samples t-test, partly because the participants contribute twice as many data points in the paired design, and partly because of within-subject correlation (Lakens 2016).

We can attempt to mitigate this violation, however, by converting the sample sizes from within-subject designs into the sample size that would achieve the same precision in a between-subjects design. In a replication candidate set composed of both within-subject and between-subject designs, converting within-subject sample size in this way should increase RV_{Cn} measurement quality by reducing measurement bias caused by variation in study design.

$$n_B = \frac{n_W a}{1 - \rho} \tag{SM2-1}$$

where n_W is the sample size of the within-subject design[1], ρ is the within-subject correlation, a is the number of groups that each subject contributes data points to, and n_B is the estimated sample size that a between-subject study would need to reach the same level of precision.

The population parameter ρ is usually estimated from the within-subject correlation r in the sample. A practical issue is that this value is very rarely reported in published manuscripts. In these cases, it is possible to calculate r from summary statistics. For example, if we have access to the t-value, Cohens $d_{average}$ (see Borenstein et al. 2009, equation 4.18), and the sample size n_W, we can calculate r by solving for r in Dunlap et al. (1996), equation 3:

$$r = \frac{2t^2 - d_{average}^2 n_W}{2t^2} \tag{SM2-2}$$

Or, if we have access to the standard error of the difference and the standard error of both groups, we could calculate r by solving for r in Lakens (see Lakens 2013, equation 8):

$$r = \frac{SD_1^2 + SD_2^2 - S_{diff}^2}{2 SD_1 SD_2} \tag{SM2-3}$$

If we do not have access to these summary statistics or the raw data, we could estimate ρ based on r in conceptually similar studies. If there are no realistic reference points for ρ whatsoever, we could potentially consider setting ρ to 0. n_W will still receive a correction in this case from being multiplied by a. Note however, that this is a very conservative assumption, and unlikely to be realistic in most cases. More importantly,

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[1] Note that we have replaced the capital N in Maxwell and Delaney (2004) with the lowercase n used to refer to sample size throughout this article. The two symbols refer to the same entity.

the choice of 0 over any other arbitrary value of ρ is motivated purely by a desire to be conservative in our assumptions about the strength of ρ, though it is not clear why one would want to be conservative.

References

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