

**Are We Comparing Apples or Squared Apples?  
The Proportion of Explained Variance Exaggerates Differences Between Effects**

Marco Del Giudice  
University of New Mexico

Marco Del Giudice, Department of Psychology, University of New Mexico. Logan Hall, 2001 Redondo Dr. NE, Albuquerque, NM 87131, USA; email: [marcodg@unm.edu](mailto:marcodg@unm.edu)

In this brief note, I wish to bring attention to a problem that has been discussed many times before, but whose implications are still not widely appreciated. As a result, many researchers (present author included) keep making distorted inferences about the relative size and importance of certain effects, by directly comparing the proportions of variance they account for. To illustrate, the narrow-sense heritability of depression (i.e., the variance in the risk for the disorder explained by additive genetic effects) is 30-40%, whereas that of bipolar disorder is at least 60% and perhaps as high as 80% (Johansson et al., 2019; Knopik et al., 2017). These figures seem to indicate that the influence of genetic factors on disease risk is approximately twice as large in bipolar disorder as in depression. But this interpretation is incorrect; as I discuss below, genetic factors play a much more similar role in the two disorders than suggested by this comparison.

In general, the proportion of explained variance is a non-intuitive and often misleading index of effect size. Variances are mathematically convenient because they combine additively; however, they are not expressed in the original units of the variable of interest—say income in dollars, intelligence in IQ points, or height in inches—but in *squared* units. When these variance units are not entirely meaningless (as with squared dollars or squared IQ points), they still fail to measure the actual trait under consideration (e.g., square inches do not measure a person’s height). In contrast, the correlation coefficient—the square root of the explained variance—quantifies the relation between two variables in terms of the (standardized) original units, and thus has a natural interpretation with respect to the size of the effect.<sup>1</sup> If the correlation between  $X$  and  $Y$  is .30, a change of one standard deviation in  $X$  predicts a change of 0.30 standard deviations in  $Y$  (and vice versa; here I do not distinguish between statistical prediction and genuine causality). The proportion of the variance of  $Y$  accounted for by  $X$  is just 9%, which makes the effect seem small and unimportant. But, as noted above, explained variance is expressed in *squared* units of  $Y$ , and relates to the real-world effect of  $X$  on  $Y$  in a highly nonlinear fashion. Over the years, many have noted that the proportion of explained variance may lead researchers to dramatically underestimate the importance of certain effects, and have recommended the use of correlations (or other unsquared indices such as Cohen’s  $d$ ) to quantify and interpret effect sizes (e.g., Abelson, 1985; Beatty, 2002; Breugh, 2003; D’Andrade & Dart, 1990; Funder & Ozer, 2019; Hunter & Schmidt, 1990, 2014; Rosenthal & Rubin, 1979).

An important corollary, but one that is seldom discussed explicitly, is that *comparing* effects based on their respective proportions of explained variance tends to exaggerate the differences among them—often by a large margin (Hunter & Schmidt, 1990, 2014).<sup>2</sup> Consider a

---

<sup>1</sup> In some scenarios, the *unsquared* correlation between two variables measures the variance explained by a third variable of interest (see Johnson, 2011; Ozer, 1985). For example, the correlation between monozygotic twins reared apart is a direct estimate of trait heritability (i.e., the proportion of variance explained by additive genetic factors); the correlation between two parallel forms of a scale is a direct estimate of their reliability (i.e., the proportion of variance explained by the latent construct). In these scenarios, the effect of interest is *not* the association between the two measured variables, but that between each of them and a third, unobserved variable (the genetic factor; the latent construct). As usual, the effect of interest is quantified by the square root of the proportion of explained variance—in this case, the square root of the heritability or reliability.

<sup>2</sup> Interestingly, an entire line of methodological research seeks to supplement multiple regression coefficients with indices that quantify the amount of variance explained by each predictor (see Johnson & LeBreton, 2004; Tonidandel & LeBreton, 2011). The rationale is that, unlike regression coefficients, such indices of “relative importance” are additive and sum to the total  $R^2$  of the model. While this is a convenient property, this approach overlooks the fact that variance-based indices provide a grossly distorted picture of how predictors compare with

variable  $Z$  that correlates .60 with  $Y$ . A change of one standard deviation in  $Z$  predicts a change of 0.60 standard deviations in  $Y$ . That is, a given change in  $Z$  has twice the effect on  $Y$  than the same amount of change in  $X$ . But the variance explained by  $Z$  (36%) is *four times* as large as that explained by  $X$ —a ratio that distorts, and grossly exaggerates, the real-world difference between the respective effects of  $X$  and  $Z$  on  $Y$ .

In general, the ratio between two correlations (henceforth the “effect ratio”) is simply the square root of the ratio between the corresponding squared correlations (i.e., the proportions of explained variance). Of course, it is not always sensible to compare two standardized effect sizes, and depending on context, *unstandardized* effects may be more informative than standardized ones. But when it makes sense to compare proportions of explained variance in the context of continuous variables, the effect ratio provides a much more realistic index of the relative importance of the respective effects. Note that the ratio between correlations is not the same as the ratio between values of Cohen’s  $d$ , because  $d$  is nonlinearly related to the correlation coefficient. Thus, when the proportion of explained variance refers to the difference between two groups, the simple effect ratio described here does not correspond to the ratio between  $d$  values, except in special cases.<sup>3</sup> In the rest of this paper, I only consider examples in which the relevant variables are continuous and the correlation coefficient is the natural effect size.

Going back to the example of depression and bipolar disorder, the ratio of the heritabilities of these disorders is about two; the square root of this ratio is about 1.41, meaning that genetic factors contribute about 40% more to the risk of bipolar disorder compared with that of depression (instead of twice as much, as suggested by the heritabilities). Indeed, one standard deviation increase in the genetic predisposition for depression increases risk by  $\sqrt{.30} \approx 0.55$  standard deviations, whereas one standard deviation increase in the genetic predisposition for bipolar disorder increases risk by  $\sqrt{.60} \approx 0.77$  standard deviations. For another example, consider this quote from Plomin and von Stumm (2018): “One of the most interesting developmental findings about intelligence is that its heritability as estimated in twin studies increases dramatically from infancy (20%) to childhood (40%) to adulthood (60%)” (p. 152). Although the heritability increases threefold, the relative impact of genetic factors is only about 70% larger in adulthood than in infancy ( $\sqrt{3} \approx 1.73$ ). In the same paper, the authors predicted that genomewide polygenic scores “will explain substantially more than 10% of the variance in intelligence, which is more than 20% of the 50% heritability of intelligence”, and commented “Nonetheless, 10% is a long way from the heritability estimate of 50% obtained from twin studies of intelligence” (p. 151). However, a polygenic score that explains “only” 10% of the variance can be expected to predict the phenotype almost half as well as the full genotype ( $\sqrt{.10/.50} \approx 0.45$ ), assuming that the estimate from twin studies is correct.

---

respect to their real-world effects on the outcome. A similar criticism applies to the heterogeneity indices I proposed to quantify the relative difference in the contributions of individual variables to multivariate effect sizes, such as Mahalanobis’  $D$  (Del Giudice, 2017, 2018). Those indices rely on a decomposition of the total squared effect size into a weighted sum of squared univariate effect sizes; hence, they arguably provide an inflated sense of the amount of heterogeneity in the data.

<sup>3</sup> For equal-sized groups, the conversion is  $d = \frac{2r}{\sqrt{1-r^2}}$ . Hence, the ratio between two  $d$  values is  $\frac{d_1}{d_2} = \frac{r_1}{r_2} \sqrt{\frac{1-r_2^2}{1-r_1^2}}$ . The ratio of  $d$ ’s closely approximates the ratio of  $r$ ’s only if the two correlations are both small or very similar to each other, so that the “correction factor” on the right becomes approximately 1.

In quantitative genetics, the routine use of variance components as indices of effect size may have led researchers to underestimate the impact of shared environmental factors (i.e., those aspects of the environment that tend to increase the similarity between siblings). In their comprehensive meta-analysis of 50 years of human twin studies (including cognitive and behavioral traits but also morphological, metabolic, reproductive traits, etc.), Polderman et al. (2015) estimated the mean heritability across traits at 48.8% and the mean shared environmental component at 17.4%. Taken at face value, these figures seem to suggest that additive genetic factors are almost three times as influential as the shared environment (explained variance ratio: 2.80); but in terms of real-world effects on the phenotype, the impact of genes is only 60-70% larger than that of the shared environment (effect ratio:  $\sqrt{2.80} \approx 1.67$ ). Similarly, the heritable and shared environmental components of criminality and substance use have been estimated at about 50% and 20%, respectively (Kendler et al., 2016, 2019). Translated into real-world effects, this corresponds to a ratio of about  $\sqrt{.50/.20} \approx \sqrt{2.50} \approx 1.58$  (or its reciprocal 0.63), meaning that shared environmental factors are about 60% as influential as genetic factors.<sup>4</sup>

It is important to note that these distortions become more pronounced as the effects being compared grow more different from one another. For example, consider a trait that is 50% heritable and has a 5% shared environmental component (ten times smaller than the heritability). Many would regard that 5% of variance as very small, or even practically negligible; but in fact, the effect ratio is only  $\sqrt{10} \approx 3.16$  (reciprocal 0.32), meaning that the impact of the shared environment on the phenotype is about one third of that of genes (!). Even a shared environmental component of just 1% is not as tiny as it looks against a heritability of 50%. The effect ratio in this case is  $\sqrt{50} \approx 7.07$ , meaning that genetic factors are seven times more influential than the shared environment—a substantial difference, but not nearly as large as indicated by the size of the variance components.<sup>5</sup>

Psychometrics is another discipline in which variance components are routinely calculated and interpreted by researchers. In classical test theory, the reliability of a scale is the proportion of *true score variance* (i.e., variance shared with the latent construct being measured) on the total variance, with the remainder accounted for by measurement error. Thus, directly comparing the reliabilities of different scales may give a distorted picture of their relations with the latent construct of interest. To illustrate, if two scales have reliabilities of .60 and .80, the higher-quality scale correlates with the latent construct only 15% more strongly than the lower-quality one (effect ratio:  $\sqrt{.80/.60} \approx \sqrt{1.33} \approx 1.15$ ).

This kind of distortion may become more insidious when the variance is parsed at a finer scale of analysis. For example, McCrae (2015, Table 1) reported that measured scores on the

---

<sup>4</sup> Hunter and Schmidt (1990, 2014) illustrated this point with a similar example from behavior genetics: if intelligence is 80% heritable and 20% environmental (which may be the case in older adults; see Plomin & Deary, 2015), the proper ratio between the genetic and environmental effects is two, not four as suggested by the size of the variance components.

<sup>5</sup> Here I am assuming that the 1% or 5% of shared environmental variance in these examples represents a reliable effect, and not a spurious estimate resulting from sampling error or other forms of bias. At least in some cases, it is reasonable to treat small variance components as effectively zero; my argument only applies to genuine nonzero effects that happen to account for a small proportion of the variance.

facets of the Big Five personality domains contain an average of 34% common trait variance (i.e., variance shared with the broader domain) and 9% facet-specific variance. (To illustrate: in this model of personality, the broad domain of Extraversion has six narrower facets: Warmth, Gregariousness, Assertiveness, Activity, Excitement seeking, and Positive emotions.) These figures suggest that a person's true score on a given personality domain (e.g., Extraversion) contributes to their measured score on a facet of that domain (e.g., Assertiveness) almost four times as much as their true score on the facet itself. However, the effect ratio is markedly smaller:  $\sqrt{.34/.09} \approx \sqrt{3.78} \approx 1.94$ , meaning that personality domains contribute to facet scores about twice as much as facets (instead of almost four times as much).

Later in the same paper, McCrae (2015) estimated variance components for scores on single personality items. On average, the total score variance consists of 12% common trait variance; 24% item-specific variance; 13% method variance (regarded as systematic error); and 51% random error. McCrae concluded: "The observed values are sobering: In the typical item, nearly two thirds of the variance is either random or systematic error [...], which is why single items are notoriously unreliable; of the remaining true-score variance [...], only a third is due to the common trait" (p. 106). However, the picture painted by effect ratios is somewhat less sobering: measurement error contributes only 33% more than true score variation ( $\sqrt{(.51 + .13)/(.24 + .12)} \approx \sqrt{1.78} \approx 1.33$ ), and the contribution of common trait variation is about 70% as large as that of item-specific variation ( $\sqrt{.12/.24} = \sqrt{0.50} \approx 0.71$ ).

In sum: using the proportion of explained variance as an index of effect size does not just distort the interpretation of individual effects, but also exaggerates the *differences* between effects, which may lead to strikingly incorrect judgements of relative importance. Luckily, a meaningful and interpretable "effect ratio" can be easily calculated as the square root of the ratio between proportions of explained variance. In several real-world examples, effect ratios tell a different story than variance components, and might prompt one to rethink the interpretation of certain canonical results (e.g., regarding the role of the shared environment in the development of psychological traits). This simple but consequential point should be understood more widely; with no pretense of originality, I hope that this note will contribute to raise awareness and prevent fallacious interpretations of research findings.

### Acknowledgments

I wish to thank Mike Bailey, Steve Gangestad, and Emil Kirkegaard for their helpful comments on a previous draft of this manuscript.

### References

- Abelson, R. P. (1985). A variance explanation paradox: When a little is a lot. *Psychological Bulletin*, 97, 129-133.
- Beatty, M. J. (2002). Do we know a vector from a scalar? Why measures of association (not their squares) are appropriate indices of effect. *Human Communication Research*, 28, 605-611.
- Breaugh, J. A. (2003). Effect size estimation: Factors to consider and mistakes to avoid. *Journal of Management*, 29, 79-97.
- D'Andrade, R., & Dart, J. (1990). The interpretation of  $r$  versus  $r^2$ , or why percent of variance accounted for is a poor measure of size of effect. *Journal of Quantitative Anthropology*, 2, 47-59.

- Del Giudice, M. (2017). Heterogeneity coefficients for Mahalanobis'  $D$  as a multivariate effect size. *Multivariate Behavioral Research*, *52*, 216-221.
- Del Giudice, M. (2018). Addendum to: Heterogeneity coefficients for Mahalanobis'  $D$  as a multivariate effect size. *Multivariate Behavioral Research*, *53*, 571-573.
- Funder, D. C., & Ozer, D. J. (2019). Evaluating effect size in psychological research: Sense and nonsense. *Advances in Methods and Practices in Psychological Science*, *2*, 156-168.
- Hunter, J. E., & Schmidt, F. L. (1990). *Methods of meta-analysis: Correcting error and bias in research findings* (1<sup>st</sup> ed.). Sage.
- Hunter, J. E., & Schmidt, F. L. (2014). *Methods of meta-analysis: Correcting error and bias in research findings* (3<sup>rd</sup> ed.). Sage.
- Johansson, V., Kuja-Halkola, R., Cannon, T. D., Hultman, C. M., & Hedman, A. M. (2019). A population-based heritability estimate of bipolar disorder—In a Swedish twin sample. *Psychiatry Research*, *278*, 180-187.
- Johnson, J. W., & LeBreton, J. M. (2004). History and use of relative importance indices in organizational research. *Organizational Research Methods*, *7*, 238-257.
- Johnson, W. (2011). Correlation and explaining variance: To square or not to square? *Intelligence*, *39*, 249-254.
- Knopik, V. S., Neiderhiser, J. M., DeFries, J. C., & Plomin, R. (2017). *Behavioral genetics* (7<sup>th</sup> ed.). Worth.
- McCrae, R. R. (2015). A more nuanced view of reliability: Specificity in the trait hierarchy. *Personality and Social Psychology Review*, *19*, 97-112.
- Ozer, D. J. (1985). Correlation and the coefficient of determination. *Psychological Bulletin*, *97*, 307-315.
- Plomin, R., & Deary, I. J. (2015). Genetics and intelligence differences: Five special findings. *Molecular Psychiatry*, *20*, 98-108.
- Plomin, R., & von Stumm, S. (2018). The new genetics of intelligence. *Nature Reviews Genetics*, *19*, 148-159.
- Polderman, T. J., Benyamin, B., De Leeuw, C. A., Sullivan, P. F., Van Bochoven, A., Visscher, P. M., & Posthuma, D. (2015). Meta-analysis of the heritability of human traits based on fifty years of twin studies. *Nature Genetics*, *47*, 702-709.
- Rosenthal, R., & Rubin, D. B. (1979). A note on percent variance explained as a measure of the importance of effects. *Journal of Applied Social Psychology*, *9*, 395-396.
- Tonidandel, S., & LeBreton, J. M. (2011). Relative importance analysis: A useful supplement to regression analysis. *Journal of Business and Psychology*, *26*, 1-9.