



Kemp, J. P., Sayers, A., Davey Smith, G., Tobias, J. H., & Evans, D. M. (2016). Authors' response to Hartwig and Davies. *International Journal of Epidemiology*, 45(5), 1678-1679.
<https://doi.org/10.1093/ije/dyw241>

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Authors' response to Hartwig and Davies

International Journal of Epidemiology, 2016, 1678–1679

doi: 10.1093/ije/dyw241

Advance Access Publication Date: 20 September 2016



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In their letter, Hartwig and Davies¹ raise an important issue that was not discussed in the original Mendelian randomization Egger regression (MR Egger) paper by Bowden *et al.*² Hartwig and Davies point out that, similar to other varieties of MR, MR-Egger is also susceptible to weak instrument bias. In the case of single-sample MR-Egger, this means that estimates of the causal effect may be biased towards the observational association when weak instruments are used in the analysis (as is the case with traditional single-sample MR). Hartwig and Davies also point out a potential solution to this problem, the utilization of more precise externally derived estimates of the relevant single nucleotide polymorphism (SNP)-exposure association (i.e. from larger publicly available genome-wide association meta-analyses).

We agree with Hartwig and Davies' conclusions that weak instrument bias is a problem in MR-Egger as it is in traditional MR analyses, and that it is critically important that users of the technique are aware of this possibility. Hartwig and Davies also refer to a recent study of ours³ in the *International Journal of Epidemiology*, where we used several different types of MR analyses (including MR-Egger) to examine a possible causal effect of adiposity on bone mineral density (BMD). As Hartwig and Davies fairly acknowledge in their letter, not only did we discuss the possibility of weak instrument bias in our study, we also performed preliminary simulations to investigate its effect on MR-Egger (the results of which broadly agree with their assertions). As Hartwig and Davies note, MR-Egger was only one small component of our paper and none of our key results (which we believe

to be robust) rely on the results of these analyses in isolation, and indeed many of the other analyses reported in our paper do not suffer from potential bias due to weak instruments.

Hartwig and Davies did, however, suggest that we could have used estimates from an external source to obtain less biased results in our MR-Egger analyses. Whereas we agree that this would be good practice in most situations, we do not feel that it would have been appropriate in our study, for two reasons. First, the focus of our article was not on a possible causal relationship between body mass index and BMD (which is well-known and widely accepted), but rather on a possible causal relationship between adiposity [as operationalized as fat mass calculated from total body dual-energy X-ray absorptiometry (DXA)] and BMD. There are no publicly available genome-wide association studies of total body fat mass as measured by total body DXA, and therefore no external estimates that we could have applied in our analyses (i.e. as far as we are aware, we are currently the largest such study). We could have used external estimates for analyses involving body mass index, but this

would have been of limited utility since body mass index is a far from perfect measure of adiposity. Second, our study involved 9-year-old children from the Avon Longitudinal Study of Parents and Children. It is unclear the extent to which effect sizes of adiposity-associated variants in adults reflect effect sizes of adiposity-associated variants in children (as Hartwig and Davies recognize), and we therefore feel it would have been inappropriate to use adult-derived external estimates in our study of children.

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Response to Hartwig and Davies

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International Journal of Epidemiology, 2016, 1679–1680

doi: 10.1093/ije/dyw252

Advance Access Publication Date: 20 September 2016



Thank you for the opportunity to respond to the thoughtful and timely letter by Hartwig and Davies.¹ They do indeed raise a very important practical issue with the implementation of MR-Egger regression in the single-sample setting, or with the use of so called ‘internal’ weights, namely weak instrument bias. They are right to point out the unsatisfactory nature of our analysis of the height data in our original publication,² and that our use of weak instruments had the likely effect of biasing the MR-Egger estimate towards that of the observational association. Their re-analysis of these data with external weights appears to provide a much more satisfactory answer and, when such weights are available, it is both a simple and an attractive way to circumvent the problem.

Although previous simulation studies have highlighted this fact, further research is needed to completely understand the issue of weak instrument bias for MR-Egger in

the single-sample context. What is clear however, is that the standard notion of instrument strength, as quantified by the F statistic, cannot naively be applied to estimate the magnitude of this bias; new (or at least newly borrowed) theory is required. Before covering initial progress in this vein, we now briefly discuss related (and more mature) work in the two-sample context.

Recent work on weak instrument bias in the two-sample context

A strength of MR-Egger regression, along with the weighted median³ and inverse-variance weighted (IVW)⁴ methods, is that they do not require gene, exposure and outcome data on a single sample of subjects at the individual level. MR-Egger regression can be implemented with only summary data estimates of the single nucleotide polymorphism (SNP)-exposure and SNP-outcome associations, making it most