mrrobust: A Stata package implementing MR-Egger regression type analyses

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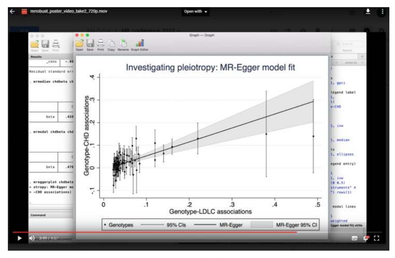
Summary

- **Scan QR code for a short video explaining the package!**



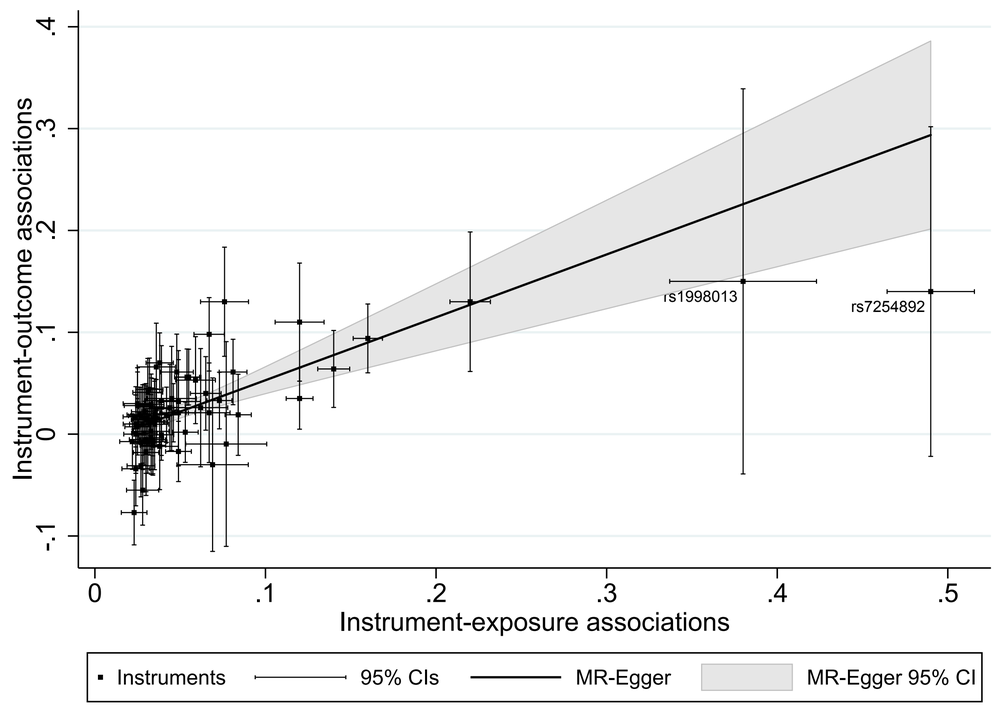
- Mendelian randomization studies using summary data from genome-wide association studies are becoming increasingly common.
- `mrrobust` is a Stata package implementing several of the latest methods.
- It is a free download from `https://raw.github.com/remlapmot/mrrobust`
- See Spiller *et al.* (2017) for further details.

Introduction

- The `mrrobust` package includes the following commands:
  - `mrratio`: ratio (Wald) estimator for a single genotype/instrumental variable (IV);
  - `mrivests`: generate ratio estimates in current dataset;
  - `mregger`: inverse-variance weighted (IVW) and MR-Egger estimators, and I^2_{GX} statistic (Bowden *et al.*, 2015, 2016a);
  - `mrmedian`: median estimators (Bowden *et al.*, 2016b);
  - `mrmodal`: zero modal estimator (Hartwig *et al.*, 2017);
  - `mreggerplot`: Egger regression type plot;
  - `mrforest`: Forest plot of IV estimates.

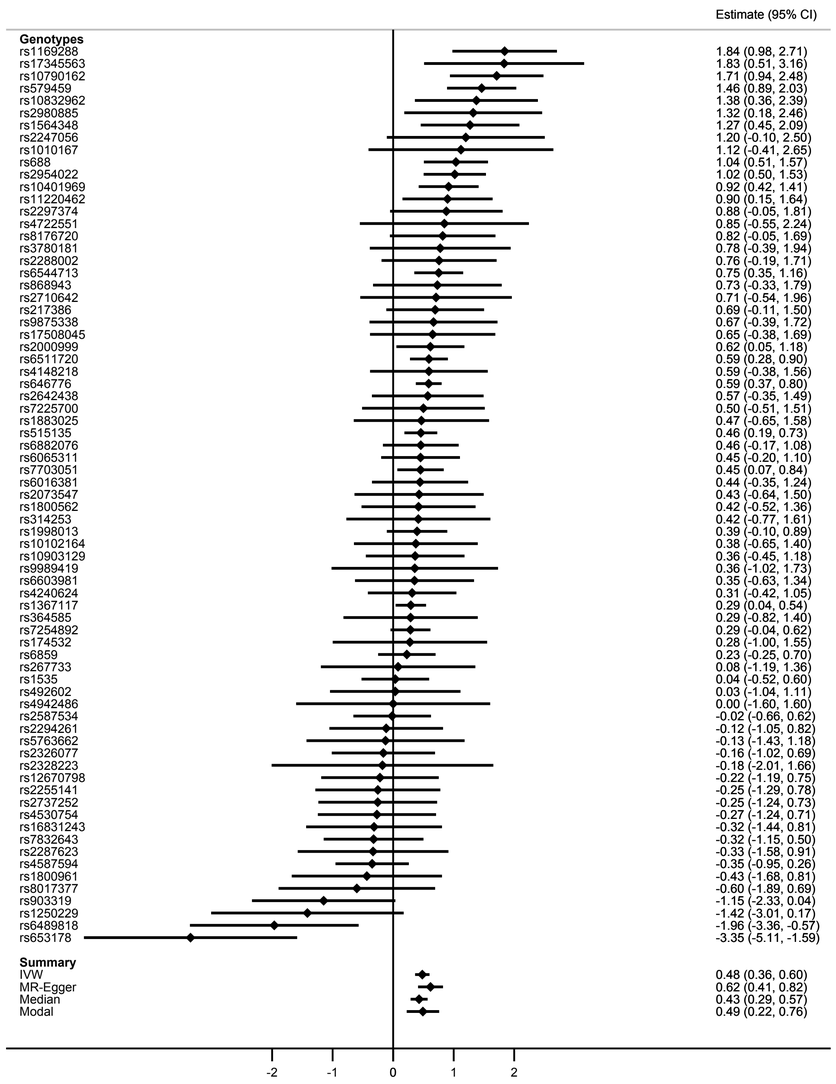
Example analysis

- The package assumes that you have imported summary data, possibly from a repository such as MR-Base `http://www.mrbase.org` (Hemani *et al.*, 2016a).
- The package also assumes that you have appropriately harmonised your data (Hartwig *et al.*, 2016).
- We use summary data provided by Do & et al. (2013) to investigate the causal effect of low-density lipoprotein cholesterol (LDL-C) on the risk of coronary heart disease (CHD).
- 73 genotypes achieved genome-wide statistical significance ($p < 1 \times 10^{-8}$) for their association with LDL-C.
- Plot of the individual IV estimates and MR-Egger fitted line with 95% CI:



- The modal estimate is similar to the IVW estimator.
- The MR-Egger estimate is the largest and the median estimate the smallest.
- The I^2_{GX} statistic of 98.5% shows that there should be less that 1.5% bias in the MR-Egger estimate due to regression dilution bias.
- The MR-Egger intercept of -0.009 (95% CI -0.020, 0.002) provides no strong evidence against the null hypothesis of no pleiotropy.

- Forest plot of genotype specific and summary IV estimates:



I_{GX}^2=98.5%

Discussion

- The `TwoSampleMR` package (Hemani *et al.*, 2016b) and the `MendelianRandomization` package (Yavorska & Burgess, 2016, 2017) provide similar functionality in R.

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Feedback zone

- Vote on these potential great new features!

Feature	Tally marks
Extract data from MR-Base	
Better forest-type plot with lots of genotypes	
SIMEX for MR-Egger	

- Any other comments: