# Including multiple instrumental variables in Mendelian randomization analyses

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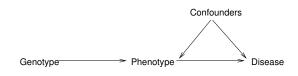
## Outline

- ▶ Introduction to Mendelian randomization
- ▶ Multiple instruments example using ALSPAC data:
  - instrument strength
  - over-identification
  - allele scores
- Multiple instruments discussion

#### Introduction

## Mendelian randomization approach:

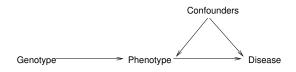
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IV assumptions, genotype should be:

- (i) independent of confounders
- (ii) associated with phenotype
- (iii) independent of disease given phenotype and confounders

#### Problem:

- MR analyses have low power:
  - Weak instruments bias IV estimate & wide CI
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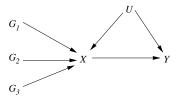
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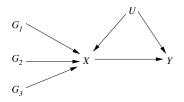
#### Solutions:

- Increase study sample size
- Stronger instrument
- Multiple instruments
- (Meta-analysis)

▶ Ideal situation (Didelez & Sheehan, 2007):

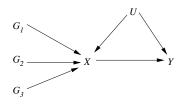


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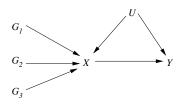
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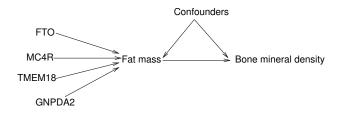
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- Over-identification: Sargan/Hansen test

▶ Outcome: bone mineral density

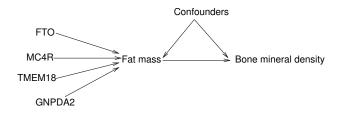
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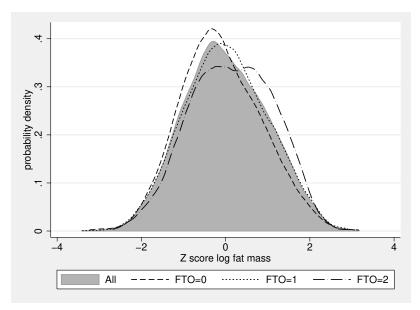
► FTO & MC4R: 0.2-0.4 kg/m² inc BMI OR: 1.1-1.3 for obesity (BMI > 30 kg/m²)

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- Estimation:
  - TSLS
  - AR/LIML, LM, CLR (Mikusheva & Poi, 2006)

# CDFs of BMD by FTO genotypes



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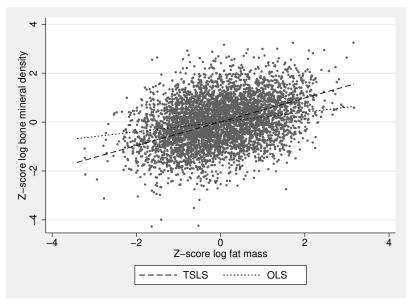
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4 SNPs AR/LIML LM CLR	1.63 (1.28, 2.06) 1.66 (1.29, 2.23) (1.30, 2.21) (1.30, 2.20)	< 0.001	18.6 <sub>16.9</sub>	0.015	0.013	0.16	4796

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AR/LIML	1.66 (1.29, 2.23)						
ĹM	(1.30, 2.21)						
CLR	(1.30, 2.20)						
Allele sc.	1.40 (0.99, 1.98)	0.06	33.2	0.007	0.43	NA	4796

IV estimates of the causal assoc. between std. BMD & std. fat mass

# Second stage regression



OLS: 1.22 (1.19, 1.26); IV allele score: 1.40 (0.99, 1.98)

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- ► This work in:

  Lawlor, Palmer, et al., Statistical Methods in Medical Research, submitted

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#### References I

- Cragg, J. G., & Donald, S. G. (1993). Testing Identifiability and Specification in Instrumental Variable Models. *Econometric Theory*, *9*, 222–240.
- Davey Smith, G., & Ebrahim, S. (2003). 'Mendelian randomization': can genetic epidemiology contribute to understanding environmental determinants of disease. *International Journal of Epidemiology, 32*, 1–22.
- Didelez, V., & Sheehan, N. (2007). Mendelian randomization as an instrumental variable approach to causal inference. Statistical Methods in Medical Research, 16, 309–330.
- Frayling, T. M., Timpson, N. J., Weedon, M. N., Zeggini, E., Freathy, R. M., Lindgren, C. M., et al. (2007). A Common Variant in the FTO Gene Is Associated with Body Mass Index and Predisposes to Childhood and Adult Obesity. Science, 316(5826), 889–894.
- Lawlor, D. A., Harbord, R. M., Sterne, J. A. C., Timpson, N., & Davey Smith, G. (2008). Mendelian randomization: Using genes as instruments for making causal inferences in epidemiology. Statistics in Medicine, 27(8), 1133–1163.
- Loos, R. J. F., Lindgren, C. M., Li, S., Wheeler, E., Zhao, J. H., Prokopenko, I., et al. (2008). Common variants near mc4r are associated with fat mass, weight and risk of obesity. *Nature Genetics*, 40(6), 768–775. Available from http://dx.doi.org/10.1038/ng.140
- Mikusheva, A., & Poi, B. (2006). Tests and confidence sets with correct size when instruments are potentially weak. *The Stata Journal*, *6*(3), 335–347.

#### References II

- Stock, J. H., Wright, J. H., & Yogo, M. (2002). A Survey of Weak Instruments and Weak Identification in Generalized Method of Moments. *Journal of Business and Economic Statistics*, 20(4), 518–529.
- Weedon, M. N., Lango, H., Lindgren, C. M., Wallace, C., Evans, D. M., Mangino, M., et al. (2008). Genome-wide association analysis identifies 20 loci that influence adult height. *Nature Genetics*, 40(5), 575–583.
- Willer, C. J., Speliotes, E. K., Loos, R. J., Li, S., Lindgren, C. M., Heid, I. M., et al. (2009). Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. *Nature Genetics*, *41*, 25–34.