

# Meta-analysis of Mendelian randomization studies

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ISCB 28,  
1 August 2007



# Outline

- 1 Brief introduction to Mendelian randomization
- 2 Concepts in the meta-analysis model
- 3 Description of the example and the meta-analysis model
- 4 An extension to the meta-analysis model
- 5 Summary and discussion

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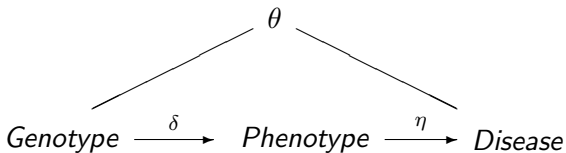
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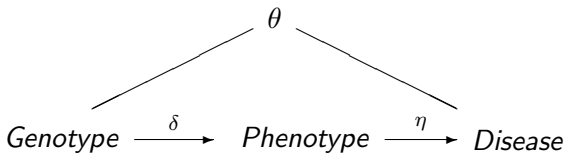
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  - Phenotype on pathway between gene and disease



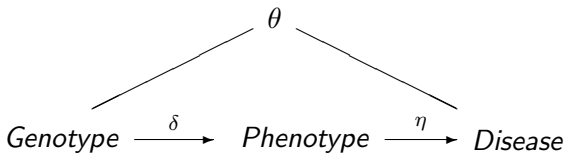
$\theta$ : Gene-Disease log odds-ratio,  $\delta$ : difference in mean phenotypes,  
 $\eta$ : Phenotype-Disease log odds-ratio





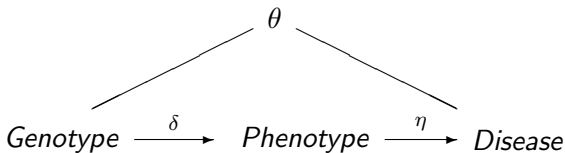
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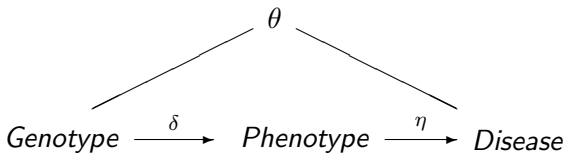
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$$\eta_{[k]} \approx \frac{k\theta}{\delta}$$

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	gg	Gg	GG
Controls	$y_{01}$	$y_{02}$	$y_{03}$
Cases	$y_{11}$	$y_{12}$	$y_{13}$
log odds-ratios		$\theta_2$	$\theta_3$
Mean phenotype levels (controls)	$\mu_1$	$\mu_2$	$\mu_3$
difference in mean phenotypes		$\delta_2$	$\delta_3$

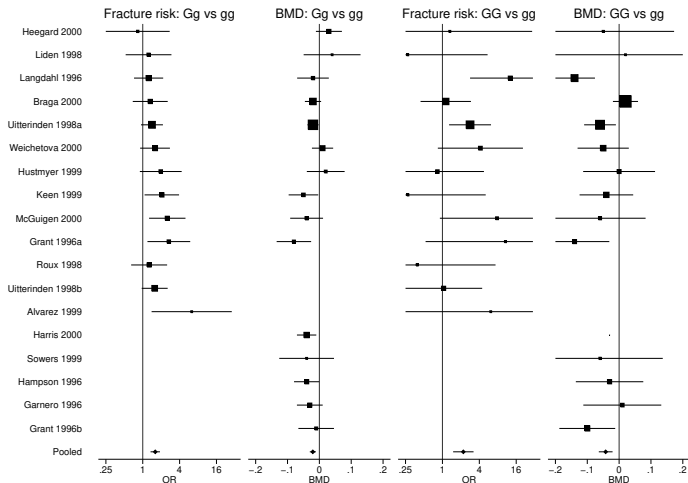
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$$\begin{bmatrix} \theta_{2i} \\ \delta_{2i} \\ \theta_{3i} \\ \delta_{3i} \end{bmatrix} \sim \text{MVN} \left( \begin{bmatrix} \eta\delta_2 \\ \delta_2 \\ \eta\delta_3 \\ \delta_3 \end{bmatrix}, \mathbf{V}_i + \mathbf{B} \right)$$

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Gg vs gg	0.57	0.42	0.77
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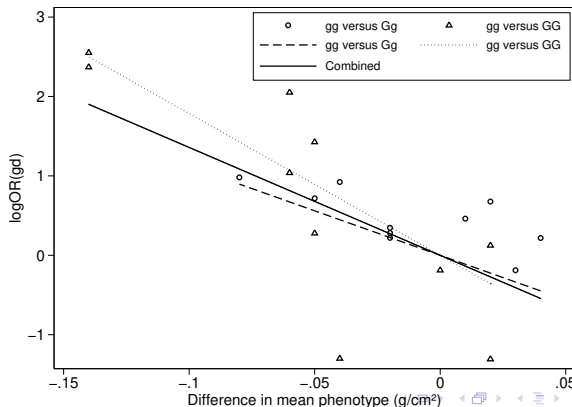
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$$\delta, \eta \sim N(0, 1 \times 10^6), \quad \lambda \sim \text{Beta}(0.5, 0.5)$$

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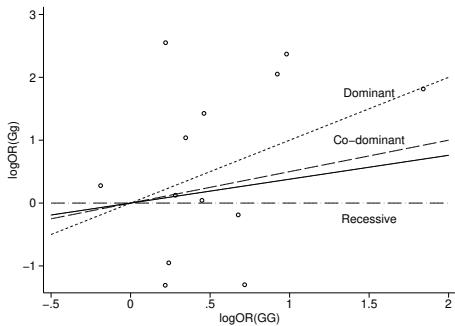
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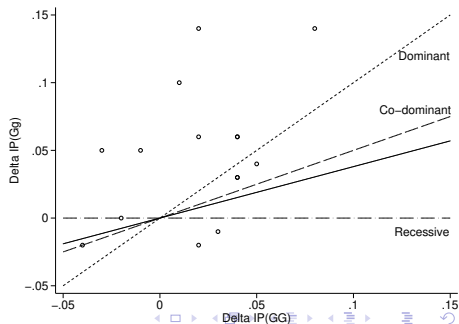
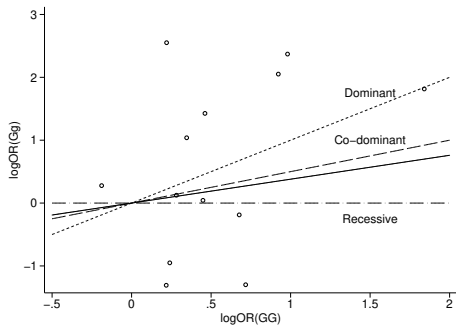
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Method of estimation	$OR_{pd,0.05}$	95% C.I./Cr.I.			$\lambda$	95% C.I./Cr.I.	
ML - MVN	0.42	0.28	0.61		0.33	0.19	0.47
Bayesian - PNF	0.46	0.32	0.61		0.30	0.17	0.45





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- Meta-analysis analysis of two genotype comparisons; extended to include the genetic model-free approach
- Meta-analysis of genetic association studies using merged genotype comparisons [Salanti and Higgins, 2007]



# Acknowledgements

- Student conference award



- Medical Research Council Capacity Building PhD Studentship in Genetic Epidemiology (G0501386).
- Dr. Martin Tobin is funded by a Medical Research Council Clinician Scientist Fellowship (G0501942).

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