MR studies in R

How to use genetics for identifying modifiable risk factors

Daniela Mariosa

Genetic Epidemiology group, IARC

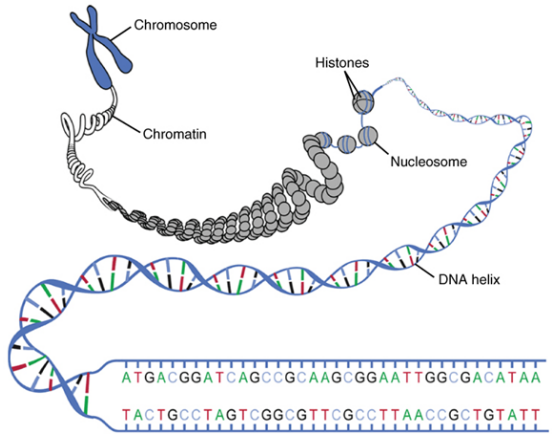
Lyon, France

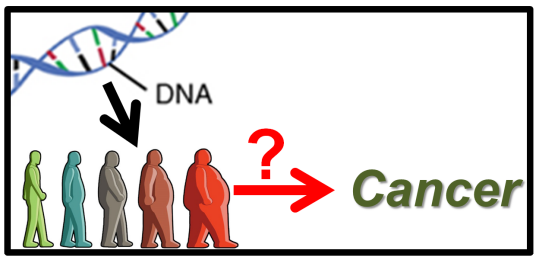
International Agency for Research on Cancer

World Health Organization

The method: Mendelian Randomization

Instrumental variable approach when instruments are genetic





Genetic variants are randomly assigned at conception

Genome**W**ide **A**ssociation **S**tudies (GWAS)

	1	2	3	4	5	6	7	8
1	SNP	CHR	BP	ChrBp	CA	NCA	BETA	SE
2	rs10733051	1	167280354	1:167280354	A	G	0.0106	0.0019
3	rs10798918	1	33275981	1:33275981	T	C	0.0157	0.0026
4	rs10917502	1	19961679	1:19961679	A	G	0.0163	0.0027
5	rs10920678	1	190239907	1:190239907	A	G	0.0166	0.0019
6	rs10923724	1	119546842	1:119546842	T	C	-0.0112	0.0019

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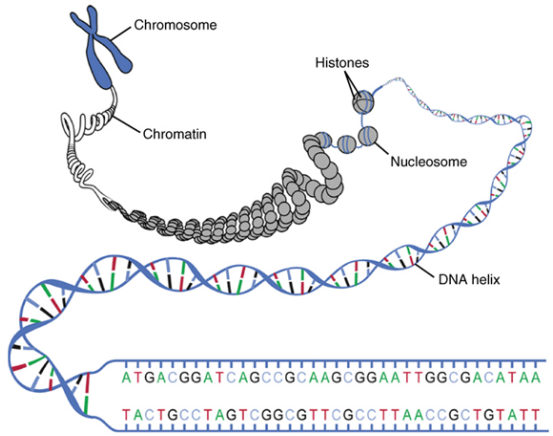

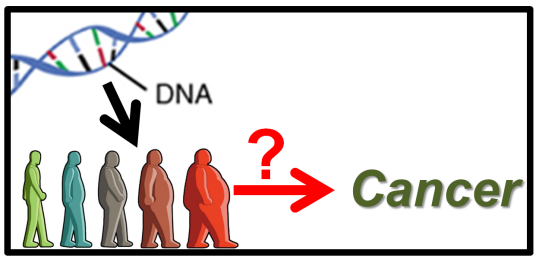

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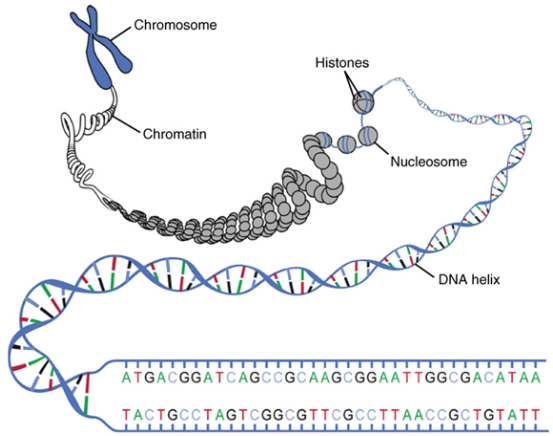

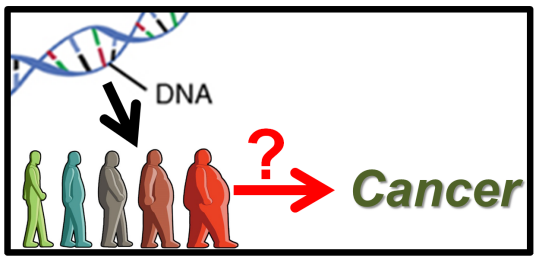

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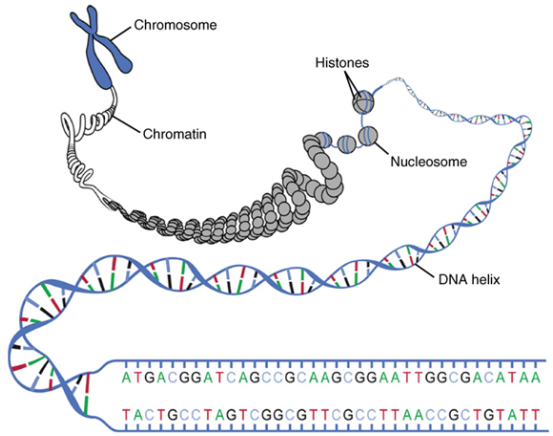

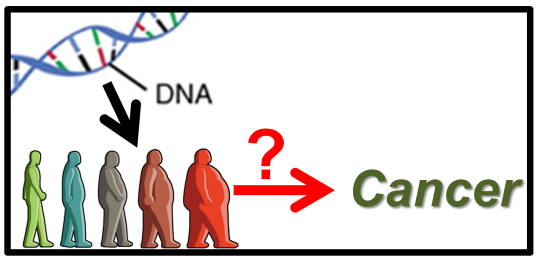

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The example: is Obesity a cause of Ovarian Cancer?

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1. GWAS results for *BMI* (instrument)
2. GWAS results for *Ovarian Cancer*

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STEPS	**2SMR**	**Meta-Analysis**	**Other**
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Harmonisation	TwoSampleMR		
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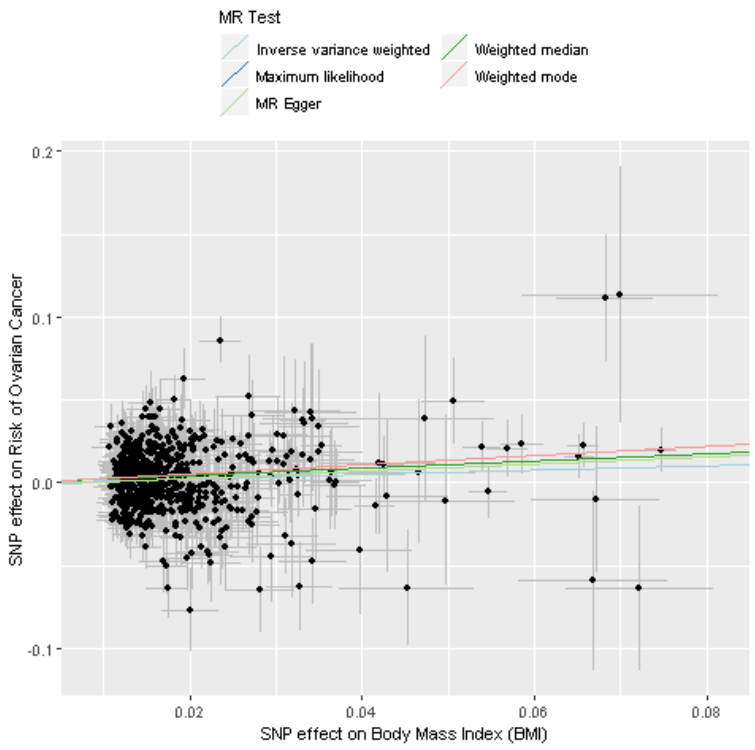
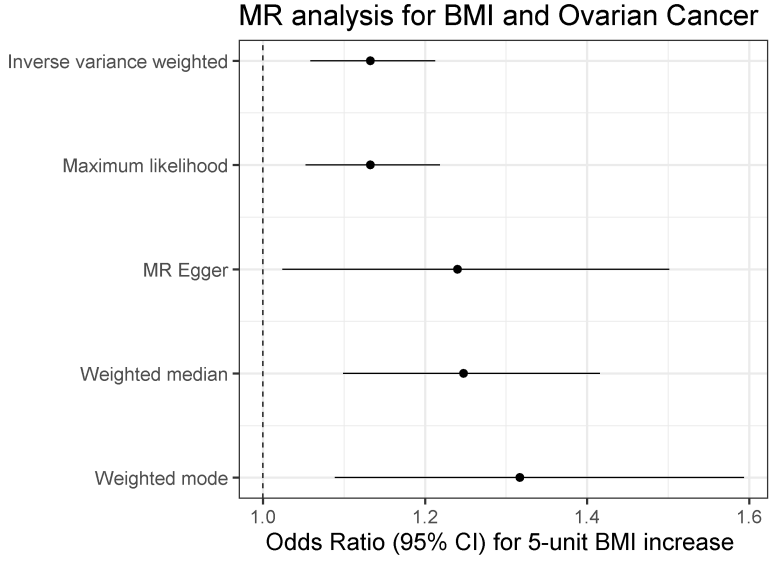


R packages: TwoSampleMR ggplot2



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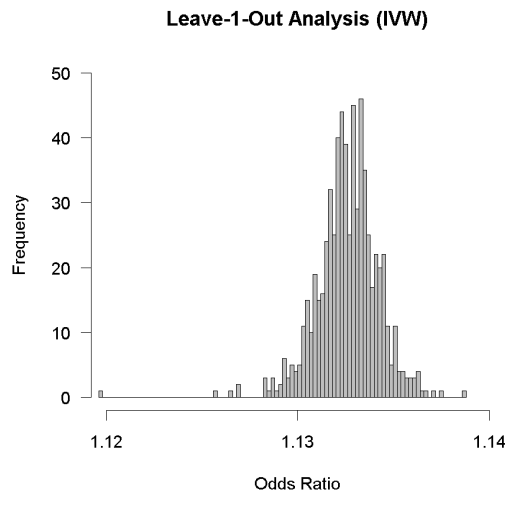

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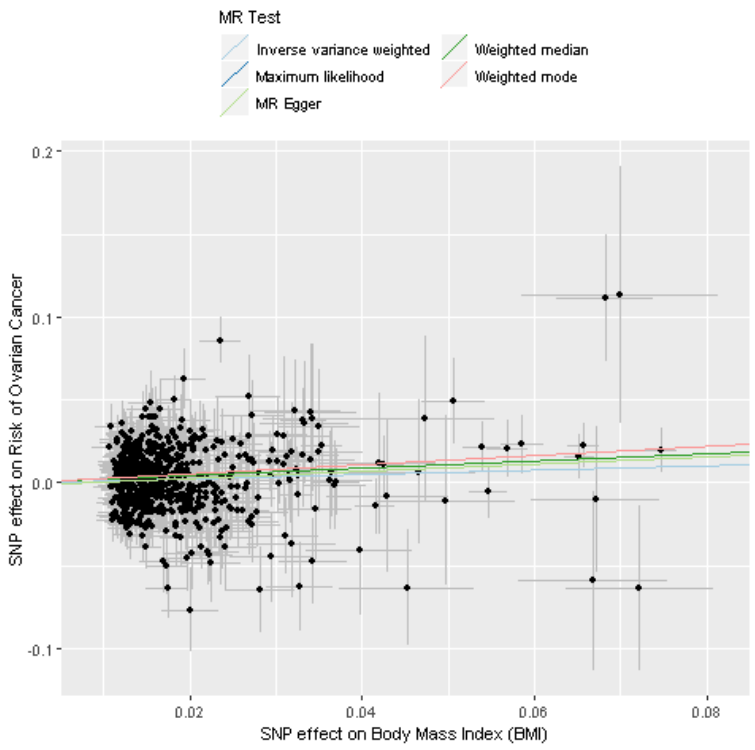

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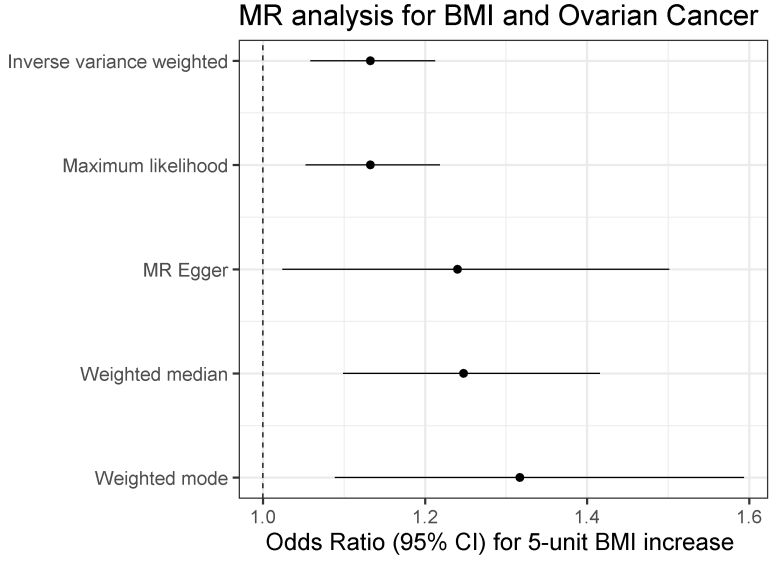

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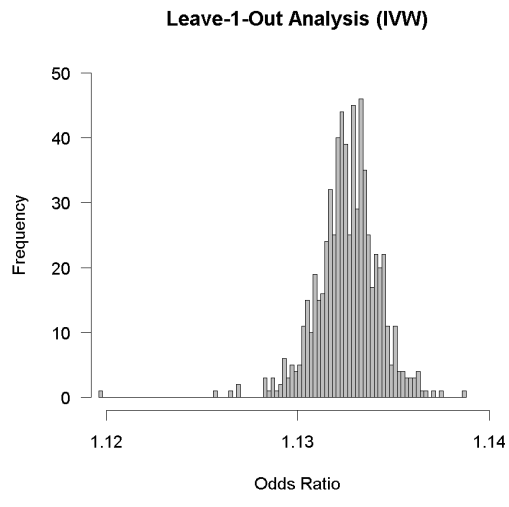

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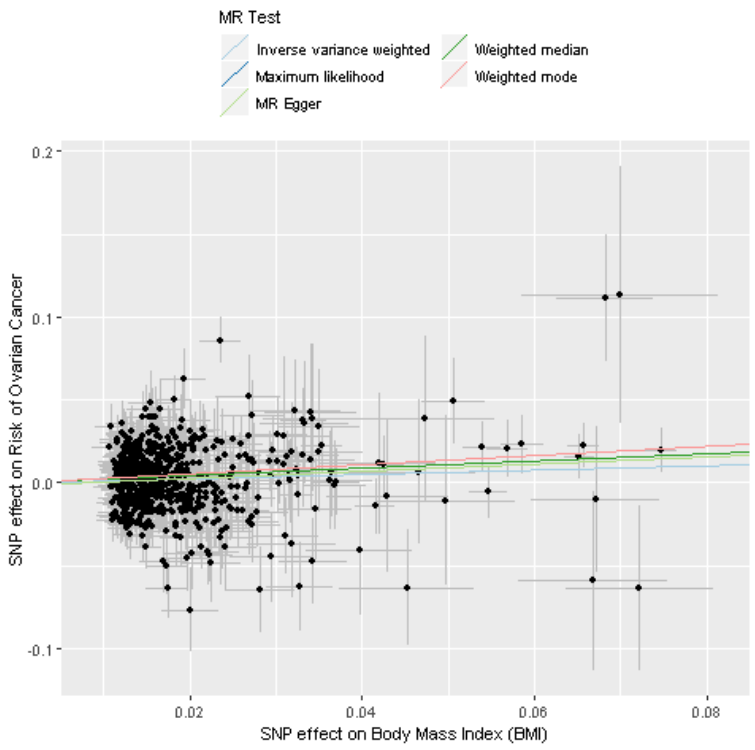

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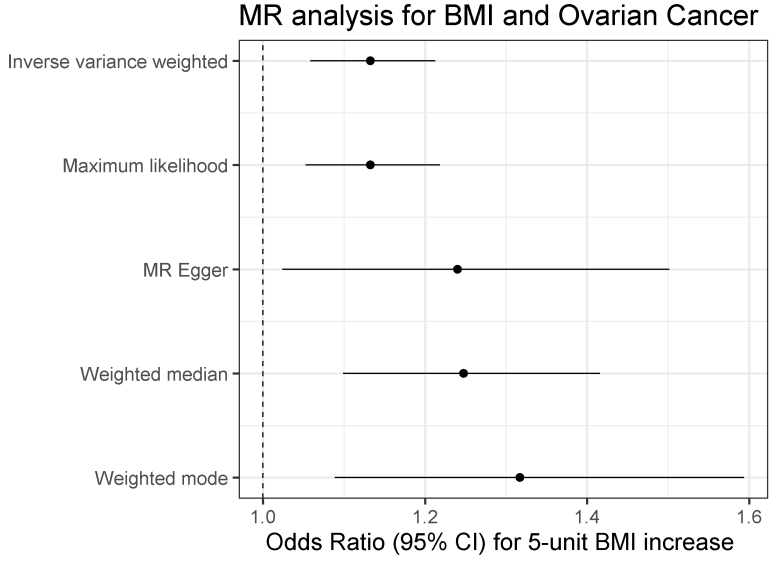

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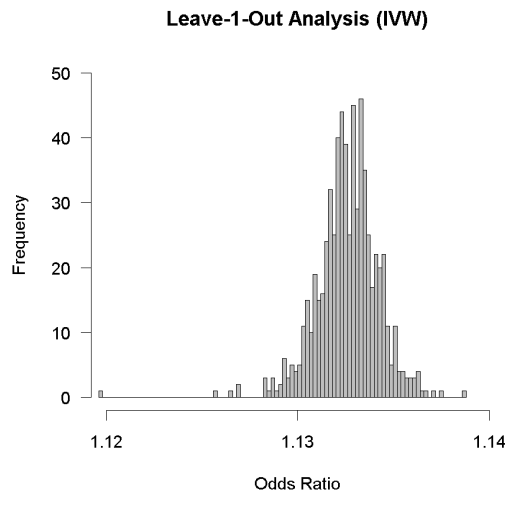

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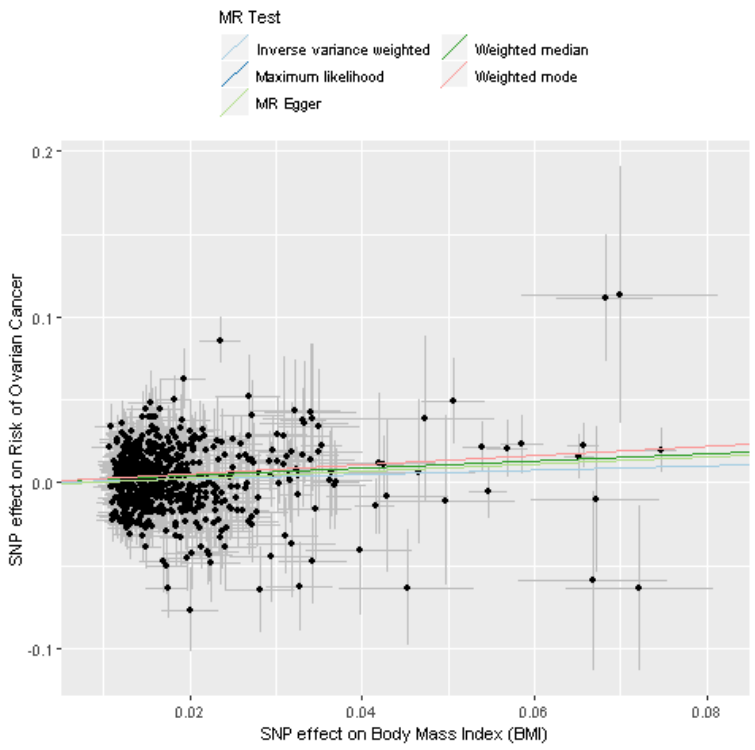

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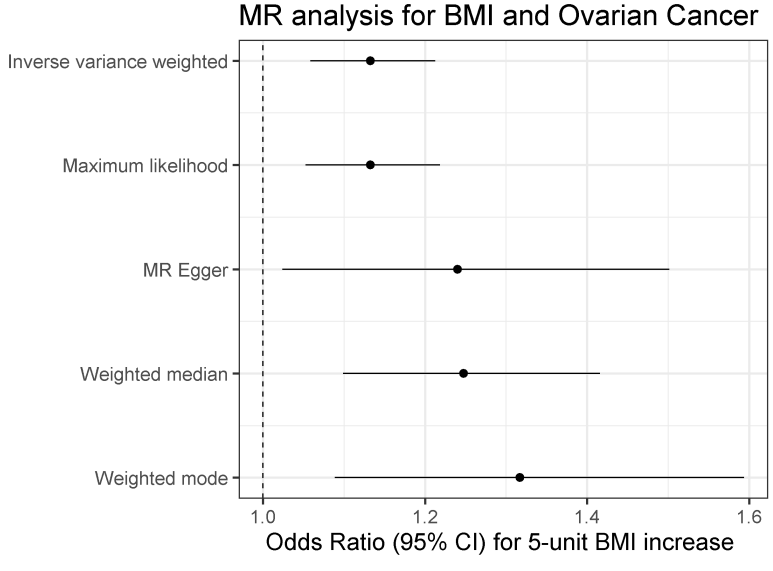

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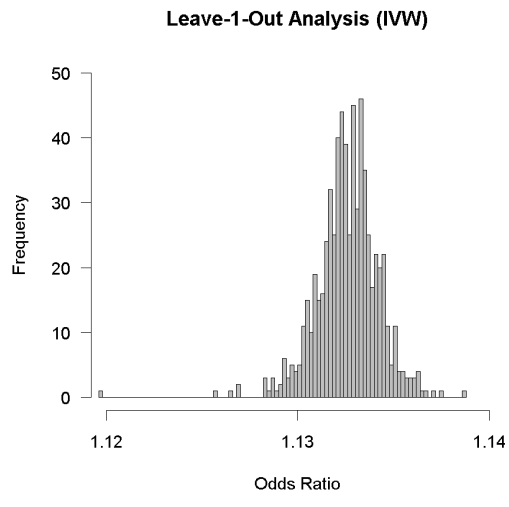
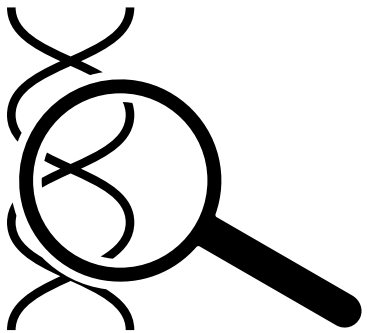


Conclusions on Mendelian randomization

Pros

- Easy to perform in R
- Genetic information is important
- Data availability



Cons

- Large sample sizes needed
- Assumptions!

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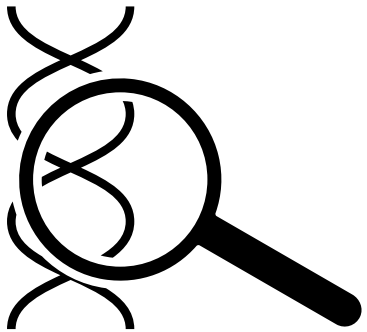

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Questions? mariosad@fellows.iarc.fr