MR studies in R

How to use genetics for identifying modifiable risk factors

Daniela Mariosa

Genetic Epidemiology group, IARC

Lyon, France
The method: Mendelian Randomization

Instrumental variable approach when instruments are genetic

Genetic variants are randomly assigned at conception

Genome Wide Association Studies (GWAS)
The method: Mendelian Randomization

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**Genome Wide Association Studies (GWAS)**

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<thead>
<tr>
<th>SNP</th>
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The example: is Obesity a cause of Ovarian Cancer?

2-Sample Mendelian Randomization (2SMR)

1. GWAS results for \textit{BMI} (instrument)
2. GWAS results for \textit{Ovarian Cancer}

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MR Test
- Inverse variance weighted
- Maximum likelihood
- MR Egger
- Weighted median
- Weighted mode

SNP effect on Body Mass Index (BMI)

SNP effect on Risk of Ovarian Cancer

R package: TwoSampleMR

MR analysis for BMI and Ovarian Cancer

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Odds Ratio (95% CI) for 5-unit BMI increase

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Leave-1-Out Analysis (IVW)

Frequency

Odds Ratio
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SNP effect on Body Mass Index (BMI) vs. SNP effect on Risk of Ovarian Cancer

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Questions? mariosad@fellows.iarc.fr