4. Results

Contents

A summary is shown in Table 1 and 2

Table 1: Summary of 1000 Simulated Mendelian Randomisation Studies With Null Causal Effect

N	Proportion of Invalid IVs	*F*	R^2	Weighted Median		MR Hevo	
				Mean Estimate (Mean SE)	Positive Rate	Mean Estimate (Mean SE)	Positive Rate
Scenario 1: Balanced pleiotropy, InSIDE assumption satisfied							
10,000	0.1	6.9	1.7%	-0.001 (0.101)	0.015	0.000 (0.001)	0.007
10,000	0.2	8.2	2%	0.002 (0.105)	0.013	0.002 (0.002)	0.008
10,000	0.3	11.1	2.7%	-0.003 (0.112)	0.029	-0.002 (0.002)	0.006
Scenario 2: Directional pleiotropy, InSIDE assumption satisfied							
10,000	0.1	6.9	1.7%	0.014 (0.101)	0.017	0.033 (0.001)	0.016
10,000	0.2	8.2	2%	0.033 (0.106)	0.019	0.083 (0.002)	0.032
10,000	0.3	11.1	2.7%	0.064 (0.112)	0.063	0.163 (0.003)	0.114

IV: Instumental Variable, SE: Standard Error
Data from 1000 Simulated Mendelian Randomisation Studies
Null Causal Effect (β = 0)

Table 2: Summary of 1000 Simulated Mendelian Randomisation Studies With Positive Causal Effect

N	Proportion of Invalid IVs	*F*	R^2	Weighted Median		MR Hevo	
				Mean Estimate (Mean SE)	Positive Rate	Mean Estimate (Mean SE)	Positive Rate
Scenario 1: Balanced pleiotropy, InSIDE assumption satisfied							
10,000	0.1	6.9	1.7%	0.028 (0.102)	0.024	0.041 (0.001)	0.020
10,000	0.2	8.2	2%	0.030 (0.106)	0.029	0.043 (0.002)	0.020
10,000	0.3	11.1	2.7%	0.024 (0.112)	0.032	0.040 (0.002)	0.011
Scenario 2: Directional pleiotropy, InSIDE assumption satisfied							
10,000	0.1	6.9	1.7%	0.043 (0.102)	0.030	0.074 (0.001)	0.052
10,000	0.2	8.2	2%	0.062 (0.107)	0.046	0.127 (0.002)	0.105
10,000	0.3	11.1	2.7%	0.091 (0.113)	0.087	0.209 (0.003)	0.234
Scenario 3: Directional pleiotropy, InSIDE assumption not satisfied							
10,000	0.1	8.5	2.1%	0.096 (0.106)	0.115	0.086 (0.001)	0.072
10,000	0.2	22.0	5.2%	0.192 (0.112)	0.297	0.157 (0.003)	0.186
10,000	0.3	10.3	2.5%	0.321 (0.119)	0.498	0.306 (0.004)	0.403

IV: Instumental Variable, SE: Standard Error
Data from 1000 Simulated Mendelian Randomisation Studies
Positive Causal Effect (β = 0.1)

```
##
## CHECKING DATA AND PREPROCESSING FOR MODEL 'MRHevo.summarystats' NOW.
##
## COMPILING MODEL 'MRHevo.summarystats' NOW.
##
## STARTING SAMPLER FOR MODEL 'MRHevo.summarystats' NOW.

##
## CHECKING DATA AND PREPROCESSING FOR MODEL 'MRHevo.summarystats' NOW.
##
## COMPILING MODEL 'MRHevo.summarystats' NOW.
##
## STARTING SAMPLER FOR MODEL 'MRHevo.summarystats' NOW.

## # A tibble: 2 x 7
##       N WME_Av WME_SE Hevo_Av Hevo_SE Hevo_Causal citation
##   <int>  <dbl>  <dbl>   <dbl>   <dbl> <lgl>       <chr>
## 1     1  0.386  0.228   0.227   0.004 FALSE       [@bowden_consistent_2016]
## 2     2  0.386  0.228   0.227   0.004 FALSE       [@bowden_consistent_2016]
```

Table reference[1]

Word count: 20

1. Bowden J, Smith GD, Haycock PC, Burgess S. Consistent Estimation in Mendelian Randomization with Some Invalid Instruments Using a Weighted Median Estimator. Genetic Epidemiology [Internet]. 2016 Apr [cited 2024 Oct 22];40(4):304. Available from: https://pmc.ncbi.nlm.nih.gov/articles/PMC4849733/