

```
In [ ]: # 导入TwoSampleMR包
library(TwoSampleMR)
```

```
In [ ]: exposure_dat=extract_instruments("ieu-a-2") # 从ieu-a-2中提取数据
outcome_data=extract_outcome_data(snps=exposure_dat$SNP,outcomes="ieu-a-7") # 从ieu-a-7中提取数据
```

```
API: public: http://gwas-api.mrcieu.ac.uk/

Extracting data for 79 SNP(s) from 1 GWAS(s)
```

```
In [ ]: dat=harmonise_data(exposure_dat,outcome_data) # harmonise_data()函数用于合并数据集
```

```
In [ ]: res=mr(dat) # 两样本MR分析
```

```
In [ ]: res # 查看结果
```

A data.frame: 5 × 9

id.exposure	id.outcome	outcome	exposure	method	nsnp	b	se	pval
<chr>	<chr>	<chr>	<chr>	<chr>	<int>	<dbl>	<dbl>	<dbl>
ieu-a-2	ieu-a-7	Coronary heart disease id:ieu-a-7	Body mass index id:ieu-a-2	MR Egger	79	0.5024935	0.14396056	8.012590e-04
ieu-a-2	ieu-a-7	Coronary heart disease id:ieu-a-7	Body mass index id:ieu-a-2	Weighted median	79	0.3870065	0.07372113	1.524295e-07
ieu-a-2	ieu-a-7	Coronary heart disease id:ieu-a-7	Body mass index id:ieu-a-2	Inverse variance weighted	79	0.4459091	0.05898302	4.032020e-14
ieu-a-2	ieu-a-7	Coronary heart disease id:ieu-a-7	Body mass index id:ieu-a-2	Simple mode	79	0.3401554	0.15679452	3.309491e-02
ieu-a-2	ieu-a-7	Coronary heart disease id:ieu-a-7	Body mass index id:ieu-a-2	Weighted mode	79	0.3888249	0.09934087	1.928836e-04

```
In [ ]: mr_pleiotropy_test(dat) # 用于检验多重性
```

A data.frame: 1 × 7

id.exposure	id.outcome	outcome	exposure	egger_intercept	se	pval
<chr>	<chr>	<chr>	<chr>	<dbl>	<dbl>	<dbl>
ieu-a-2	ieu-a-7	Coronary heart disease id:ieu-a-7	Body mass index id:ieu-a-2	-0.001719304	0.003985962	0.6674266

```
In [ ]: mr_heterogeneity(dat) # 用于检验异质性
```

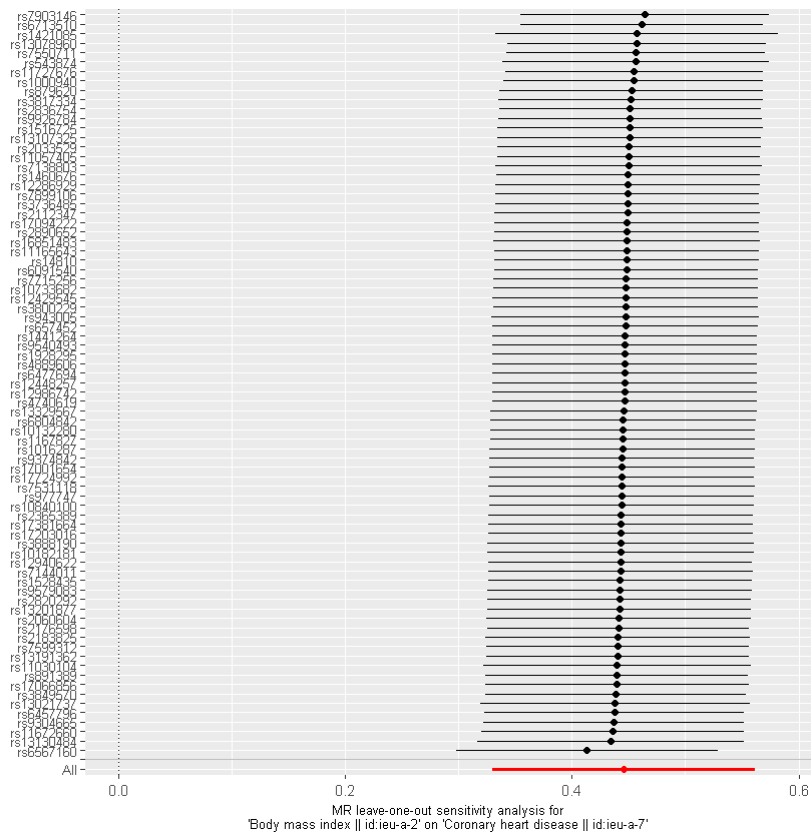
A data.frame: 2 × 8

id.exposure	id.outcome	outcome	exposure	method	Q	Q_df	Q_pval
<chr>	<chr>	<chr>	<chr>	<chr>	<dbl>	<dbl>	<dbl>
ieu-a-2	ieu-a-7	Coronary heart disease id:ieu-a-7	Body mass index id:ieu-a-2	MR Egger	143.3046	77	6.841585e-06
ieu-a-2	ieu-a-7	Coronary heart disease id:ieu-a-7	Body mass index id:ieu-a-2	Inverse variance weighted	143.6508	78	8.728420e-06

```
In [ ]: res_loo=mr_leaveoneout(dat) # 用于检验留一法
mr_leaveoneout_plot(res_loo) # 用于绘制留一法图
```

Warning message:
 "Removed 1 rows containing missing values (`geom_errorbarh()`)."
 Warning message:
 "Removed 1 rows containing missing values (`geom_point()`)."
 `\$ieu-a-2.ieu-a-7`

```
attr("split_type")
[1] "data.frame"
attr("split_labels")
  id.exposure id.outcome
1    ieu-a-2    ieu-a-7
```



```
In [ ]: mr_scatter_plot(res,dat) # 用于绘制散点图
```

```
$`ieu-a-2.ieu-a-7`
```

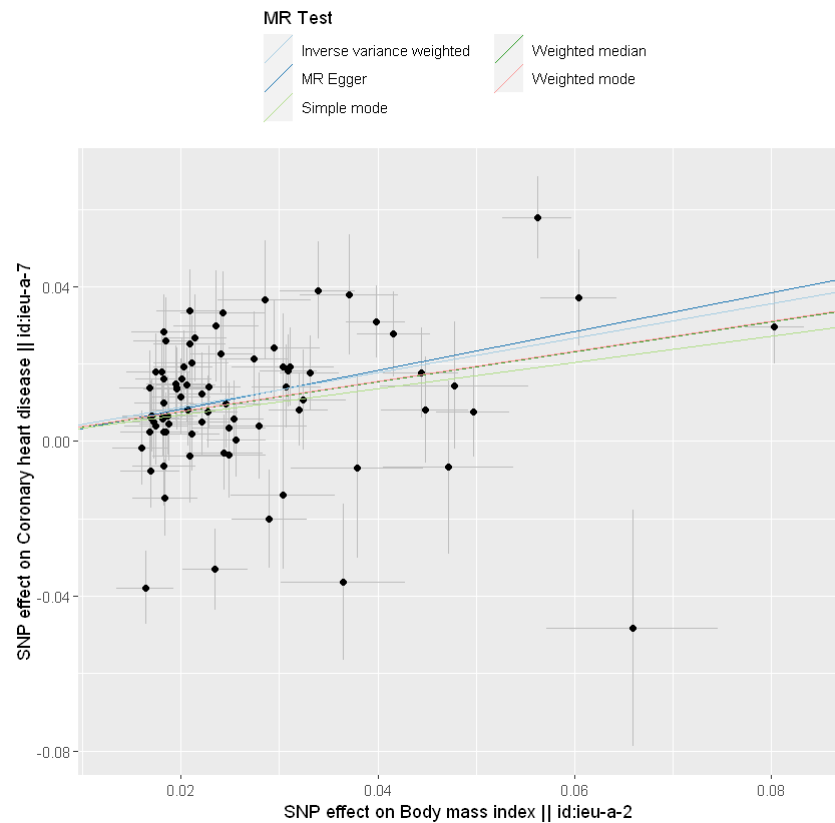
```
attr("split_type")
```

```
[1] "data.frame"
```

```
attr("split_labels")
```

```
id.exposure id.outcome
```

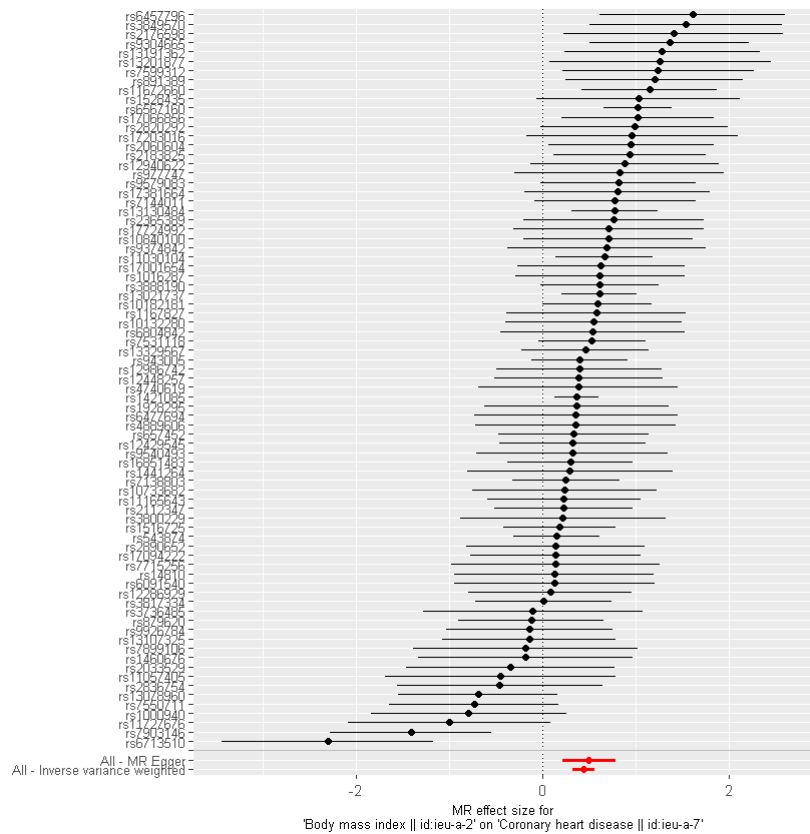
```
1 ieu-a-2 ieu-a-7
```



```
In [ ]: res_single=mr_singlesnp(dat) # 用于检验单个SNP
mr_forest_plot(res_single) # 用于绘制森林图
```

Warning message:
 "Removed 1 rows containing missing values (`geom_errorbarh()`)."
 Warning message:
 "Removed 1 rows containing missing values (`geom_point()`)."
 \$`ieu-a-2.ieu-a-7`

```
attr("split_type")
[1] "data.frame"
attr("split_labels")
  id.exposure id.outcome
1 ieu-a-2 ieu-a-7
```



```
In [ ]: mr_funnel_plot(res_single) # 用于绘制漏斗图
```

```
$`ieu-a-2.ieu-a-7`
```

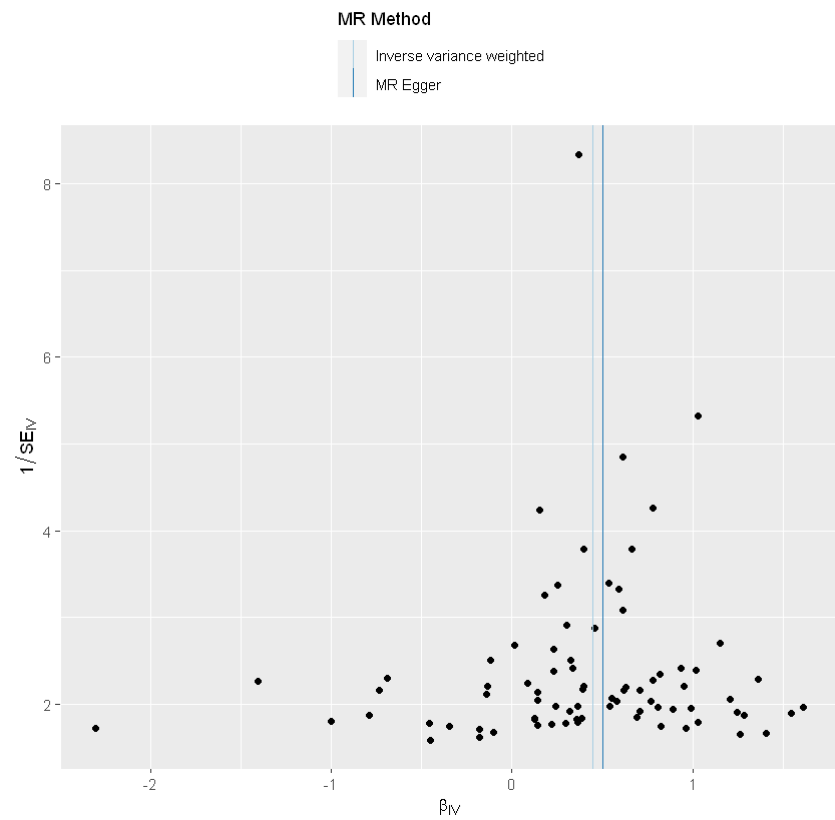
```
attr("split_type")
```

```
[1] "data.frame"
```

```
attr("split_labels")
```

```
id.exposure id.outcome
```

```
1 ieu-a-2 ieu-a-7
```



```
In [ ]: p1=mr_funnel_plot(res_single) # 用于绘制漏斗图
p1
```

```
$`ieu-a-2.ieu-a-7`
```

```
attr(,"split_type")
```

```
[1] "data.frame"
```

```
attr(,"split_labels")
```

```
id.exposure id.outcome
```

```
1 ieu-a-2 ieu-a-7
```

MR Method

- Inverse variance weighted
- MR Egger

