

```
In [ ]: # 多变量孟德尔随机化 — R语言
```

```
# Author: 坚定的唯物主义鼠鼠
```

```
library(TwoSampleMR)
```

```
In [ ]: id_exposure <- c("ieu-a-299", "ieu-a-300", "ieu-a-302") # 三个暴露分别是HDL cholesterol, LDL cholesterol和Triglycerides  
id_outcome <- "ieu-a-7" # 结果是冠心病
```

```
# 更多的暴露和结果的GWAS_ID可以在这里找到: http://cywd.f3322.net/minephp/IEU-GWAS/
```

```
In [ ]: exposure_dat <- mv_extract_exposures(id_exposure, clump_r2 = 0.001, clump_kb = 1e5) #提取暴露数据  
outcome_dat <- extract_outcome_data(exposure_dat$SNP, id_outcome) #提取结局数据
```

```
#提取暴露数据的参数clump_r2和clump_kb是用来剔除连锁不平衡的参数, 可以根据需要进行调整
```

```
mvdat <- mv_harmonise_data(exposure_dat, outcome_dat) # 对数据进行harmonisation
```

```
In [ ]: mv_lasso_feature_selection(mvdat) # 进行Lasso回归, 筛选出最佳的SNP组合
```

```
# Apply LASSO feature selection to mvdat object
```

```
# 在进行MVMR研究时, 我们不建议使用很多的暴露, 因为这会带来比较严重的共线性问题, 一般3~5个为宜。
```

```
# 如果暴露间的共线性问题比较严重, 建议使用mv_lasso_feature_selection()函数来帮助你去除不必要的暴露。
```

```
# 官方文档: https://mrcieu.github.io/TwoSampleMR/reference/mv\_lasso\_feature\_selection.html
```

```
In [ ]: mv_ivw(mvdat) # 进行IVW分析
```

```
# Performs modified multivariable MR analysis.
```

```
# For each exposure the instruments are selected then all exposures for those SNPs are regressed against-
```

```
# - the outcome together, weighting for the inverse variance of the outcome.
```

```
# 官方文档: https://mrcieu.github.io/TwoSampleMR/reference/mv\_ivw.html
```

```
In [ ]: mv_multiple(mvdat, intercept = FALSE, instrument_specific = FALSE, plots = FALSE) # 进行多重暴露的IVW分析
```

```
# Performs modified multivariable MR analysis.
```

```
# For each exposure the instruments are selected then all exposures for those SNPs are regressed against-
```

```
# - the outcome together, weighting for the inverse variance of the outcome.
```

```
# 这个函数算法与mv_ivw()函数类似。
```

```
# intercept = FALSE: 用来控制是否在模型中加入截距项
```

```
# instrument_specific = FALSE: 用来控制是否对每个暴露都进行IVW分析
```

```
# plots = FALSE: 用来控制是否绘制IVW分析的图形
```

```
# 官方文档: https://mrcieu.github.io/TwoSampleMR/reference/mv\_multiple.html
```

```
In [ ]: mv_basic(mvdat) # 进行基本的分析
```

```
# Performs initial multivariable MR analysis from Burgess et al 2015.
```

```
# For each exposure the outcome is residualised for all the other exposures, then unweighted regression is applied.
```

```
# 官方文档: https://mrcieu.github.io/TwoSampleMR/reference/mv\_basic.html
```

```
In [ ]: mv_residual(mvdat,intercept = FALSE,instrument_specific= FALSE,plots = FALSE)
```

```
# Performs initial multivariable MR analysis from Burgess et al 2015.
```

```
# For each exposure the outcome is residualised for all the other exposures, then unweighted regression is applied.
```

```
# 这个函数算法与mv_basic()函数类似。
```

```
# intercept = FALSE: 用来控制是否在模型中加入截距项
```

```
# instrument_specific = FALSE: 用来控制是否对每个暴露都进行IVW分析
```

```
# plots = FALSE: 用来控制是否绘制IVW分析的图形
```

```
# 官方文档: https://mrcieu.github.io/TwoSampleMR/reference/mv\_residual.html
```

```
In [ ]: mv_subset(mvdat,  
  features = mv_lasso_feature_selection(mvdat),  
  intercept = FALSE,  
  instrument_specific = FALSE,  
  pval_threshold = 5e-08,  
  plots = FALSE)
```

```
  # Perform multivariable MR on subset of features
```

```
# The function proceeds as follows:
```

```
# 1. Select features (by default this is done using LASSO feature selection).
```

```
# 2. Subset the mvdat to only retain relevant features and instruments.
```

```
# 3. Perform MVMR on remaining data.
```

```
# features: 要保留的数据,默认是mv_lasso_feature_selection(mvdat)
# intercept = FALSE: 用来控制是否在模型中加入截距项
# instrument_specific = FALSE: 用来控制是否对每个暴露都进行IVW分析
# plots = FALSE: 用来控制是否绘制IVW分析的图形

# 官方文档: https://mrcieu.github.io/TwoSampleMR/reference/mv\_subset.html
```