

# MAIVE in R:

## Instructions to the User

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This document provides some instructions on the implementation of the MAIVE meta-analysis estimator in R.<sup>1</sup> The code consists of two files: *maive.r* and *maivefunction.r*. The execution file is *maive.r*, which internally calls *maivefunction.r*. Both files should be stored in the same folder.

### 1. Input

The code requires the user to supply the meta-analysis data in an Excel file to be called *inputdata.xlsx*, which should be in the same folder as the R files. The Excel file should have the following structure:

- Column 1, to be labelled ‘bs’, should contain the primary estimates.
- Column 2, to be labelled ‘sebs’, should contain the standard errors.
- Column 3, to be labelled ‘Ns’, should contain the sample sizes.
- Column 4, to be labelled ‘study\_id’, should contain a study identification number. (This column is only necessary if the user chooses clustering or study-level fixed effects. See below.)

Figure 1 shows the structure of the input Excel file.

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<sup>1</sup>“Spurious Precision in Meta-Analysis,” by Zuzana Irsova, Pedro Bom, Tomas Havranek, and Heiko Rachinger.

Figure 1: Example of the input file with the meta-analysis data

	A	B	C	D	
1	bs	sebs	Ns	studyid	
2	2.4841	0.8427	58	4	
3	-2.2383	1.1934	38	3	
4	1.5497	0.5759	183	4	
5	0.5149	0.2603	930	9	
6	0.0755	0.5233	258	3	
7	0.9914	1.3905	30	7	
8	0.0449	0.2212	1389	5	
9	0.7615	0.3594	560	5	
10	0.4205	0.1769	2105	4	
11	0.6170	0.2845	629	2	
12	-0.2377	0.9119	83	9	
13	-0.3250	0.5504	201	5	
14	3.3882	1.1907	50	4	
15	1.2926	0.5684	169	8	
16	1.0893	0.5249	201	3	
17	0.2577	0.1941	1766	1	
18	1.5449	0.5761	185	10	
19	1.0222	0.4833	240	3	
20	-0.0677	0.3537	482	10	
21	0.2497	0.2218	1277	5	
22	1.9761	0.8772	95	3	

## 2. Options

The default MAIVE meta-estimator is MAIVE-PET-PEESE with instrumented standard errors and no weights. However, the user can choose other options in lines 26-35 of *maive.r*. The code allows for the user to change the meta-analysis method (PET, PEESE, PET-PEESE, or EK), the weighting (no weights, standard inverse-variance weights, or MAIVE-adjusted weights), the instrumentation of standard errors (yes or no), and the accounting for study-level correlation (none, study fixed effects, or cluster-robust methods).

- Method: PET=1, PEESE=2, PET-PEESE=3, EK=4. The default method option is PET-PEESE=3. This option can be changed in line 28 by inserting the corresponding number.
- Weighting: no weights=0, inverse-variance weights=1, adjusted weights=2. The default weighting option is no weights=0. This option can be changed in line 30 by inserting the corresponding number.
- Instrumenting the SEs: no=0, yes=1. The default instrumenting option is yes=1.

This option can be changed in line 32 by inserting the corresponding number.

- Study-level correlation: none=0, study fixed effects=1, cluster-robust standard errors=2. The default study-level correlation option is none=0. This option can be changed in line 34 by inserting the corresponding number.

### 3. Output

The code returns:

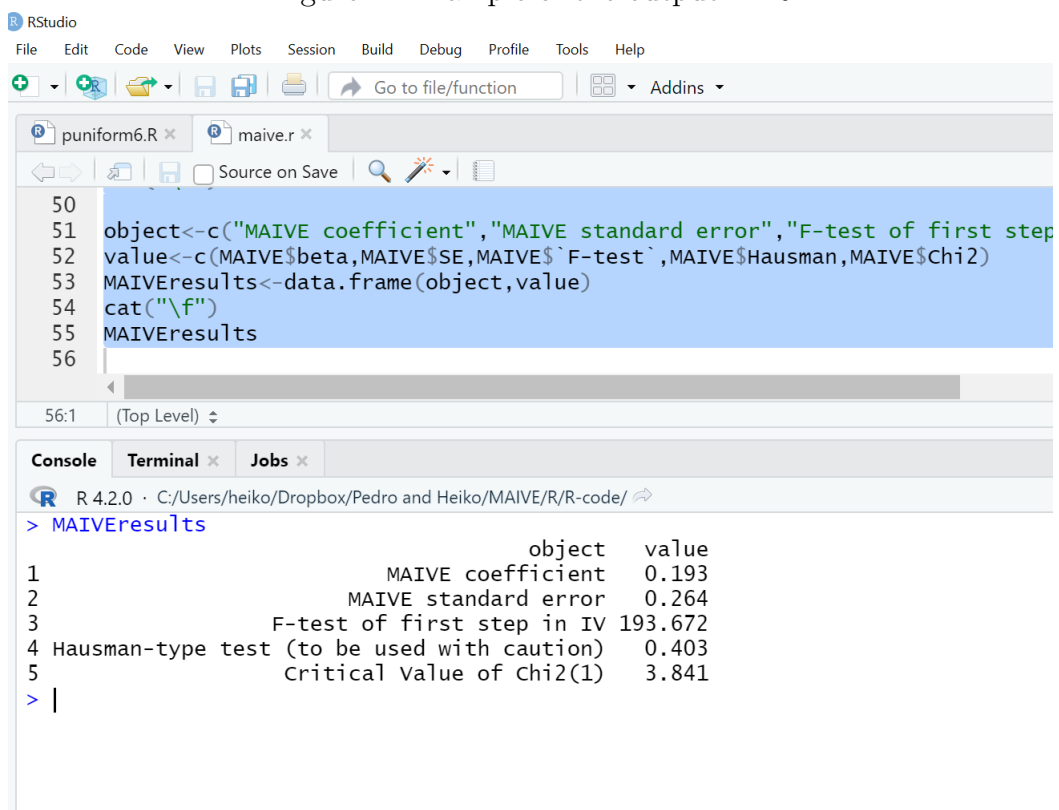
1. A MAIVE point estimate and a standard error.
2. A Hausman-type test statistic and a 5% critical value. The test statistic consists of a weighted squared difference between the MAIVE point estimate and a standard point estimate. The latter is obtained from the same method as chosen for MAIVE but with inverse-variance weights and without instrumenting the standard errors.
3. When instrumenting the standard errors, the code also returns a heteroskedasticity-robust F test of the first-stage regression.

Figure 2 provides an example of the output in R.

### 4. Technical comments

- In the first-stage, we regress the variances on a constant and the inverse sample sizes.
- The Hausman-type test is weighted by the variance of the MAIVE estimator and is, consequently, a conservative test. It only compares the intercepts.
- If study fixed effects are included, the dummy variables are demeaned so that the intercept measures a grand mean.
- If the user does not provide a ‘study-id’ column, the program assumes that the study-level correlation option is *none*.

Figure 2: Example of the output in R



The screenshot shows the RStudio interface. The top menu bar includes File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, and Help. Below the menu is a toolbar with icons for file operations and a search bar. The main editor window displays a script with the following R code:

```
50  
51 object<-c("MAIVE coefficient","MAIVE standard error","F-test of first step  
52 value<-c(MAIVE$beta,MAIVE$SE,MAIVE$`F-test`,MAIVE$Hausman,MAIVE$Chi2)  
53 MAIVEResults<-data.frame(object,value)  
54 cat("\nf")  
55 MAIVEResults  
56
```

The console window at the bottom shows the output of the code:

```
> MAIVEResults  
      object      value  
1      MAIVE coefficient      0.193  
2      MAIVE standard error      0.264  
3      F-test of first step in IV 193.672  
4 Hausman-type test (to be used with caution)      0.403  
5      Critical value of Chi2(1)      3.841  
> |
```