

Jason & Glenwick, eds.

Methodological Approaches to Community-Based Research

Chapter 7/Web Appendix guide

Chapter 7/Meta-Analysis in Community-Oriented Research: Practice Dataset Guide

Introduction to Meta-Data

As described in the chapter, studies included in a meta-analysis in the social sciences usually report multiple outcome variables. Therefore, two data sets are required to conduct analysis at the level of (1) individual studies, and (2) for separate outcome measures. It is assumed that you have coded, entered, and cleaned your data of any errors by this point. All datasets and syntax are in SPSS/PASW format. *N.B.: The studies in the sample datasets used here have been simplified for practice purposes, and do not fully reflect the results of the studies or their authors.*

The practice data sets in this appendix use meta-analysis macros created by David Wilson and Mark Lipsey, first published with their book *Practical Meta-Analysis* (2001). More comprehensive information, macros, and tutorials are available at <http://mason.gmu.edu/~dwilsonb/ma.html>.

Study level. Refer to data set Phase1_Studylevel. This data set includes all identifying information, methodological variables, and demographic data related to the studies. Notice that some study identification numbers have a letter after them (e.g., 0912A). As described in Chapter 7, these cases are derived from multiple distinct studies reported in the same resource, usually the same journal article. This is the Phase 1 stage of the study-level data set. You can run descriptive analyses in this data set as you wish.

Outcome level. Refer to data set Phase1a_Outcomelevel. This dataset includes study identification numbers, with multiple cases for each study that correspond to multiple outcome variables. Note that each outcome variable has its own sample size, as some participants may not have completed every outcome measure.

Using the Practice Datasets

The data sets in this Web Appendix are intended to help novice meta-analysts practice the steps required to run a meta-analysis. Many transformations and rearrangements of the data are required before meta-analyses can produce results. The steps in this guide are not the only valid methods to meta-analysis. Instead, this guide encompasses basic steps that are useful with many kinds of data.

The statistical methods applied in this guide assume that the reader is familiar with basic features of SPSS, descriptive statistics, and univariate statistics. Generally, graduate students in psychology who have taken one to two basic statistics courses should have no trouble following this guide. Meta-analytic techniques are explained in text and in the syntax, but certain skills such as maneuvering within the SPSS interface are assumed.

This guide is organized in three phases, with corresponding SPSS datasets, syntax, and sample outputs. Datasets are provided for each step along the way, so that readers may check their work or practice specific steps without having to go through all the transformations every time. A table is provided at the end of this Web Appendix to indicate which SPSS files are associated with each step.

Phase 1: Preparing the data

- a) Winsorizing sample sizes and standard mean differences (SMDs)
- b) Winsorizing standard mean differences (SMDs)
- c) Weighting SMDs

Phase 2: Appending and Aggregating

- a) Aggregate the outcome level data
- b) Append outcome variables to the study level data

Phase 3: Major meta-analyses

- a) Mean SMDs
- b) Meta-ANOVA
- c) Meta-Regression

Phase 1: Preparing the data

Trim outliers. As described in Chapter 7, it is often useful to trim outliers in the sample sizes and effect sizes. Trimming is not always necessary, but it is important to inspect the obtained distributions to see if extreme values are present. You should check the chapter and references for more information on the process of trimming outliers. When trimming is appropriate, we prefer a winsorizing procedure, as shown in the Winsorizing and weighting syntax. Winsorizing entails replacing outliers with a set value and is explained in Chapter 7..

Other valid methods of trimming meta-analysis data exist, and may be familiar to the reader from managing outliers in normal statistical analysis. One approach is to rank order the data and delete a specific number of cases at the high and low ends. In SPSS interface, click Data, Sort Cases, and select the variable to be trimmed, then delete or cap the number of desired outlying cases. If the variable of interest does not have a normal distribution, then it is possible to transform values to z-scores and trim outliers from this distribution.

1a) Winsorizing sample sizes. To run the Winsorizing syntax for sample sizes, first open the data set Phase1a_Outcomelevel.sav and the syntax Phase1_WinsorizingWeighting.sps. Look at lines 14–28. In the outcome level data set, sample sizes for the experimental and control groups are reported separately. The experimental n and the control group n must be combined to come up with a total n for each study, at post-test and at follow up. Run lines 14–28 (highlight and press Control+R). Look in the outcome data set to verify that four new variables were created:

```
postn_sum
follupn_sum
wpostn
wfollupn.
```

The variables postn_sum and follupn_sum refer to the total samples sizes (experimental + control group) for each study at post-test and follow up test. The variables wpostn and wfollupn refer to the Winsorized post n and Winsorized follow up n . Descriptive labels for each of these variables are coded into the syntax. At this stage, postn_sum and wpostn should be equal, because the variables were just created and not yet Winsorized. Run lines 30–32 to create a

descriptives table to check that the post variables are equivalent, and the follow up variables are equivalent. The next step is to Winsorize wpostn and wfollupn.

The sample sizes in this meta-analysis range from 22 to 18,875. For practice purposes, the Winsorization point for this dataset will be $n < 2000$, which was selected because only 4 studies had sample sizes greater than 2000, with the remaining sample sizes composing a fairly normal distribution with positive skewness. Read lines 34–35 in the syntax, and notice that the syntax commands represent a logical argument that can be read as:

If any value for the variable for Winsorized post n is greater than 2,000, then delete the higher value and replace it with a value of 2000.

Run lines 34–38. Next, run the descriptives statistics in lines 40–42. Notice that in the previous descriptives (from lines 30–32), the Winsorization variables have been created but not finished. In this second descriptives table, the maximum values for wpostn (Winsorized total post N) and wfollupn (Winsorized total follow up N) should be 2,000. Check your work with the table below before moving to the next step.

Descriptive Statistics					
	N	Minimum	Maximum	Mean	Std. Deviation
total post N	369	22.00	18875.00	569.9214	1376.65121
Winsorized total post N	369	22.00	2000.00	426.9485	546.59372
total follow up N	60	46.00	2448.00	326.2000	485.31349
Winsorized total follow up N	60	46.00	2000.00	318.7333	454.58955
Valid N (listwise)	14				

The ceiling values (in lines 35 and 38) can be adjusted to suit your data needs. Try changing the values in the syntax from 2,000 to 1,500, then rerun the descriptives and see if it changes. Return to the Winsorized sample size at 2,000, and save the data set.

Now that the total sample sizes have been trimmed, it is necessary to redistribute the winsorized sample sizes into experimental and control groups. Run lines 44–59 to create these four new variables:

```
wexpostn
wctrlpostn
wexpfollupn
wctrlfollupn.
```

Check your data to see if they appear at the end of the data set, then run lines 61–65 to examine descriptive statistics of your new variables. The output should match with the table below:

Descriptive Statistics					
	N	Minimum	Maximum	Mean	Std. Deviation
experimental post N	369	10	1633	246.57	357.279
Winsorized experimental post N	369	10.00	1090.12	213.7738	265.69611
control post N	369	12	17758	323.35	1178.390
Winsorized control post N	369	12.00	1881.64	213.1747	335.71627
experimental follow up N	60	21	1224	199.52	323.340
Winsorized experimental follow up N	60	21.00	1076.00	195.7833	312.41987
control follow up N	60	23	1224	126.68	186.192
Winsorized control follow up N	60	23.00	1000.00	122.9500	164.83854
Valid N (listwise)	14				

At this point, the sample sizes are Winsorized. Your data set should now match Phase1b_Outcomelevel.sav. Check that the data set you just created matches this practice dataset and continue on to the next step for Winsorization of effect sizes. (Hint: a good way to check your work is to run descriptive statistics, like those displayed above, for both files and see if you get the same results.)

1b) Winsorizing SMDs. As discussed in Chapter 7, effect sizes in this meta-analysis are referred to as Standardized Mean Differences (SMD). As also discussed in Chapter 7, outliers beyond two to three standard deviations are often Winsorized (trimmed and replaced with the upper or lower bounds of the second or third standard deviation distribution). In this practice syntax, the threshold of two standard deviations is used. You may alter this syntax to fit your desired Winsorization levels.

Open the data set you created or open Phase1b_Outcomelevel.sav. In the Phase1_WinsorizingWeighting.sps syntax, read and run lines 72–83 to create the new variables you will need for SMD Winsorization. Check that these three variables appear at the end of your data set for the pre-test, post-test, and follow up SMDs, respectively:

```
wpreSMD
wpostSMD
wfollupSMD
```

Run the descriptives statistics in lines 85–88, and check that your output matches the table below:

Descriptive Statistics

	N	Minimum	Maximum	Mean	Std. Deviation
preSMD	29	-1.32	.60	-.1355	.42731
Winsorized pre SMD	29	-1.32	.60	-.1355	.42731
post SMD overall	369	-.72	2.26	.2269	.37387
Winsorized post SMD	369	-.72	2.26	.2269	.37387
follow up SMD overall	60	-.42	1.19	.1945	.32592
Winsorized follow up SMD	60	-.42	1.19	.1945	.32592
Valid N (listwise)	1				

Using the means and standard deviations obtained, calculate the values two standard deviations away from the means for pretest, posttest, and follow up. These numbers are listed in the table below, as well as in the comment lines of the Winsorizing syntax.

Variable	Raw SMD mean	Standard Dev * 2	Floor and Ceiling
Pre SMD	-0.1355	$(0.4273 * 2) = 0.8546$	-0.9901, 0.7191
Post SMD	0.2269	$(0.3739 * 2) = 0.7478$	- 0.5208, 0.9746
Follow up SMD	0.1945	$(0.3259 * 2) = 0.6518$	-0.4573, 0.8463

Input these numbers into the syntax as shown in the comments of syntax lines 90–107, then run these lines. Always double-check your calculations of the ceilings and floors. Run the descriptives in lines 109–111. The results should match the table below. Notice the differences from the previous table, where the Winsorized SMDs have been trimmed:

Descriptive Statistics

	N	Minimum	Maximum	Mean	Std. Deviation
preSMD	29	-1.32	.60	-.1355	.42731
Winsorized pre SMD	29	-.99	.60	-.1241	.39804
post SMD overall	369	-.72	2.26	.2269	.37387
Winsorized post SMD	369	-.52	.97	.2085	.30754
follow up SMD overall	60	-.42	1.19	.1945	.32592
Winsorized follow up SMD	60	-.42	.85	.1886	.31053
Valid N (listwise)	1				

Now the sample sizes and SMDs are trimmed of outliers. The data set you created should now match Phase1c_Outcomelevel.sav. The next step is to weight the data.

1c) Weighting SMDs. As described in Chapter 7, it is standard practice to multiply each effect size by its inverse weight, for the purpose of giving larger studies with more participants a more powerful “vote” in the analyses. This process does not change the effect sizes, but the weight variables are used in the analyses to adjust results according to the contributions of each study.

Lines 113–135 in the Phase1_WinsorizingWeighting syntax create several variables with somewhat confusing names, which are abbreviations for various weights, which correspond to variable names in the meta-analysis syntax. In the dataset you have created thus far (which should match Phase1c_Outcomelevel.sav), run lines 113–135 of the syntax and check that your data file now has these additional variables:

```
weighnumpo
weighdenpo
invweighpo
w_espo
w_essqpo
wsqpo
weighnumfu
weighdenfu
invweighfu
w_esfu
w_essqfu
wsqfu
```

Now, you have successfully Winsorized outliers and weighted the data. The SMDs are ready for analysis. At this point, Phase 1 of preparing the data is complete, and the dataset you created should now match Phase2_Outcomelevel.sav. Check that your newly created data set matches this practice data set before proceeding.

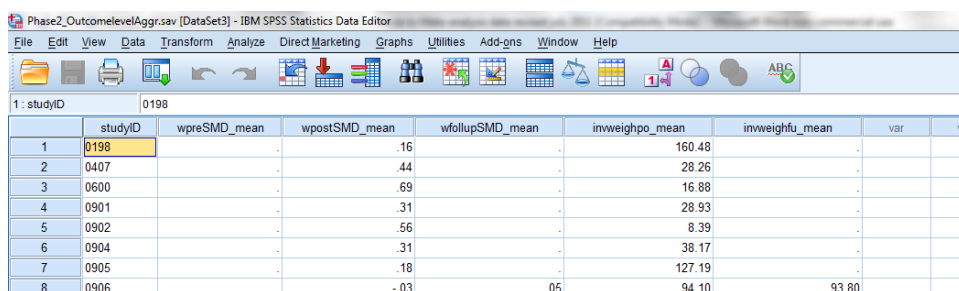
Phase 2: Aggregating and Appending

In the steps above, the k (number of studies) for each statistic was 415. However, the current meta-analysis includes only 75 studies. This disparity is caused by the fact that many of the studies collected data on multiple outcome measures, ranging from one to 15 per study. As described in Chapter 7, each study in a meta-analysis gets “one vote” in the results (that is, each study should contribute only one data point in each analysis). For calculating a mean effect across all the studies, this theory translates into aggregating (i.e., averaging) all outcomes for each study into one master outcome effect size. In this step, you will create a study level data set with one aggregated mean effect size per study to obtain the grand mean of the meta-analysis across all the studies. Later, you will create specific data sets to analyze categories of outcomes.

2a) Aggregating the Outcome data. Open the Phase2_Outcomelevel.sav file and the Phase2_AggrAppend.sps syntax. Run line 14 to sort the entire dataset by the variable studyID. Next, read over lines 16–26 to aggregate the outcome variables into one meta-outcome variable for each study. The new variables will be saved under the file name Phase2_OutcomelevelAggr.sav. You must specify the location on your computer where you would like this file to be saved, in line 20 of the syntax. Currently, it is set to save the file to the

owner user's desktop in Windows 7. This may not be a valid option for some users, so it is important to save this file in your desired location by editing line 20 according to your preference.

After you enter the directory where you would like to save the aggregate file, run lines 16–26. Run lines 28–30 to open the aggregate file you just created (or use the interface to click on this file with your mouse, if you prefer). Take a moment to examine the Phase2_OutcomelevelAggr.sav file. If you have successfully aggregated the data, there should be 75 studies in the file. Each studyID should be associated with Winsorized effect sizes and inverse weights. Several data points will be missing, because many studies did not report pre-test data or follow-up data. The database should look like the screenshot below. After you have confirmed that the aggregation procedure was successful, save and close this dataset.



	studyID	wpreSMD_mean	wpostSMD_mean	wfollupSMD_mean	invweighpo_mean	invweighfu_mean	var	v2
1	0198	.	.16	.	160.48	.	.	.
2	0407	.	.44	.	28.26	.	.	.
3	0600	.	.69	.	16.88	.	.	.
4	0901	.	.31	.	28.93	.	.	.
5	0902	.	.56	.	8.39	.	.	.
6	0904	.	.31	.	38.17	.	.	.
7	0905	.	.18	.	127.19	.	.	.
8	0906	.	-.03	.05	94.10	93.80	.	.

2b) Append the Aggregated Outcome–level data to the Study-level data. For the sake of simplicity (and because of how SPSS designates active datasets), it is easiest to close all syntax, output files, and data sets before starting Phase 2b. Open the Phase1_Studylevel.sav file. In the syntax Phase2_AggrAppend.sps, run line 37 to sort by studyID. Notice that line 42 requires you to type in the location of the Phase2_OutcomelevelAggr.sav file that you specified in Phase 2a. Next, run lines 39–44 to add the aggregated variables to the study-level data set. After you run these lines of syntax, look to see that the following variables appeared in the data set Phase1_Studylevel.sav:

```
wpreSMD_mean
wpostSMD_mean
wfollupSMD_mean
invweighpo_mean
invweighfu_mean
```

Save this file as Phase3a_Merged.sav. You should now see all of the Winsorized variables in your study-level file. The data are now ready to be meta-analyzed.

Major Analyses

Before you run major analyses, it is recommended to run descriptive statistics on the studies in your meta-analysis. Such analyses are similar to traditional descriptive statistics, and therefore they are not described in this guide. Refer to the references in Chapter 7 for more detailed information on meta-analytic descriptives.

3a) Overall mean effect. Save the folder “SPSS_Macros” directly to your hard drive, usually the C:/ drive. If you do not save the folder directly to your hard drive, the syntax will not

run properly. If your hard drive is labeled something other than C:/, you must alter the syntax to correct the path name in both of the Master Instructions files. You will not need to open the MeanES, MetaF, and MetaReg files. Instead, the Master Instructions files will connect to these macros. These analyses will work only if the path names are correct.

Open the data set Phase3a_Merged.sav and the syntax Phase3_Master_Instructions_short.sps.¹ Run lines 13–16, and examine the SPSS output created. The results of this syntax should produce two output matrices, for post and follow up SMD (standard mean differences), respectively. Compare your results to the output file Phase3a_MeanSMD.spv. The output provides both fixed and random effects. In this guide, only random effects results are used, and there is ample literature elsewhere regarding the debate over the uses of fixed and random effects (see Lipsey & Wilson, 2001).

Results for the first matrix in Phase3a_MeanSMD.spv refer to the post-test standardized mean effects, included below. Take some time to examine your results and put these effects into your own words, for best understanding. To determine if the results are significant, examine the confidence intervals of the random mean effect. If the 95% CI does not include zero, then the results are significantly different from zero.

Matrix: Mean SMD at post-test

Run MATRIX procedure:	
***** Meta-Analytic Results *****	
Number of studies reporting post SMD	----- Distribution Description ----- N Min ES Max ES Wgtd SD 68.000 .160 .779 .233
	----- Fixed & Random Effects Model ----- Mean ES -95%CI +95%CI SE Z P Fixed .1823 .1554 .2092 .0137 13.2925 .0000 Random .2154 .1519 .2789 .0324 6.6475 .0000
Random mean SMD, 95% CI	----- Random Effects Variance Component ----- $\tau^2 = .043295$
	----- Homogeneity Analysis ----- Q df p 288.2134 67.0000 .0000
Q-statistic is significant	Random effects τ^2 estimated via noniterative method of moments.
----- END MATRIX -----	

In the above results, $n=68$, indicating that 68 out of the 75 studies reported data at post-test (7 studies reported only follow-up outcomes). The random mean SMD = 0.2154, with a 95% Confidence Interval = {0.1519, 0.2789}. All obtained results can be rounded to two decimal places. As this confidence interval does not include zero, then it can be concluded that the overall effect size for this body of studies is significant. Finally, the Q-statistic is significant, indicating that the body of studies in this sample is not homogeneous. A significant Q-statistic indicates that the meta-analyst should search the database for one or more variables (i.e., moderators) that can

¹ The long version of Lipsey and Wilson's (2001) syntax is provided in the SPSS Macros folder with comments explaining analytic options, but the short version will be used here.

explain the variability that has been obtained in effect sizes (i.e., that explains why the distribution of effects as denoted by the Q -statistic is not homogeneous. Therefore, it is logical to proceed to the next step of analyzing moderators through ANOVA and regression.

3b) Moderator analyses. Moderator analyses can be conducted when there is a significant Q -statistic (found in the Homogeneity Analysis in the output), indicating underlying group differences in the mean effect. This is the case in the practice data set for both post and follow-up data. First, methodological factors will be examined that may contribute to variability in SMDs. Next, this guide will outline how to select and examine hypothesized moderators, to determine which types of programs work best. The guide does not explore all the assumptions required for ANOVA (independent observations, homogeneity of variance across groups, sphericity, and normal distribution of each group). It is recommended that the reader explore these issues through descriptive statistics before continuing with meta-ANOVA.

Study level moderators. Any of the study-level variables can be assessed with the same study-level dataset used to obtain the mean SMD. For example, the syntax on lines 20-24 in the Master Instructions short file calculates ANOVA F -tests between studies with a structured, active intervention (group 1), and studies that lacked a structured intervention protocol (group 2), at posttest and follow up test. Results are displayed in the output file Phase3bi_MetaANOVA.spv. To determine if the results are significant, compare the confidence intervals of the two categories. If they do not overlap, you can conclude that the two groups are significantly different at the $p < 0.01$ level. In this case, there is no overlap, and the structured, active interventions in group 1 have higher SMD's than group 2.

If they overlap slightly, refer to Cumming & Finch (2005) for comparison procedures:

“For a comparison of two independent means, p is less than 0.05 when the overlap of the 95% CIs is no more than about half the average margin of error, that is, when the proportion overlap is about .50 or less. In addition, p is less than 0.01 when the two CIs do not overlap, that is, when proportion overlap is about 0 or there is a positive gap” (p. 176)

To assess other study level variables, you can substitute the Structure variable with any other variable entered at the study level. Note that the groups being compared correspond to the numerical value labels for the randomized variable in the dataset.

Outcome-level moderators. Extra steps are required to assess outcome level moderators. As in all meta-analyses, each study must get only one data point per analysis. When comparing categories of outcome variables, the outcome-level file must be aggregated again on the basis of the variable of interest. To try this with your own data, refer to the previous sections 2a and 2b on aggregating and appending.

In the practice data set, start by opening the data file Phase2_Outcomelevel.sav. This file includes all the Winsorized sample sizes, SMDs, and weights, but it is not yet aggregated. Open the syntax Phase3b_AggrAppend.sps. In line 21, the break variables should include studyID and the outcome variable of interest for the ANOVA. In this exercise, the additional break variable will be OC_category, which indicates the type of outcome data that was collected. Run lines 13-14 to sort the dataset by studyID and OC_category.

As before, the aggregated outcome file must be named in line 20. Enter the name and directory location where you would like to save this file on your computer. In this practice, the aggregated file is saved as Phase3b_OutcomelevelAggr. Run lines 19–26.

Save and close all data files. Then open Phase1_studylevel.sav. Run lines 36–37 to sort the study level file by studyID and OC_category. Adjust line 42 to indicate the correct directory location of the file Phase3b_AggrAppend.sps. Then run lines 39–44 to append the aggregated outcome file to the study-level file, and save. The variable OC_category is merged so that each study contributes one case per condition. For example, some studies measured more than one outcome variable in the category of social skills. For meta-analysis, these two outcomes were merged to create one effect size for social skills from that study. The data set should now match Phase3b_Merged.sav.

Open Phase3b_Merged.sav. Next, open the syntax Master_Instructions_short.sps. Run lines 28–31. Results of this analysis are saved in the output file Phase3bii_MetaANOVA.spv. As with the studylevel moderator analysis, the group numbers in the output correspond to their value labels for the OC_category variable in the dataset. In interpreting the results, first look at the Q -statistics and check if any are significant at the $p < 0.05$ level. In this output, none of the Q -statistics are significant, indicating that the outcome categories are sufficiently specific for moderator analysis.

Compare the confidence intervals of these outcome categories. Check if any of the confidence intervals include zero, to see if the effects of the programs are significant for these variables.

Look at the follow up matrix as well. Note that in the follow-up results, SPSS returned the following error:

Error encountered in source line # 1293

Error # 12431

Degree of freedom is less than or equal to zero for CHICDF or TCDF.
Execution of this command stops.

Do not panic! This error does not mean that the results are somehow in error but only refers to the fact that one of the categories had an insufficient sample size at follow-up test. The Effect Size Results display that category 72 (grades) has a sample size of 1, and $df = 0$. Therefore, no effect size can be calculated for this category. You can review the df for other categories to judge the stability and generalizability of SMDs. When testing moderators, it is common to realize that certain categories are either too broad or too narrow. If the category is too broad, that group will have a significant Q -statistic. If it is too narrow, there will be insufficient df to analyze this group.

As with the study-level analyses, compare the 95% CIs, and utilize the Cumming & Finch procedures if necessary. To analyze other outcome level variables, repeat the aggregation and merging procedure for each variable, and then run the meta-ANOVA script. Remember, for each analysis you conduct, each study should have one vote (or case) per condition (or category).

Q -statistic. When conducting moderator analyses, the homogeneity analysis Cochrane's Q -statistic is a useful tool for judging whether the moderator variable sufficiently explains variability in SMDs. For example, in the mean SMD analysis, displayed in Phase3_meanSMD.spv, the mean effects for all studies are summarized with no moderators taken into account. The Q -statistic is significant at both post-test and follow up, suggesting that the studies in this meta-analysis have significant variability. The right moderators are likely to explain more of this variance, thereby differentiating the qualities of studies that have higher SMDs.

Within the past decade, another method of estimating homogeneity has become more popular. Cochrane's Q is distributed as the chi-square, with $k - 1$ degrees of freedom, where k = the number of studies in the meta-analysis. When the sample size is small, Cochrane's Q has too low power. When sample size is excessively large, Q has too much power. For the practice dataset, Cochrane's Q is appropriate. However, it is useful to get into the habit of calculating the I^2 statistic as well. $I^2 = 100\% (Q - df) / Q$ (Higgins et al., 2003). For the mean SMD calculated above, $I^2 = (324.06 - 67) / 324.06 \times 100\% = 79.34\%$. This is considered a large magnitude of variability (see Higgins et al., 2003, for how to interpret different values of I^2).

If Q -statistics are significant, then the results suggest that these moderators, even if they are significant, do not account for all the variance in the sample. It is possible to combine two or more variables by coding them into discrete categories, aggregating, and running another ANOVA. Another option is to run a meta-regression.

3c) Meta-regression. In some cases it is desirable to assess the impact of multiple variables on the standardized mean difference. In meta-regression, it is possible to run simultaneous entry regressions using the Lipsey & Wilson (2001) syntax on this disc.²

To learn more about the options available in meta-regression, open the file MetaReg.sps in the SPSS_Macros folder. The syntax in lines 10-16 describes different options for fixed effects models (FE), random effects via method of moments (MM), and maximum likelihood (ML). When using your own data, refer to other sources to decide which method best fits your data. In this practice dataset, MM will be used for random effects.

Regression is useful for distinguishing the relative contributions of methodological variables and theoretical variables. This practice meta-regression will assess two study-level variables, but it is possible to include outcome-level variables that have been appropriately aggregated.

To run meta-regression, first open the dataset Phase3a_Merged.sav and the syntax file Phase3_Master_Instructions_short.sps. In line 36, the dependent variable is the aggregated winsorized post SMD ($ES = wpostSMD_mean$), and the independent variables are structured, interactive intervention, and year of publication ($IVS = Structure\ Year$). The model selected is method of moments (MM), for random effects. Run lines 35–36 and examine the output. These results should match Phase3c_MetaRegression.spv.

The results can be interpreted in the same way as an ordinal multiple regression analysis. In this example, the independent variables account for 24.6% of the total variance. The significance of the model is determined by the $Q_R (Model)$, which is the homogeneity statistic of the regression model. In this practice regression, Q_R is significant. Additionally, $Q_E (Error)$ is not significant, indicating that other moderators are unlikely to improve the fit of the model. Lastly, the regression coefficients can be analyzed in the same way as an ordinal multiple regression. In this example, Structure is significant ($p < 0.001$), but Year is not. Therefore, the data indicate that a structured intervention is likely to produce higher SMDs, whereas the lack of significance for the Year moderator indicates that, when Structure is already accounted for, more recent studies do not necessarily produce better results than earlier studies.

² It is also possible to run stepwise, forward, and backward regressions in the SPSS interface using the inverse weight variables as the WLS weight, but this approach is less conventional. The benefits and drawbacks of using SPSS interface are beyond the scope of this guide.

Conclusion

The exercises in this practice dataset are an introduction to basic data preparation and meta-analysis. First, if you attempt to create your own meta-analysis from scratch, more reading is recommended. In particular, Lipsey and Wilson's (2001) book, *Practical Meta-Analysis*, is an essential explanation to using their macros. Second, many of the references listed in this chapter are wonderful resources for developing meta-analytic skills. Also, it is recommended to collaborate with a researcher who has successfully conducted meta-analyses. Through these steps and with the guidance of an experienced meta-analyst, you will be well equipped to conduct your own analyses.

REFERENCES

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