

STATA META-ANALYSIS COMMANDS

Meta-analysis commands: Stata commands for meta-analysis are not an integral part of the original Stata software—they are additional, user-written, add-on programs that can be freely downloaded and added to the Stata ado file list. Once the meta-analysis programs have been added to the pre-existing ado list, they function like any usual Stata command.

How to download and install user-written, meta-analysis commands:

1. Make sure your Stata package is up-to-date by typing, “update all” when your system is logged on to the internet. Stata will automatically connect to www.stata.com and download all updates that are required.
2. Search for all the meta-analysis user-written programs by typing “search meta.” Stata will again connect to www.stata.com and display all the programs that are available. The display will appear like this:

```
STB-61 sbe19.4 . . . . . Update to metabias to work under
version 7
(help metabias if installed) . . . . . T. J. Steichen
5/01 p.11; STB Reprints Vol 10, pp.71--72
updated for use with Stata 7

STB-61 sbe39.2 . . . . . Update of metatrim to work under
version 7
(help metatrim if installed) . . . . . T. J. Steichen
5/01 p.11; STB Reprints Vol 10, p.118
updated for use with Stata 7
and so on...
```

3. Click on each sbe number—it will be highlighted in a different color (e.g. [sbe19.4](#)). Another window will open with a display that will look like this:

```
TITLE
STB-61 sbe19_4. Update to metabias to work under version 7

DESCRIPTION/AUTHOR(S)
STB insert by Thomas J. Steichen, RJRT
Support: steicht@rjrt.com
After installation, see help metabias

INSTALLATION FILES \(click here to install\)
sbe19_4/metabias.ado
sbe19_4/metabias.hlp
```

Click “click here to install.” Stata will download and store it in its list of ado files.

4. To check if a specific command is available after installation, type “help command_name” (e.g. help metabias). If the help screen for that command pops up, it indicates successful installation of that specific program.
5. As of July 2003, we are aware of 14 Stata commands (see the following pages). Make sure you have installed all on your system.

Stata commands available (as of July 2003): meta, metan, metap, metareg, metacum, funnel, funnel2, labbe, metannt, metainf, metaninf, galbr, metabias, and metatrim.

General note: All Stata commands must be typed in lower case letters. The variables should be typed in whichever case was originally used [as it is in the dataset]. Stata allows you to shorten several commands and almost all variables.

General Stata syntax: command variable_names, options

Commonly used syntax for meta commands: command logor selogor, options.

Most meta-analysis commands require the user to provide the measure of effect (odds ratio, risk ratio, etc.) and its standard error or variance. So, before the command can be used, the user will need to generate the measure of effect and the standard error. For example, if the effect measure of interest is the odds ratio, the following simple commands will generate the logor and the selogor:

Command for generating odds ratios:

gen or=((a*d)/(b*c)), where a, b, c, and d are the 4 cell values in a 2x2 table.

Commands for generating log odds ratios:

gen lnor=ln(or)

Command for generating standard errors of log or:

gen selnor=sqrt((1/a)+(1/b)+(1/c)+(1/d))

Similarly, the log of the effect measure and its standard error can be computed for other measures such as risk ratio, hazard ratio, risk difference, etc.

Options for each command: Each of the following meta-analysis commands come with several options. The options are usually specified after the command and a comma.

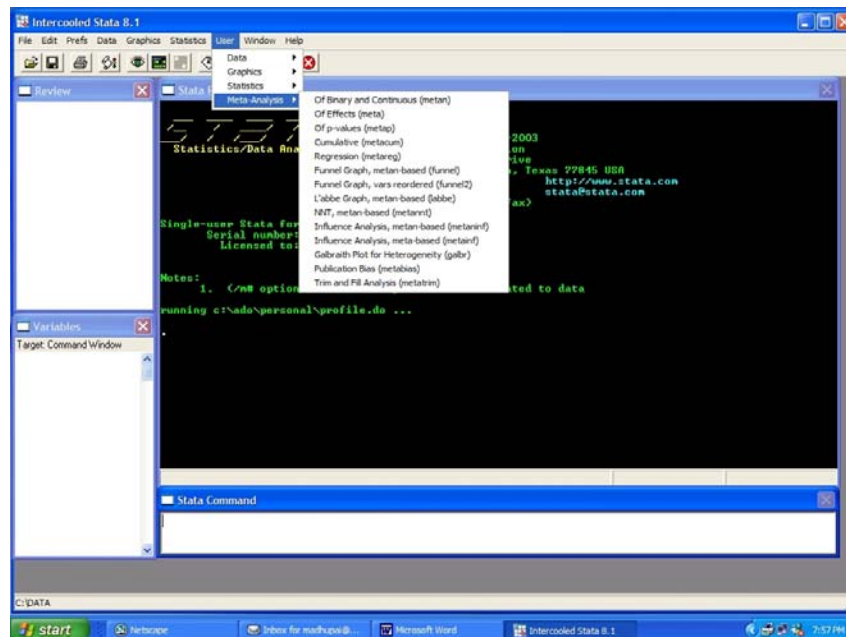
E.g. metan tdeath tnodeath cdeath cnodeath, **or random** – where **or** and **random** are options for specifying odds ratios and random effects model. If the same command were written as: metan tdeath tnodeath cdeath cnodeath, **rr fixed**, the program will return risk ratios rather than odds ratios, and the summary measure will be computed using the fixed effects model. Options also include graphics and labeling. To see all the options for each command, type “help command_name.”

Help for any Stata command: Simply type “help command_name” in the command box. E.g. typing “help metabias” will open a window that describes the metabias command, its options, etc.

Menu-driven (dialog box) options for meta-analysis in Stata 8:

This is a new feature, available only in Stata 8. To install the files necessary to use pull-down menus and dialog boxes, do the following:

1. First make sure all 14 Stata commands are already installed on your system.
2. Then pull down the help menu in Stata, select “search” and search for “meta_dialog” with the “search all” option checked. Install the meta_dialog module.
3. Once you install the meta_dialog module on your system, you will need to create a profile.do file and add it to your Stata do file list. The profile.do file will launch itself automatically each time you open Stata. The profile.do file should contain the program given below (look under “Menu Creation Commands”). Cut and paste the program into an empty do file and save the file in some path that Stata will recognize at the time of initialization: C:\data\stata\profile.do OR C:\ado\personal\profile.do.
4. Once the profile.do file is saved in the right path, open Stata. You should see a line like this coming up on your opening screen: running c:\ado\personal\profile.do ... this indicates that the profile.do commands are being run automatically.
5. Now look in the top menu bar and pull down the menu called “USER”. You should see a new pull-down menu called “Meta-analysis” (see picture below). When you open the Meta-analysis menu, you should see all 14 commands. Click on any command and it will open the dialog box.



Description of meta_dialog

Package meta_dialog provides Stata Version 8 dialog boxes (.dlg files) and the commands needed to create a Meta-Analysis sub-menu that contains the publicly available meta-analysis commands. The 14 commands included in this package that may be placed on the menu are: meta, metan, metap, metareg, metacum, funnel, funnel2, labbe, metant, metainf, metainf, galbr, metabias, and metatrim.

The menu commands (shown below) are placed in your personal Stata profile.do file. They create the sub-menu on the StataCorp-defined User menu.

You can determine if you have defined a profile.do file by starting Stata and observing whether a line of the form:

```
running C:\data\stata\profile.do ...
```

Version 6, March 2004

Madhukar Pai, Michael McCulloch, Jack Colford
Systematic Reviews Group, UC Berkeley: www.medepi.org/meta
madhupai@uclink.berkeley.edu

appears on the screen as part of the initiation sequence. If it does, then add the commands below to that file and resave the file. If the line does not appear then you have not defined a profile. Create a plain text file containing the commands below, name it profile.do and save it somewhere in the Stata path.

You may choose not to create the menu and run the dialogs directly from the Stata8 command line via the db name command. If so,

```

-----
command...  runs...      description...
-----
db meta     meta 2.02     Meta-analysis of Effects
db metan    metan 1.74     Meta-analysis of Binary and Continuous
db metap    metap 2.0.0    Meta-analysis of p-values
db metareg  metareg 1.06  Meta-analysis Regression
db metacum  metacum 1.02  Cumulative Meta-analysis
db funnel   funnel 1.04    Metan-based Funnel Graph (original)
db funnel2  funnel2 1.051  Funnel Graph (funnel, vars reordered)
db labbe    labbe 1.21     Metan-based L'abbe Graph
db metannt  metannt 1.0    Metan-based NNT
db metaninf metaninf 1.0.1  Metan-based Influence Analysis
db metainf  metainf 3.0.0  Meta-based Influence Analysis
db galbr    galbr 2.0      Galbraith Plot for Heterogeneity
db metabias metabias 1.2.2  Publication Bias in Meta-analysis
db metatrim metatrim 1.0.5  Trim and Fill Analysis
-----

```

Menu Creation Commands

Put the following commands in your profile.do:

```

-----
if _caller() >= 8 {
  window menu clear
  window menu append submenu "stUser" "&Meta-Analysis"
  window menu append item "Meta-Analysis" "Of Binary and Continuous (meta&n)" "db metan"
  window menu append item "Meta-Analysis" "Of Effects (&meta)" "db meta"
  window menu append item "Meta-Analysis" "Of p-values (meta&p)" "db metap"
  window menu append item "Meta-Analysis" "Cumulative (meta&cum)" "db metacum"
  window menu append item "Meta-Analysis" "Regression (meta&reg)" "db metareg"
  window menu append item "Meta-Analysis" "Funnel Graph, metan-based (f&funnel)" "db
funnel"
  window menu append item "Meta-Analysis" "Funnel Graph, vars reordered (funnel&2)" "db
funnel2"
  window menu append item "Meta-Analysis" "L'abbe Graph, metan-based (&labbe)" "db labbe"
  window menu append item "Meta-Analysis" "NNT, metan-based (metann&t)" "db metannt"
  window menu append item "Meta-Analysis" "Influence Analysis, metan-based (metan&inf)"
"db metaninf"
  window menu append item "Meta-Analysis" "Influence Analysis, meta-based (metainf)" "db
metainf"
  window menu append item "Meta-Analysis" "Galbraith Plot for Heterogeneity (&galbr)" "db
galbr"
  window menu append item "Meta-Analysis" "Publication Bias (meta&bias)" "db metabias"
  window menu append item "Meta-Analysis" "Trim and Fill Analysis (metatrim)" "db
met&atrim"
  window menu refresh
}
-----

```

Notes

Dialogs are available in Stata8 only, thus the leading if _caller() >= 8 { and trailing } lines above are needed only if you also run Stata7, but leaving them in will not cause problems. The easiest way to capture these commands is to open this help file in your text editor, copy the lines, then paste them into profile.do.

Author: Thomas J. Steichen, RJRT, steicht@rjrt.com

COMMAND	DESCRIPTION (from Stata help files)	EXAMPLES
meta	<p>meta provides pooled estimates, confidence limits, and a test that the true pooled effect is zero, obtained from fixed and random effects meta-analysis, a test for heterogeneity between studies and an estimator of between studies variance, and, optionally, plots the individual and pooled estimates.</p> <p>The user provides the effect estimate as theta (i.e., a log risk ratio, log odds ratio, or other measure of effect). Likewise, the user supplies a measure of theta's variability (i.e., its standard error, se_theta, or its variance, var_theta).</p> <p>Alternatively, the user provides exp(theta) (i.e., a risk ratio or odds ratio) and its confidence interval, (ll, ul)).</p> <p>meta is most useful when data are extracted from published reports as effect measures and confidence intervals. If the raw data for the effect measure are available (i.e. all cell values in a 2x2 table), then metan is preferable to meta (see below).</p> <p>Note:</p> <p>If some of the trials in the analysis have zero cells in the 2x2 table, it is important to first add 0.5 to each of the 4 cells before proceeding with the analysis using meta command. If some trials have no events at all, such trials have to be dropped from the analysis.</p>	<pre>meta logor selogor, eform gr(f) cline xline(1) id(trialnam) xlab meta meandiff vardiff, var gr(r) eb print meta rr ll ul, ci gr(e)</pre>

COMMAND	DESCRIPTION (from Stata help files)	EXAMPLES
metan	<p>metan provides methods for the meta-analysis of either binary (event) or continuous data with two groups. There are several methods (random and fixed effects) available for pooling the study results, and performing formal tests on the data. Additionally, the results may be displayed graphically by a forest plot.</p> <p>The user provides the raw data (the 4 cell values of a 2x2 table) in a specific order [see 2x2 table format below] after the metan command.</p> <p>Note: the metan command automatically corrects for the zero cell problem by adding 0.5 to each cell—there is no need to do this manually! However, if the data were already corrected for zero cells, metan will not work! Metan will not accept fractions.</p> <p><u>Updates to the metan command:</u></p> <p>An updated version of the metan program is now available [download: http://www.ihs.ox.ac.uk/csm/staff/mikestats.html]. The updated command can pool data if presented as effect sizes (e.g. OR) along with standard errors or confidence intervals; the raw 2x2 table frequencies are not mandatory.</p> <p>The updated metan command can also perform subgroup analyses using the “by” option. For further information, see: http://www.ihs.ox.ac.uk/csm/staff/mikestats.html</p>	<p>Binary data:</p> <pre>metan tdeath tnodeath cdeath cnodeath, or random label(namevar=trialid)</pre> <pre>metan tdeath tnodeath cdeath cnodeath, rd fixed</pre> <p>Continuous data:</p> <pre>metan n1 m1 sd1 n2 m2 sd2, random xlab(-2,-1,0,1,2)</pre> <p>Syntax for pooling effect measures (only in the updated metan command):</p> <pre>metan logrr selogrr, options</pre> <pre>metan effect_size lowerlimit upperlimit, options</pre>

Stata 2x2 table format for the “metan” command:

	Disease	No Disease
Exposed	a	b
Not exposed	c	d

Syntax for metan command for **binary** data: metan a b c d, options

Syntax for **continuous** data: metan n1 m1 sd1 n2 m2 sd2, options

COMMAND	DESCRIPTION (from Stata help files)	EXAMPLES
metacum	<p>metacum provides cumulative pooled estimates, confidence limits, and a test that the true pooled effect is zero, obtained from fixed or random effects meta-analysis and, optionally, plots the cumulative pooled estimates in the style of Lau et al. (1992).</p> <p>The user provides the effect estimate as theta (i.e., a log risk ratio, log odds ratio, or other measure of effect). Likewise, the user supplies a measure of theta's variability (i.e., its standard error, se_theta, or its variance, var_theta). Alternatively, the user provides exp(theta) (e.g. a risk ratio or odds ratio) and its confidence interval, (ll, ul).</p>	<pre>metacum logor selogor, effect(f) eform graph cline xline(1) id(trialnam) xlab metacum meandiff vardiff, effect(r) var graph metacum rr ll ul, ci effect(r) eform</pre>
metareg	<p>metareg extends a random effects meta-analysis to estimate the extent to which one or more covariates, with values defined for each study in the analysis, explain heterogeneity in the treatment effects. Examples of such study-level covariates might be average duration of follow-up, some measure of study quality, or a measure of geographical location of each study.</p> <p>metareg fits models with two additive components of variance, one representing the variance within units, the other the variance between units, and therefore is applicable both to the meta-analysis situation, where each unit is one study, and to other situations such as multi-center trials, where each unit is one center.</p>	<pre>metareg logor covariate1 covariate2, wsse(selogor) metareg logor dur, wsvar(vlor) bs(eb) noit metareg meandiff qual avchol, wsse(sediff) bs(ml) tol(5) l(90)</pre>
metap	metap provides combination of p-values from each study. The user provides the one-tail p-values as pvar.	<pre>metap pvar metap pvar, method(ea) metap pvar, method(en)</pre>
metainf	metainf investigate the influence of a single study on the overall meta-analysis estimate. This command shows graphically the results of an influence analysis, in which the meta-analysis estimates are computed omitting one study in each turn.	<pre>metainf logor selogor, eform id(trialname) metainf logrr logse, random print id(studyid) metainf logrr logse, random eform id(studyid) format(%4.2f)</pre>
galbr	galbr provides a graphical display to get a visual impression of the amount of heterogeneity from a meta-analysis. For each trial, the z statistic theta/setheta is plotted against the reciprocal standard error 1/setheta. The (unweighted) regression line constrained through the origin, with its 95% confidence interval, has a slope equal to the overall log rate ratio, or log odds ratio, or log hazard ratio in a fixed effects meta-analysis. The position of each trial on the horizontal axis gives an indication of the weight allocated to it in a meta-analysis. The position on the vertical axis gives the contribution of each trial to the Q statistic for heterogeneity. In the absence of heterogeneity we could expect all the points to lie within the confidence bounds (positioned 2 units over and below the regression line). The user provides theta (effect estimated from the individual study), and setheta (its standard error). For example theta might be a log odds ratio, or a log hazard ratio.	<pre>galbr logrr selogrr, id(study) yline(0)</pre>

COMMAND	DESCRIPTION (from Stata help files)	EXAMPLES
metabias	<p>metabias performs the Begg and Mazumdar adjusted rank correlation test for publication bias and performs the Egger, et al., regression asymmetry test for publication bias. As options, it provides a funnel graph or the regression asymmetry plot. The user provides the effect estimate, theta, to metabias as a log risk ratio, log odds ratio, or other direct measure of effect. Along with theta, the user supplies a measure of theta's variability (i.e., its standard error, se_theta, or its variance, var_theta).</p> <p>The Begg adjusted rank correlation test is a direct statistical analogue of the visual funnel graph. Note that both the test and the funnel graph have low power for detecting publication bias. The Begg and Mazumdar procedure tests for publication bias by determining if there is a significant correlation between the effect estimates and their variances. metabias carries out this test by, first, standardizing the effect estimates to stabilize the variances and, second, performing an adjusted rank correlation test based on Kendall's tau.</p> <p>The Egger, et al., regression asymmetry test and the regression asymmetry plot tend to suggest the presence of publication bias more frequently than the Begg approach. The Egger test detects funnel plot asymmetry by determining whether the intercept deviates significantly from zero in a regression of the standardized effect estimates against their precision.</p>	<pre>metabias logor selogor, graph(begg) metabias logrr varlogrr if site==3, var graph(egger) metabias rr ll ul, ci by(site) metabias logor selogor if region==4, graph(egger) level(90)</pre>
metatrim	<p>metatrim performs the Duval and Tweedie nonparametric "trim and fill" method of accounting for publication bias in meta-analysis. The method, a rank-based data augmentation technique, formalizes the use of funnel plots, estimates the number and outcomes of missing studies, and adjusts the meta-analysis to incorporate the theoretical missing studies. The authors claim that the method is effective and consistent with other adjustment techniques.</p> <p>The user provides the effect estimate, theta, to metatrim as a log risk ratio, log odds ratio, or other direct measure of effect. Along with theta, the user supplies a measure of theta's variability (i.e., its standard error, se_theta, or its variance, var_theta). Alternatively, the user may provide the exponentiated form, exp(theta), (i.e., a risk ratio or odds ratio) and its confidence interval, (ll, ul).</p>	<pre>metatrim logrr selogrr, funnel print metatrim logrr varlogrr if site==3, var graph metatrim rr ll ul, ci eform reffect metatrim logor selogor if region==4, funnel level(90)</pre>

COMMAND	DESCRIPTION (from Stata help files)	EXAMPLES
metaninf	<p>metaninf investigates the influence of each individual study on the overall meta-analysis summary estimate. The command presents a table and a graph of the results of an influence analysis in which the meta-analysis is reestimated omitting each study in turn.</p> <p>The table numerically provides the results, with the rows of the table being the meta-analysis of all studies except the "omitted" study named in that row, and the usual, full meta-analysis (omitting none of the studies) being given as the "combined" results at the bottom of the table.</p> <p>The graph visually provides the same results in a plot, naming the omitted study on the left margin and presenting the resulting "omitted" meta-analytic summary statistics as a horizontal confidence interval. The full, "combined" results are shown as the solid vertical lines.</p> <p>No formal test of influence is given; rather, the program provides and displays results to which some general guidelines can be applied to assess influence. One such guideline is that an individual study is suspected of excessive influence if the point estimate of its "omitted" analysis lies outside the confidence interval of the "combined" analysis. Another guideline is that a study is excessively influential if its "omitted" meta-analytic estimate differs in significance relative to the "combined" analysis. Neither of these guidelines provides definitive proof that such a study should, or should not, be removed from the analysis; they merely provide a suggestion that some attention be paid to potential reasons for its influence.</p> <p>metaninf uses program metan as its meta-analysis engine and its options are a direct subset of metan's. It is expected that users will merely edit a metan command line by adding the "inf" suffix to the program name to run metaninf.</p> <p>Like metan, metaninf requires either four or six variables to be declared. When four variables are specified, analysis of binary data is performed. When six variables are specified, the data are assumed continuous.</p> <p>Binary data is presented as the 4 cell counts (a b c d) of a 2x2 table where a and b are the number of event & no-event subjects in the intervention group and c and d are similar numbers for the control group.</p> <pre>. metaninf a b c d</pre> <p>Continuous data is presented as 6 values: the n, mean and sd for the treatment (or intervention) group followed by similar values for the control group.</p> <pre>. metaninf nt mt sdt nc mc sdc</pre>	<pre>metaninf a b c d, fixedi or label(namevar=studyid, yearvar=year) metaninf nt mt sdt nc mc sdc, cohen notable</pre>

COMMAND	DESCRIPTION (from Stata help files)	EXAMPLES
funnel	funnel may be used for producing a graph of either the study sample size, standard error or precision (inverse of s.e.) against the effect size.	funnel , sample vsqrt xlabel(0.1,0.5,1,5,10) ylabel(0,500,1000)
funnel2	If the funnel2 command is invoked following metan with no parameters specified it will produce a standard funnel plot of precision (1/SE) against treatment effect. Addition of the noinvert option will produce a plot of standard error against treatment effect. The alternative sample size version of the funnel plot can be obtained by using the sample option (this automatically selects the noinvert option). Alternative plots can be created by specifying precision_var and effect_size. If the effect size is a relative risk or odds ratio, the xlog option should be used to create a symmetrical plot.	funnel2 , sample vsqrt xlab(0.1,0.5,1,5,10) ylab(0,500,1000) funnel2 or selogor, xlab(0.1,0.5,1,5,10) ylab(0,0.05,0.1) xlog
labbe	labbe draws a L'Abbe plot for event data (proportion of successes in the two groups). This is an alternative to the graph produced by metan	labbe tdeath tnodeath cdeath cnodeath, xlabel(0,0.25,0.5,0.75,1) ylabel(0,0.25,0.5,0.75,1)
metannt	<p>This program is intended to aid interpretation of meta-analyses of binary data by presenting the effect sizes in absolute terms. Both the number needed to treat (NNT) and the number of events avoided (or added) per 1000 are presented.</p> <p>The Number Needed to Treat (NNT) is the number of individuals required to experience the intervention in order to expect there to be one additional event to be observed. Assuming the event is undesirable, this is termed the "number needed to treat to benefit" (NNTB). If the intervention arm experiences more events, this is commonly referred to as the "number needed to treat to harm" (NNTH).</p> <p>metannt calculates this by deriving an effect size (e.g. a risk ratio), applying it to a population with a given event prevalence, and from this deriving a projected event rate if the population were to receive the intervention. The NNT is equal to 1/(control group event rate - treatment group event rate).</p> <p>The number of avoided or excess events (respectively) per 1000 population is the difference between the two event rates multiplied by 1000. The intervention group event rate is calculated in the same manner as with the NNT. Optionally a confidence interval is also presented, using the confidence limits of the effect size applied to the control group event rate.</p>	metannt , measure(rr) size(0.2) baseline(0.1,0.2,0.3) metan tdeath tnodeath cdeath cnodeath, or metannt , baseline(0.15)

Further reading:

1. Sterne et al. Meta-analysis in Stata. In: Egger M, Smith GD, Altman DG (editors). Systematic reviews in health care. Meta-analysis in context. London: BMJ Publishing Group, 2001: pp 347-369. This excellent book chapter is available free on the book website, along with three sample Stata datasets: <http://www.systematicreviews.com/>. Enter the website and click on "Sample Chapters and Datasets."
2. Bradburn M. Updated and new commands for meta-analysis in Stata. URL: <http://www.ihs.ox.ac.uk/csm/staff/mikestats.html>

STATA COMMANDS FOR META-ANALYSIS OF INTERVENTION TRIALS WITH BINARY OUTCOME

Michael McCulloch, UC Berkeley, 2003
mcculloch@uclink4.berkeley.edu

*This meta do file calculates the Odds Ratio and a 95% Confidence Interval by the random effects model, for categorical variables from controlled trial, then displays summary effects and confidence intervals in a table and forest plot then saves the calculated data as
c:\windows\desktop\mymeta.dta

*Instructions:

- * Open a clean instance of STATA, with no data
- * Open the Data Editor, and confirm no data in cells
- * Paste five values in from Excel, in the following order from left to right,
* and using the variable names exactly as typed here:
* StudyID, RxFail, RxTotal, CtrFail, and CtrCure
- * Stata will by default name them: RxFail=var1, RxTotal=var2, CtrFail=var3,
* CtrCure=var4

*change directory to desktop
cd c:\windows\desktop

*rename the variables
rename var1 StudyID
rename var2 RxFail
rename var3 RxTotal
rename var4 CtrFail
rename var5 CtrTotal

*label the variables
label variable RxFail "Cell a in 2x2"
label variable RxTotal "Row total N1 in 2x2"
label variable CtrFail "Cell c in 2x2"
label variable CtrTotal "Row total N2 in 2x2"

*calculate cells "b" and "d"
gen RxCure= RxTotal- RxFail
gen CtrCure= CtrTotal- CtrFail
label variable RxCure "Cell b in 2x2"
label variable CtrCure "Cell d in 2x2"

*add 0.5 to the 2x2 table where necessary
gen Rxzero=0
replace Rxzero=1 if RxFail==0|CtrFail==0|RxCure==RxTotal|CtrCure==CtrTotal
replace RxFail=RxFail+0.5 if Rxzero==1
replace CtrFail=CtrFail+0.5 if Rxzero==1
replace RxCure=RxCure+0.5 if Rxzero==1
replace CtrCure=CtrCure+0.5 if Rxzero==1

```

*calculate OR, logOR, seLogOR, & 95% CI
gen or=((RxFail*CtrCure)/( RxCure*CtrFail))
gen logor=log(( RxFail*CtrCure)/( RxCure*CtrFail))
gen seLogOR = sqrt((1/ RxFail)+(1/ RxCure)+(1/ CtrFail)+(1/ CtrCure))
gen CiLow= exp(logor-1.96*seLogOR)
gen CiUpp= exp(logor+1.96*seLogOR)
label variable or "Odds Ratio"
label variable logor "Log of Odds Ratio"
label variable seLogOR "Standard Error, Log OR"
label variable CiLow "Lower Bound, 95% CI"
label variable CiUpp "Upper Bound, 95% CI"

*perform the meta-analysis
sort StudyID
meta logor seLogOR, eform print graph(r) xline(1) xlab(.01,.1,1,10,100) id(StudyID)
b2title(Odds ratio) boxysca(1)

*save and close the file
save "mymeta.dta", replace

```

STATA 7 COMMANDS FOR META-ANALYSIS OF DIAGNOSTIC STUDIES
Madhukar Pai, UC Berkeley, 2003
madhupai@uclink.berkeley.edu

Note: some commands may not work well with Stata 8

*Variable codes: tp=true positives; fp=false positives; tn=true negatives; fn=false negatives

*FOR REPLACING ZERO CELLS IN THE 2X2 TABLE:

```
*add .5 to all zero cells
gen zero=0
replace zero=1 if tp==0|fp==0|fn==0|tn==0
replace tp=tp+.5 if zero==1
replace fp=fp+.5 if zero==1
replace fn=fn+.5 if zero==1
replace tn=tn+.5 if zero==1
```

*FOR GENERATING TRUE POSITIVE RATE (SENSITIVITY)

```
gen tpr= tp/(tp+fn)
```

*FOR GENERATING FALSE POSITIVE RATE (1-SPECIFICITY)

```
gen fpr=fp/(fp+tn)
```

*GENERATE LOGIT OF TPR

```
gen logittpr=ln(tp/fn)
```

*GENERATE LOGIT OF FPR

```
gen logitfpr=ln(fp/tn)
```

*FOR PLOTTING TPR AND FPR IN A ROC SPACE

```
gr7 tpr fpr, s(O) noaxis ysize(6) xsize(6) xline(0(.1)1) yline(0(.1)1) tlab(0(.1)1) xlab(0(.1)1)
ylab(0(.1)1) t1(1-Specificity) l1(Sensitivity) b2(1-Specificity) b1(ROC Plot of Sensitivity vs
Specificity)
```

*LOOK FOR A CORRELATION BETWEEN TPR AND FPR

```
gr7 logittpr logitfpr
spearman logittpr logitfpr
```

*FOR META-ANALYSIS OF DIAGNOSTIC ODDS RATIOS

```
metan tp fn fp tn, or random nowt sortby(author) xlab(.01,1,100) label(namevar=author,
yearvar=pubyear) t1(Summary Diagnostic Odds Ratio, Random Effects)
```

*FOR META-ANALYSIS OF LIKELIHOOD RATIO POSITIVE

metan tp fn fp tn, rr random nowt sortby(author) xlab(.01,1,100) label(namevar=author, yearvar=pubyear) t1(Summary LR+, Random Effects)

*FOR META-ANALYSIS OF LIKELIHOOD RATIO NEGATIVE

metan fn tp tn fp, rr random nowt sortby(author) xlab(.01,1,100) label(namevar=author, yearvar=pubyear) t1(Summary LR-, Random Effects)

*FOR META-ANALYSIS BY SUBGROUPS (STRATIFYING VARIABLE=COVARIATE)

*FOR DOR

metan tp fn fp tn if covariate==1, or random nowt sortby(author) xlab(.01,1,100) label(namevar=author, yearvar=pubyear) t1(Summary Diagnostic Odds Ratio, Random Effects)

metan tp fn fp tn if covariate==0, or random nowt sortby(author) xlab(.01,1,100) label(namevar=author, yearvar=pubyear) t1(Summary Diagnostic Odds Ratio, Random Effects)

*FOR LR+

metan tp fn fp tn if covariate==1, rr random nowt sortby(author) xlab(.01,1,100) label(namevar=author, yearvar=pubyear) t1(Summary LR+, Random Effects)

metan tp fn fp tn if covariate==0, rr random nowt sortby(author) xlab(.01,1,100) label(namevar=author, yearvar=pubyear) t1(Summary LR+, Random Effects)

*FOR LR-

metan fn tp tn fp if covariate==1, rr random nowt sortby(author) xlab(.01,1,100) label(namevar=author, yearvar=pubyear) t1(Summary LR-, Random Effects)

metan fn tp tn fp if covariate==0, rr random nowt sortby(author) xlab(.01,1,100) label(namevar=author, yearvar=pubyear) t1(Summary LR-, Random Effects)

TESTS FOR PUBLICATION BIAS:

*generating odds ratios:

gen or=(tp*tn)/(fp*fn)

*generating log odds ratios:

gen lnor=ln(or)

*generating standard errors of log or:

gen selnor=(1/tp)+(1/fp)+(1/fn)+(1/tn)

*Begg and Egger test for publication bias with Begg's funnel plot:

metabias lnor selnor, graph(begg)

*Begg and Egger tests for subgroups (eg. Covariate=1)

metabias lnor selnor if covariate==1, graph(begg)

GENERATING SROC CURVES:

*generate sum (logit of tpr + logit of fpr)
gen sum= logittpr+ logitfpr

*generate difference (logit of tpr - logit of fpr)
gen diff= logittpr- logitfpr

*regress difference against sum and draw a fitted regression line (generic)
regress diff sum
predict yhat
gr7 diff yhat sum, ylab(3,4,5,6,7,8) xlab(-4,-3,-2,-1,0,1,2) c(.1) s(oi)

*compute transformed sensitivity for SROC curve (generic)
gen tse=1/(1+(1/(exp(_cons/1-_b)*(fpr/spec)^1+_b/1-_b)))

(constant and b are derived from the above regression model)

*plot SROC curve (generic)
gr7 se tse fpr, ysize(6) xsize(6) noaxis xline(0(.1)1) yline(0(.1)1) tlab(0(.1)1) xlab(0(.1)1)
ylab(0(.1)1) s(Oi) c(.s) l1(Sensitivity) b2(1-Specificity) ti(Summary ROC Curve) key1(" ")
key2(" ")

META-REGRESSION TO EXPLORE HETEROGENEITY:

regress diff sum covariate1 covariate2 covariate3...

*coefficients from the model can be exponentiated and interpreted as relative diagnostic odds ratios (RDOR).