meta forestplot — Forest plots+

+This command includes features that are part of StataNow.

Description

meta forestplot summarizes meta data in a graphical format. It reports individual effect sizes and the overall effect size (ES), their confidence intervals (CIs), heterogeneity statistics, and more. meta forestplot can perform random-effects (RE), common-effect (CE), and fixed-effects (FE) meta-analyses. It can also perform subgroup, cumulative, and sensitivity meta-analyses. For tabular display of meta-analysis summaries, see [META] **meta summarize**.

Quick start

Default forest plot after data are declared by using either meta set or meta esize

```
    meta forestplot
```

Same as above, but apply the hyperbolic tangent transformation to effect sizes and their CIs

```
    meta forestplot, transform(tanh)
```

Add vertical lines at the overall effect-size and no-effect values

```
    meta forestplot, esrefline nullrefline
```

Customize the overall effect-size line, and annotate the sides of the plot, with respect to the no-effect line, favoring the treatment or control

```
    meta forestplot, esrefline(lcolor(green))      ///
         nullrefline(favorsleft("Favors vaccine")  ///
         favorsright("Favors control"))
```

Add a custom diamond with a label for the overall effect-size ML estimate by specifying its value and CI limits

```
    meta forestplot, customoverall(-.71 -1.05 -.37, label("{bf:ML Overall}"))
```

Forest plot based on subgroup meta-analysis

```
    meta forestplot, subgroup(groupvar)
```

Forest plot based on cumulative meta-analysis

```
    meta forestplot, cumulative(ordervar)
```

Forest plot based on leave-one-out meta-analysis

```
    meta forestplot, leaveoneout
```

Default forest plot after data are declared with meta set but with the columns spelled out

```
    meta forestplot _id _plot _esci _weight
```

Default forest plot after data are declared with meta esize but with the columns spelled out

```
    meta forestplot _id _data _plot _esci _weight
```

Same as above, but with the weights omitted

```
meta forestplot _id _data _plot _esci
```

Same as above, but the columns are rearranged

```
meta forestplot _id _data _esci _plot
```

Same as above, but plot variables x1 and x2 as the second and last columns

```
meta forestplot _id x1 _data _esci _plot x2
```

Change the format of the _esci column

```
meta forestplot, columnopts(_esci, format(%7.4f))
```

Menu

Statistics > Meta-analysis

Syntax

meta forestplot [*column_list*] [*if*] [*in*] [, *options*]

column_list is a list of column names given by *col*. In the *Meta-Analysis Control Panel*, the columns can be specified on the **Forest plot** tab of the Forest plot pane.

options	Description
Main	
random[(*remethod*)]	random-effects meta-analysis
common[(*cefemethod*)]	common-effect meta-analysis
fixed[(*cefemethod*)]	fixed-effects meta-analysis
reopts	random-effects model options
subgroup(*varlist*)	subgroup meta-analysis for each variable in *varlist*
cumulative(*cumulspec*)	cumulative meta-analysis
leaveoneout	leave-one-out meta-analysis
Options	
level(#)	set confidence level; default is as declared for meta-analysis
citype(*citype*)	specify the type of study CI (for meta-analysis of a single proportion)
proportion	report proportions (for meta-analysis of a single proportion)
prevalence	synonym for proportion but labels the effect sizes as Prevalence in the output
+correlation	report correlations (for meta-analysis of correlations)
eform_option	report exponentiated results
transform(*transfspec*)	report transformed results
sort(*varlist*[, ...])	sort studies according to *varlist*
tdistribution	report t test instead of z test
[no]metashow	display or suppress meta settings in the output
Maximization	
maximize_options	control the maximization process; seldom used
Forest plot	
columnopts(*col*, [*colopts*])	column options; can be repeated
cibind(*bind*)	change binding of CIs for columns _esci and _ci; default is cibind(brackets)
sebind(*bind*)	change binding of standard errors for column _esse; default is sebind(parentheses)
nohrule	suppress horizontal rule
hruleopts(*hrule_options*)	change look of horizontal rule
text_options	change looks of text options such as column titles, supertitles, and more
plot_options	change look or suppress markers, restrict range of CIs, and more
test_options	suppress information about heterogeneity statistics and tests
graph_options	change the lines, labels, ticks, titles, scheme, etc. on the forest plot
nooverall	suppress row corresponding to the overall effect size
olabel(*string*)	modify default overall effect-size label under the _id column; default label is Overall

+These features are part of StataNow.

nooverall and olabel() do not appear in the dialog box.

col	Description
Default columns and order	
_id	study label
_data	summary data; _data1 and _data2 for two-group comparisons of continuous and binary outcomes (only after meta esize)
_plot	forest graph
_esci	effect size and its confidence interval
_weight	percentage of total weight given to each study
Summary-data columns and order	
Two-sample continuous data	
Treatment group	
_data1	summary data for treatment group; _n1, _mean1, and _sd1
_n1	sample size in the treatment group
_mean1	mean in the treatment group
_sd1	standard deviation in the treatment group
Control group	
_data2	summary data for control group; _n2, _mean2, and _sd2
_n2	sample size in the control group
_mean2	mean in the control group
_sd2	standard deviation in the control group
Two-sample binary data	
Treatment group	
_data1	summary data for treatment group; _a and _b
_a	number of successes in the treatment group
_b	number of failures in the treatment group
Control group	
_data2	summary data for control group; _c and _d
_c	number of successes in the control group
_d	number of failures in the control group
One-sample binary data	
_data	summary data; _e and _n
_e	number of successes
_n	study sample size
Correlation data (StataNow)	
_data	summary data; _r and _n
_r	correlation
_n	study sample size

Other columns	
_es	effect size
_ci	confidence interval for effect size
_lb	lower confidence limit for effect size
_ub	upper confidence limit for effect size
_se	standard error of effect size
_esse	effect size and its standard error
_pvalue	*p*-value for significance test with subgroup(), cumulative(), or leaveoneout
_K	number of studies with subgroup()
_size	within-group sample size with subgroup()
_order	order variable for cumulative meta-analysis with cumulative()
varname	variable in the dataset (except meta system variables)

Columns _data, _data1, _data2, and the other corresponding data columns are not available after the declaration by using meta set.

Columns _n1, _mean1, _sd1, _n2, _mean2, and _sd2 are available only after the declaration by using meta esize for a two-group comparison of continuous outcomes.

Columns _a, _b, _c, and _d are available only after the declaration by using meta esize for a two-group comparison of binary outcomes.

Columns _e and _n are available only after the declaration by using meta esize for estimating a single proportion.

Columns _r and _n are available only after the declaration by using meta esize for correlation data.

Column _pvalue is available only when option subgroup() with multiple variables is specified or when cumulative() or leaveoneout is specified.

Columns _K and _size are available only when option subgroup() with multiple variables is specified.

Column *varname* is not available when option subgroup() with multiple variables is specified.

colopts	Description
supertitle(*string*)	super title specification
title(*string*)	title specification
format(*%fmt*)	numerical format for column items
mask(*mask*)	string mask for column items
plotregion(*region_options*)	attributes of plot region
textbox_options	appearance of textboxes

text_options	Description
coltitleopts(*textbox_options*)	change look of column titles and supertitles
itemopts(*textbox_options*)	change look of study rows
overallopts(*textbox_options*)	change look of the overall row
groupopts(*textbox_options*)	change look of subgroup rows
bodyopts(*textbox_options*)	change look of study, subgroup, and overall rows
nonotes	suppress notes about the meta-analysis model, method, and more

plot_options	Description
crop(# #)	restrict the range of CI lines
ciopts(*ci_options*)	change look of CI lines (size, color, etc.)
nowmarkers	suppress weighting of study markers
nomarkers	suppress study markers
markeropts(*marker_options*)	change look of study markers (size, color, etc.)
noomarker	suppress the overall marker
omarkeropts(*marker_options*)	change look of the overall marker (size, color, etc.)
nogmarkers	suppress subgroup markers
gmarkeropts(*marker_options*)	change look of subgroup markers (size, color, etc.)
insidemarker[(*marker_options*)]	add a marker at the center of the study marker
esrefline[(*line_options*)]	add a vertical line corresponding to the overall effect size
noesrefline	suppress vertical line corresponding to the overall effect size plotted on leave-one-out forest plot
nullrefline[(*nullopts*)]	add a vertical line corresponding to no effect
customoverall(*customspec*)	add a custom diamond representing an overall effect; can be repeated

test_options	Description
ohetstatstext(*string*)	modify default text for overall heterogeneity statistics
noohetstats	suppress overall heterogeneity statistics
ohomtesttext(*string*)	modify default text for overall homogeneity test
noohomtest	suppress overall homogeneity test
osigtesttext(*string*)	modify default text for test of significance of overall effect size
noosigtest	suppress test of significance of overall effect size
ghetstats#text(*string*)	modify default text for subgroup heterogeneity statistics in the #th subgroup
noghetstats	suppress subgroup heterogeneity statistics
gwhomtest#text(*string*)	modify default text for within-subgroup homogeneity test in the #th subgroup
nogwhomtests	suppress within-subgroup homogeneity tests
gsigtest#text(*string*)	modify default text for test of significance of the subgroup effect size in the #th subgroup
nogsigtests	suppress tests of significance of subgroup effect size
gbhomtest#text(*string*)	modify default text for between-subgroup homogeneity test in the #th subgroup
nogbhomtests	suppress between-subgroup homogeneity tests

graph_options	Description
`xline(`*linearg*`)`	add vertical lines at specified x values
`xtitle(`*axis_title*`)`	specify x-axis title
`xlabel(`*rule_or_values*`)`	major ticks plus labels
`xtick(`*rule_or_values*`)`	major ticks only
`xmlabel(`*rule_or_values*`)`	minor ticks plus labels
`xmtick(`*rule_or_values*`)`	minor ticks only
`title(`*tinfo*`)`	overall title
`subtitle(`*tinfo*`)`	subtitle of title
`note(`*tinfo*`)`	note about graph
`caption(`*tinfo*`)`	explanation of graph
`t1title(`*tinfo*`)` `t2title(`*tinfo*`)`	rarely used
`b1title(`*tinfo*`)` `b2title(`*tinfo*`)`	rarely used
`l1title(`*tinfo*`)` `l2title(`*tinfo*`)`	vertical text
`r1title(`*tinfo*`)` `r2title(`*tinfo*`)`	vertical text
`scheme(`*schemename*`)`	overall look
`nodraw`	suppress display of graph
`name(`*name*`, ...)`	specify name for graph
`saving(`*filename*`, ...)`	save graph in file

nullopts	Description
`favorsleft(`*string* [, *textbox_options*]`)`	add a label to the left of the no-effect reference line
`favorsright(`*string* [, *textbox_options*]`)`	add a label to the right of the no-effect reference line
line_options	affect the rendition of the no-effect reference line

Options

Main

`random`[`(`*remethod*`)`], `common`[`(`*cefemethod*`)`], `fixed`[`(`*cefemethod*`)`], `subgroup(`*varlist*`)`, `cumulative(`*cumulspec*`)`, and `leaveoneout`; see *Options* in [META] **meta summarize**.

reopts are `tau2(`*#*`)`, `i2(`*#*`)`, `predinterval`, `predinterval(`*#*[, *line_options*]`)`, and `se(`*seadj*`)`. These options are used with random-effects meta-analysis. See *Options* in [META] **meta summarize**.

`predinterval` and `predinterval(`*#*[, *line_options*]`)` draw whiskers extending from the overall effect marker and spanning the width of the prediction interval. *line_options* affect how the whiskers are rendered; see [G-3] ***line_options***.

Options

`level(`*#*`)`, `citype()`, `proportion`, `prevalence`, `correlation`, *eform_option*, `transform()`, `sort(`*varlist*[, ...]`)`, `tdistribution`, and [`no`]`metashow`; see *Options* in [META] **meta summarize**.

Maximization

maximize_options: `iterate(#)`, `tolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, `from(#)`, and `showtrace`; see *Options* in [META] **meta summarize**.

Forest plot

`columnopts(`*col* [, *colopts*]`)` changes the look of the column identified by *col*. This option can be repeated.

colopts are the following options:

`supertitle(`*string*`)` specifies that the column's supertitle is *string*.

`title(`*string*`)` specifies that the column's title is *string*.

`format(`*%fmt*`)` specifies the format for the column's numerical values.

`mask(`*mask*`)` specifies a string composed of formats for the column's statistics. For example, *mask* for column `_weight` that identifies the column of weight percentages may be specified as `"%6.2f %%"`.

`plotregion(`*region_options*`)` modifies attributes for the plot region. You can change the margins, background color, an outline, and so on; see [G-3] ***region_options***.

textbox_options affect how the column's items (study and group) are rendered. These options override what is specified in global options `bodyopts()`, `itemopts()`, and `groupopts()`. See [G-3] ***textbox_options***.

Options `format()`, `mask()`, and *textbox_options* are ignored by `_plot`.

`cibind(`*bind*`)` changes the binding of the CIs for columns `_esci` and `_ci`. *bind* is one of `brackets`, `parentheses`, or `none`. By default, the CIs are bound by using brackets, `cibind(brackets)`. This option is relevant only when `_esci` or `_ci` appears in the plot.

`sebind(`*bind*`)` changes the binding of the standard errors for column `_esse`. *bind* is one of `parentheses`, `brackets`, or `none`. By default, the standard errors are bound by using parentheses, `cibind(parentheses)`. This option is relevant only when `_esse` appears in the plot.

`nohrule` suppresses the horizontal rule.

`hruleopts(`*hrule_options*`)` affects the look of the horizontal rule.

hrule_options are the following options:

`lcolor(`*colorstyle*`)` specifies the color of the rule; see [G-4] ***colorstyle***.

`lwidth(`*linewidthstyle*`)` specifies the width of the rule; see [G-4] ***linewidthstyle***.

`lalign(`*linealignmentstyle*`)` specifies the alignment of the rule; see [G-4] ***linealignmentstyle***.

`lpattern(`*linepatternstyle*`)` specifies the line pattern of the rule; see [G-4] ***linepatternstyle***.

`lstyle(`*linestyle*`)` specifies the overall style of the rule; see [G-4] ***linestyle***.

`margin(`*marginstyle*`)` specifies the margin of the rule; see [G-4] ***marginstyle***.

text_options are the following options:

`coltitleopts(`*textbox_options*`)` affects the look of text for column titles and supertitles. See [G-3] ***textbox_options***.

`itemopts(`*textbox_options*`)` affects the look of text for study rows; see [G-3] ***textbox_options***. This option is ignored when option `subgroup()` is specified and contains multiple variables or when option `cumulative()` or `leaveoneout` is specified.

overallopts(*textbox_options*) affects the look of text for the overall row. See [G-3] ***textbox_options***.

groupopts(*textbox_options*) (synonym subgroupopts()) affects the look of text for subgroup rows when option subgroup() is specified. See [G-3] ***textbox_options***.

bodyopts(*textbox_options*) affects the look of text for study, subgroup, and overall rows. See [G-3] ***textbox_options***.

nonotes suppresses the notes displayed on the graph about the specified meta-analysis model and method and the standard error adjustment.

plot_options are the following options:

crop($\#_1$ $\#_2$) restricts the range of the CI lines to be between $\#_1$ and $\#_2$. A missing value may be specified for any of the two values to indicate that the corresponding limit should not be cropped. Otherwise, lines that extend beyond the specified value range are cropped and adorned with arrows. This option is useful in the presence of small studies with large standard errors, which lead to confidence intervals that are too wide to be displayed nicely on the graph. Option crop() may be used to handle this case.

ciopts(*ci_options*) affects the look of the CI lines and, in the presence of cropped CIs (see option crop()), arrowheads.

ci_options are any options documented in [G-3] ***line_options*** and the following options of [G-2] **graph twoway pcarrow**: mstyle(), msize(), mangle(), barbsize(), mcolor(), mfcolor(), mlcolor(), mlwidth(), mlstyle(), and color().

nowmarkers suppresses weighting of the study markers.

nomarkers suppresses the study markers.

markeropts(*marker_options*) affects the look of the study markers.

marker_options: msymbol(), mcolor(), mfcolor(), mlcolor(), mlwidth(), mlalign(), mlstyle(), and mstyle(); see [G-3] ***marker_options***.

nowmarkers, nomarkers, and markeropts() are ignored when option subgroup() is specified and contains multiple variables or when option cumulative() or leaveoneout is specified.

noomarker suppresses the overall marker.

omarkeropts(*marker_options*) affects the look of the overall marker.

marker_options: mcolor(), mfcolor(), mlcolor(), mlwidth(), mlalign(), mlstyle(), and mstyle(); see [G-3] ***marker_options***.

nogmarkers suppresses the subgroup markers.

gmarkeropts(*marker_options*) affects the look of the subgroup markers.

marker_options: mcolor(), mfcolor(), mlcolor(), mlwidth(), mlalign(), mlstyle(), and mstyle(); see [G-3] ***marker_options***.

nogmarkers and gmarkeropts() are ignored when option subgroup() is not specified.

insidemarker and insidemarker(*marker_options*) add markers at the center of study markers. *marker_options* control how the added markers are rendered.

marker_options: msymbol(), mcolor(), mfcolor(), mlcolor(), mlwidth(), mlalign(), mlstyle(), and mstyle(); see [G-3] ***marker_options***.

insidemarker() is not allowed when option subgroup() is specified and contains multiple variables or when option cumulative() or leaveoneout is specified.

`esrefline` and `esrefline(`*line_options*`)` specify that a vertical line be drawn at the value corresponding to the overall effect size. The optional *line_options* control how the line is rendered; see [G-3] ***line_options***.

`noesrefline` suppresses the overall effect-size line plotted by default on the leave-one-out forest plot, which is produced when you specify option `leaveoneout`.

`nullrefline` and `nullrefline(`*nullopts*`)` specify that a vertical line be drawn at the value corresponding to no overall effect. *nullopts* are the following options:

`favorsleft(`*string* [`,` *textbox_options*]`)` adds a label, *string*, to the left side (with respect to the no-effect line) of the forest graph. *textbox_options* affect how *string* is rendered; see [G-3] ***textbox_options***.

`favorsright(`*string* [`,` *textbox_options*]`)` adds a label, *string*, to the right side (with respect to the no-effect line) of the forest graph. *textbox_options* affect how *string* is rendered; see [G-3] ***textbox_options***.

`favorsleft()` and `favorsright()` are typically used to annotate the sides of the forest graph (column `_plot`) favoring the treatment or control.

line_options affect the rendition of the vertical line; see [G-3] ***line_options***.

`customoverall(`*customspec*`)` draws a custom-defined diamond representing an overall effect size. This option can be repeated. *customspec* is *#es #lb #ub* [`,` *customopts*], where *#es*, *#lb*, and *#ub* correspond to an overall effect-size estimate and its lower and upper CI limits, respectively. *customopts* are the following options:

`label(`*string*`)` adds a label, *string*, under the `_id` column describing the custom diamond.

textbox_options affect how `label(`*string*`)` is rendered; see [G-3] ***textbox_options***.

marker_options affect how the custom diamond is rendered. *marker_options* are `mcolor()`, `mfcolor()`, `mlcolor()`, `mlwidth()`, `mlalign()`, `mlstyle()`, and `mstyle()`; see [G-3] ***marker_options***.

Option `customoverall()` may not be combined with option `cumulative()` or `leaveoneout`.

test_options are defined below. These options are not relevant with cumulative and leave-one-out meta-analysis.

`ohetstatstext(`*string*`)` modifies the default text for the overall heterogeneity statistics reported under the `Overall` row heading on the plot.

`noohetstats` suppresses overall heterogeneity statistics reported under the `Overall` row heading on the plot.

`ohomtesttext(`*string*`)` modifies the default text for the overall homogeneity test labeled as `Test of` θ_i=θ_j under the `Overall` row heading on the plot.

`noohomtest` suppresses the overall homogeneity test labeled as `Test of` θ_i=θ_j under the `Overall` row heading on the plot.

`osigtesttext(`*string*`)` modifies the default text of the test of significance of the overall effect size labeled as `Test of` θ=`0` under the `Overall` row heading on the plot.

`noosigtest` suppresses the test of significance of the overall effect size labeled as `Test of` θ=`0` under the `Overall` row heading on the plot.

`ghetstats#text(`*string*`)` modifies the default text for the heterogeneity statistics in the #th subgroup. These statistics are reported under the group-specific row headings when a single subgroup analysis is performed, that is, when option `subgroup()` is specified with one variable.

noghetstats suppresses subgroup heterogeneity statistics reported when a single subgroup analysis is performed, that is, when option subgroup() is specified with one variable. These statistics are reported under the group-specific row headings.

gwhomtest#text(*string*) modifies the default text for the within-subgroup homogeneity test in the #th subgroup. This test is reported when a single subgroup analysis is performed, that is, when option subgroup() is specified with one variable. The test is labeled as Test of θ_i=θ_j under the group-specific row headings.

nogwhomtests suppresses within-subgroup homogeneity tests. These tests investigate the differences between effect sizes of studies within each subgroup. These tests are reported when a single subgroup analysis is performed, that is, when option subgroup() is specified with one variable. The tests are labeled as Test of θ_i=θ_j under the group-specific row headings.

gsigtest#text(*string*) modifies the default text for the test of significance of the subgroup effect size labeled as Test of θ=0 in the #th subgroup.

nogsigtests suppresses tests of significance of the subgroup effect size labeled as Test of θ=0 within each subgroup. These tests are reported when a single subgroup analysis is performed, that is, when option subgroup() is specified with one variable.

gbhomtest#text(*string*) modifies the default text for the between-subgroup homogeneity test in the #th subgroup. The #th between-subgroup homogeneity test corresponds to the #th variable specified within option subgroup(). The test is labeled as Test of group differences on the plot.

nogbhomtests suppresses between-subgroup homogeneity tests. These tests investigate the differences between the subgroup effect sizes reported when any subgroup analysis is performed, that is, when option subgroup() is specified. The tests are labeled as Test of group differences on the plot.

graph_options: xline(), xtitle(), xlabel(), xtick(), xmlabel(), xmtick(), title(), subtitle(), note(), caption(), t1title(), t2title(), b1title(), b2title(), l1title(), l2title(), r1title(), r2title(), scheme(), nodraw, name(), and saving(); see [G-3] ***twoway_options*** for details.

The following options are available with meta forestplot but are not shown in the dialog box:

nooverall suppresses the row corresponding to the overall effect size in the forest plot.

olabel(*string*) modifies the default overall effect-size label under the _id column, which, by default, is Overall.

Remarks and examples stata.com

Remarks are presented under the following headings:

Overview

Meta-analysis results are often presented using a forest plot (for example, Lewis and Ellis [1982]). A forest plot shows effect-size estimates and their confidence intervals for each study and, usually, the overall effect size from the meta-analysis (for example, Lewis and Clarke [2001]; Harris et al. [2016]; and Fisher 2016). Each study is represented by a square with the size of the square being proportional to the study weight; that is, larger squares correspond to larger (more precise) studies. The weights depend on the chosen meta-analysis model and method. Studies' CIs are plotted as whiskers extending from each side of the square and spanning the width of the CI. Heterogeneity measures such as the I^2 and H^2 statistics, homogeneity test, and the significance test of the overall effect sizes are also commonly reported.

A subgroup meta-analysis forest plot also shows group-specific results. Additionally, it reports a test of the between-group differences among the overall effect sizes. A cumulative meta-analysis forest plot shows the overall effect sizes and their CIs by accumulating the results from adding one study at a time to each subsequent analysis. Similarly, a leave-one-out meta-analysis forest plot shows the overall effect sizes and their CIs resulting from meta-analyses omitting one study at a time. By convention, group-specific and overall effect sizes are represented by diamonds centered on their estimated values with the diamond width corresponding to the CI length.

For more details about forest plots, see, for instance, Anzures-Cabrera and Higgins (2010). Also see Schriger et al. (2010) for an overview of their use in practice.

Using meta forestplot

`meta forestplot` produces meta-analysis forest plots. It provides a graphical representation of the results produced by `meta summarize` and thus supports most of its options such as those specifying a meta-analysis model and estimation method; see [META] **meta summarize**.

The default look of the forest plot produced by `meta forestplot` depends on the type of analysis. For basic meta-analysis, `meta forestplot` plots the study labels, effect sizes and their confidence intervals, and percentages of total weight given to each study. If `meta esize` was used to declare `meta data`, summary data are also plotted. That is,

```
. meta forestplot
```

is equivalent to typing

```
. meta forestplot _id _plot _esci _weight
```

after declaration by using `meta set` and to typing

```
. meta forestplot _id _data _plot _esci _weight
```

after declaration by using `meta esize`.

If multiple variables are specified in the `subgroup()` option,

```
. meta forestplot, subgroup(varlist)
```

is equivalent to typing

```
. meta forestplot _id _K _plot _esci _pvalue, subgroup(varlist)
```

For cumulative meta-analysis,

```
. meta forestplot, cumulative(varname)
```

is equivalent to typing

```
. meta forestplot _id _plot _esci _pvalue _order, cumulative(varname)
```

For leave-one-out meta-analysis,

```
. meta forestplot, leaveoneout
```

is equivalent to typing

```
. meta forestplot _id _plot _esci _pvalue, leaveoneout
```

You can also specify any of the supported columns with `meta forestplot`, including variables in your dataset. For example, you may include, say, variables `x1` and `x2`, as columns in the forest plot by simply specifying them in the column list,

```
. meta forestplot _id x1 _plot _esci _weight x2
```

See *Plot columns* for details about the supported columns.

The CIs correspond to the confidence level as declared by `meta set` or `meta esize`. You can specify a different level in the `level()` option. Also, by default, the CIs are bound by using brackets. You can specify `cibind(parentheses)` to use parentheses instead.

As we mentioned earlier, you can produce forest plots for subgroup analysis by using the `subgroup()` option, for cumulative meta-analysis by using the `cumulative()` option, and for leave-one-out meta-analysis by using the `leaveoneout` option.

You can modify the default column supertitles, titles, formats, and so on by specifying the `columnopts()` option. You can repeat this option to modify the look of particular columns. If you want to apply the same formatting to multiple columns, you can specify these columns within `columnopts()`. See *Options* for the list of supported column options.

Options `esrefline()` and `nullrefline()` are used to draw vertical lines at the overall effect-size and no-effect values, respectively. For the leave-one-out forest plot, produced when you specify option `leaveoneout`, the overall effect-size line is drawn by default. You may suppress it by using option `noesrefline`. Suboptions `favorsleft()` and `favorsright()` of `nullrefline()` may be specified to annotate the sides (with respect to the no-effect line) of the plot favoring treatment or control.

Another option you may find useful is `crop(`$\#_1$ $\#_2$`)`. Sometimes, some of the smaller studies may have large standard errors that lead to CIs that are too wide to be displayed on the plot. You can "crop" such CIs by restricting their range. The restricted range will be indicated by the arrowheads at the corresponding ends of the CIs. You can crop both limits or only one of the limits. You can modify the default look of the arrowheads or CI lines, in general, by specifying `ciopts()`.

You may sometimes want to show the overall effect-size estimates from multiple meta-analysis models (for example, common versus random), from different estimation methods (REML versus DL), or for specific values of moderators from a meta-regression. This may be accomplished via the `customoverall(`*#es #lb #ub* [`,`*customopts*]`)` option. This option may be repeated to display multiple diamonds depicting multiple custom-defined overall effect sizes.

You can specify many more options to customize the look of your forest plot such as modifying the look of text for column titles in `coltitleopts()` or the column format in `format()`; see *Syntax* for details.

`meta forestplot` uses the following default convention when displaying the results. The results from individual studies—individual effects sizes—are plotted as blue squares with areas proportional to study weights. The overall effect size is plotted as a green (or, more precisely, forest green using Stata's color convention) diamond with the width corresponding to its CI. The results of a single subgroup analysis—subgroup effect sizes—are plotted as red diamonds with the widths determined by the respective CIs. The results of multiple subgroup analyses are plotted as red circles with the CI lines. The cumulative meta-analysis results—cumulative overall effect sizes—are displayed as green circles with CI lines. Similarly, the leave-one-out meta-analysis results—overall effect size with one study omitted—are also displayed as green circles with CI lines.

Options itemopts(), nomarkers, and markeropts() control the look of study rows and markers, which represent individual effect sizes. These options are not relevant when individual studies are not reported such as with multiple subgroup analysis, cumulative meta-analysis, and leave-one-out meta-analysis.

Options groupopts(), nogmarkers, and gmarkeropts() control the look of subgroup rows and markers and are relevant only when subgroup analysis is performed by specifying the subgroup() option.

Options overallopts(), noomarker, and omarkeropts() control the look of overall rows and markers, which represent the overall effect sizes. These options are always applicable because the overall results are always displayed by default. With cumulative and leave-one-out meta-analysis, these options affect the displayed overall effect sizes.

Graphs created by meta forestplot cannot be combined with other Stata graphs using graph combine.

Plot columns

meta forestplot supports many columns that you can include in your forest plot; see the list of supported columns in *Syntax*. The default columns plotted for various analyses were described in *Using meta forestplot* above. Here we provide more details about some of the supported columns.

meta forestplot provides individual columns such as _es and _se and column shortcuts such as _esse. Column shortcuts are typically shortcuts for specifying multiple columns. For instance, when dealing with two-group comparison of binary or continuous outcomes, column _data is a shortcut for columns _data1 and _data2, which themselves are shortcuts to individual summary-data columns. For a two-group comparison of continuous outcomes, _data1 is a shortcut for columns _n1, _mean1, and _sd1, and _data2 is a shortcut for _n2, _mean2, and _sd2. For a two-group comparison of binary outcomes, _data1 corresponds to the treatment-group numbers of successes and failures, _a and _b, and _data2 to the respective numbers in the control group, _c and _d. For estimating a single proportion, the case of one-sample binary data, columns _data1 and _data2 are not available. In this case, column _data corresponds to columns _e and _n, which are the number of successes and the study sample size, respectively. Similarly, for correlation data, column _data corresponds to columns _r and _n, which are the correlation and the study sample size, respectively. Column _data and the corresponding summary-data columns are available only after declaration by using meta esize.

The other column shortcuts are _ci, _esci, and _esse. In addition to serving as shortcuts to the respective columns (_lb and _ub; _es, _lb, and _ub; and _es and _se), these shortcut columns have additional properties. For instance, when you specify _ci, the lower and upper CI bounds are separated with a comma, bounded in brackets, and share a title. That is,

```
. meta forestplot _ci
```

is similar to specifying

```
. meta forestplot _lb _ub,
> columnopts(_lb _ub, title(95% CI))
> columnopts(_lb, mask("[%6.2f,"))
> columnopts(_ub, mask("%6.2f]"))
```

Similarly, _esci additionally combines _es and _ci with the common column title, and _esse combines _es and _se and bounds the standard errors in parentheses. _ci, _esci, and _esse also apply other properties to improve the default look of the specified columns such as modifying the default column margins by specifying `plotregion(margin())`.

If you want to modify the individual columns of the shortcuts, you need to specify the corresponding column names in `columnopts()`. For instance, if we want to display the effect sizes of the `_esci` column with three decimal digits but continue using the default format for CIs, we can type

```
. meta forestplot _esci, columnopts(_es, format(%6.3f))
```

If we specify `_esci` instead of `_es` in `columnopts()`,

```
. meta forestplot _esci, columnopts(_esci, format(%6.3f))
```

both effect sizes and CIs will be displayed with three decimal digits. On the other hand, if we want to change the default title and supertitle for `_esci`, we should specify `_esci` in `columnopts()`,

```
. meta forestplot _esci, columnopts(_esci, supertitle("My ES") title("with my CI"))
```

Also see example 7 and example 8 for more examples of customizing the default look of columns.

Column `_plot` corresponds to the plot region that contains graphical representation of the effect sizes and their confidence intervals. You can modify the default look of the plot by specifying the *plot_options* in *Syntax*.

Column `_es` corresponds to the plotted effect sizes. For basic meta-analysis, this column displays the individual and overall effect sizes. For subgroup meta-analysis, it also displays subgroup-specific overall effect sizes. For cumulative meta-analysis, it displays the overall effect sizes corresponding to the accumulated studies. For leave-one-out meta-analysis, it displays the overall effect sizes corresponding to the meta-analyses omitting one study at a time.

Some of the columns such as `_pvalue`, `_K`, `_size`, and `_order` are available only with specific meta-analyses. `_pvalue` is available only with multiple subgroup analyses, with cumulative analysis, or with leave-one-out analysis; it displays the p-values of the significant tests of effect sizes. `_K` is available with multiple subgroup analyses and displays the number of studies within each subgroup. `_order` is available only with cumulative meta-analysis; it displays the values of the specified ordering variable.

You may also add variables in your dataset to the forest plot. For instance, if you want to display variables `x1` and `x2` in the second and last columns, you may type

```
. meta forestplot _id x1 _plot _esci _weight x2
```

Duplicate columns are ignored with `meta forestplot`. Also, column shortcuts take precedence. That is, if you specified both `_es` and `_esci`, the latter will be displayed.

Examples of using meta forestplot

In this section, we demonstrate some of the uses of `meta forestplot`. The examples are presented under the following headings:

▷ Example 1: Forest plot for two-group comparison of binary outcomes

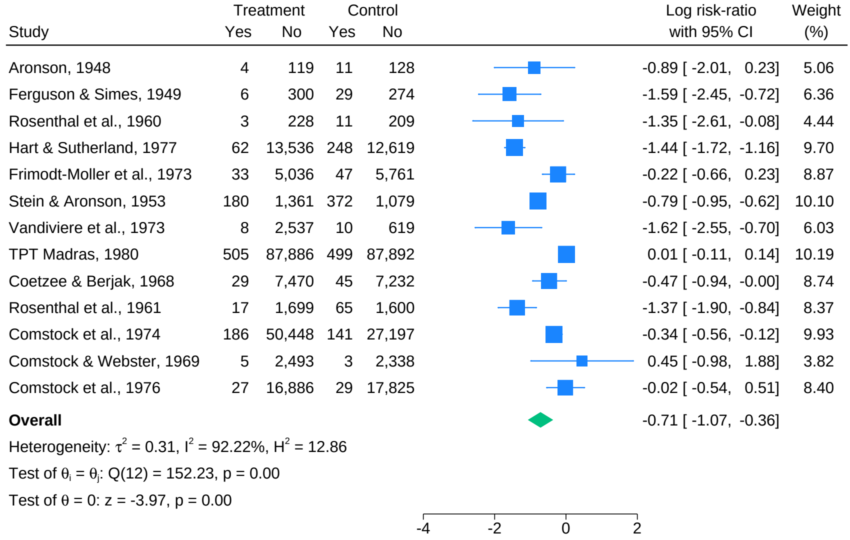
Consider the dataset from Colditz et al. (1994) of clinical trials that studies the efficacy of a Bacillus Calmette-Guérin (BCG) vaccine in the prevention of tuberculosis (TB). This dataset was introduced in *Efficacy of BCG vaccine against tuberculosis (bcg.dta)* of [META] **meta**. In this section, we use its declared version and focus on the demonstration of various options of `meta forest`.

```
. use https://www.stata-press.com/data/r18/bcgset
(Efficacy of BCG vaccine against tuberculosis; set with -meta esize-)
```

Let's construct a basic forest plot by simply typing

```
. meta forestplot

  Effect-size label: Log risk-ratio
        Effect size: _meta_es
          Std. err.: _meta_se
        Study label: studylbl
```



Study	Treatment Yes	Treatment No	Control Yes	Control No	Log risk-ratio with 95% CI	Weight (%)
Aronson, 1948	4	119	11	128	-0.89 [-2.01, 0.23]	5.06
Ferguson & Simes, 1949	6	300	29	274	-1.59 [-2.45, -0.72]	6.36
Rosenthal et al., 1960	3	228	11	209	-1.35 [-2.61, -0.08]	4.44
Hart & Sutherland, 1977	62	13,536	248	12,619	-1.44 [-1.72, -1.16]	9.70
Frimodt-Moller et al., 1973	33	5,036	47	5,761	-0.22 [-0.66, 0.23]	8.87
Stein & Aronson, 1953	180	1,361	372	1,079	-0.79 [-0.95, -0.62]	10.10
Vandiviere et al., 1973	8	2,537	10	619	-1.62 [-2.55, -0.70]	6.03
TPT Madras, 1980	505	87,886	499	87,892	0.01 [-0.11, 0.14]	10.19
Coetzee & Berjak, 1968	29	7,470	45	7,232	-0.47 [-0.94, -0.00]	8.74
Rosenthal et al., 1961	17	1,699	65	1,600	-1.37 [-1.90, -0.84]	8.37
Comstock et al., 1974	186	50,448	141	27,197	-0.34 [-0.56, -0.12]	9.93
Comstock & Webster, 1969	5	2,493	3	2,338	0.45 [-0.98, 1.88]	3.82
Comstock et al., 1976	27	16,886	29	17,825	-0.02 [-0.54, 0.51]	8.40
Overall					-0.71 [-1.07, -0.36]	

Heterogeneity: τ^2 = 0.31, I^2 = 92.22%, H^2 = 12.86
Test of $\theta_i = \theta_j$: Q(12) = 152.23, p = 0.00
Test of θ = 0: z = -3.97, p = 0.00

Random-effects REML model

By default, the basic forest plot displays the study labels (column `_id`), the summary data (`_data`), graphical representation of the individual and overall effect sizes and their CIs (`_plot`), the corresponding values of the effect sizes and CIs (`_esci`), and the percentages of total weight for each study (`_weight`). You can also customize the columns on the forest plot; see example 7 and example 12.

In the graph, each study corresponds to a blue square centered at the point estimate of the effect size with a horizontal line (whiskers) extending on either side of the square. The centers of the squares (the values of study effect sizes) may be highlighted via the `insidemarker()` option; see example 10. The horizontal line depicts the CI. The area of the square is proportional to the corresponding study weight.

The overall effect size corresponds to the green diamond centered at the estimate of the overall effect size. The width of the diamond corresponds to the width of the overall CI. Note that the height of the diamond is irrelevant. It is customary in meta-analysis forest plots to display an overall effect size as a diamond filled inside with color. This, however, may overemphasize the actual area of the diamond whereas only the width of it matters. If desired, you may suppress the fill color by specifying the `omarkeropts(mfcolor(none))` option.

Under the diamond, three lines are reported. The first line contains heterogeneity measures I^2, H^2, and $\widehat{\tau}^2$. The second line displays the homogeneity test based on the Q statistic. The third line displays the test of the overall effect size being equal to zero. These lines may be suppressed by specifying options `noohetstats`, `noohomtest`, and `noosigtest`. Alternatively, the default text in these lines may be modified via options `ohetstatstext()`, `ohomtesttext()`, and `osigtesttext()`, respectively; see example 16. See [META] **meta summarize** for a substantive interpretation of these results.

Some forest plots show vertical lines at the no-effect and overall effect-size values. These may be added to the plot via options `nullrefline()` and `esrefline()`, respectively; see example 5. Also, you may sometimes want to plot custom-defined overall effect sizes such as based on multiple meta-analysis models. This may be accomplished via the `customoverall()`; see example 12.

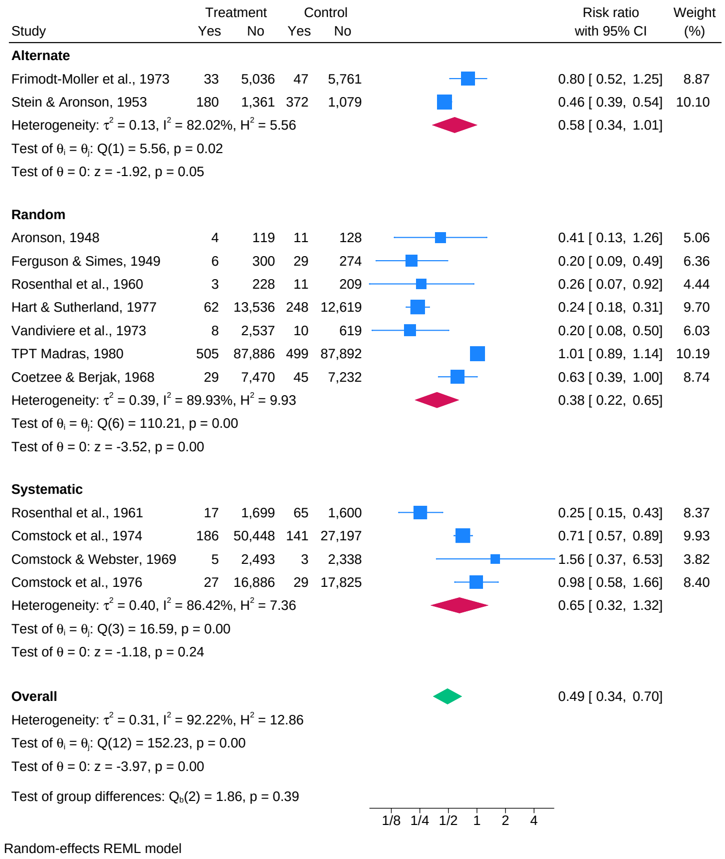
`meta forestplot` provides a quick way to assess between-study heterogeneity visually. In the absence of heterogeneity, we would expect to see that the middle points of the squares are close to the middle of the diamond and the CIs are overlapping. In these data, there is certainly evidence of some heterogeneity because the squares for some studies are far away from the diamond and there are studies with nonoverlapping CIs.

◁

▷ Example 2: Subgroup-analysis forest plot

Continuing with example 1, let's now perform a subgroup meta-analysis based on the method of treatment allocation recorded in variable `alloc`. We specify `subgroup(alloc)` and also use the `eform` option to display exponentiated results, risk ratios (RRs) instead of log risk-ratios in our example.

```
. meta forestplot, subgroup(alloc) eform
  Effect-size label: Log risk-ratio
        Effect size: _meta_es
          Std. err.: _meta_se
        Study label: studylbl
```



In addition to the overall results, the forest plot shows the results of meta-analysis for each of the three groups. With subgroup meta-analysis, each group gets its own red diamond marker that represents the group-specific overall effect size. Just like with the overall diamond, only the widths (not the heights) of the group-specific diamonds are relevant on the plot. Similarly to the overall marker, you can specify the `gmarkeropts(mfcolor(none))` option to suppress the fill color for the group-specific diamonds.

Heterogeneity measures, homogeneity tests, and significance tests are reported at the bottom (below the group-specific diamond marker) within each group. These provide information regarding the heterogeneity among the studies within each group and the statistical significance of the group-specific overall effect size. They may be suppressed with options `noghetstats`, `nogwhomtests`, and `nogsigtests`, respectively. Alternatively, you may specify options `ghetstats#text()`, `gwhomtest#text()`, and `gsigtest#text()` to modify the default text reported within the #th subgroup (# can be 1, 2, or 3 in this case); see example 16.

A test of between-group differences based on the Q_b statistic is reported at the bottom. This test investigates the difference between the group-specific overall effect sizes. It may be suppressed with nogbhomtests. Alternatively, the default text for this test may be modified using option gbhomtest#text(); see example 16.

You may also specify multiple variables in subgroup(), in which case a separate subgroup analysis is performed for each variable; see example 6 for details.

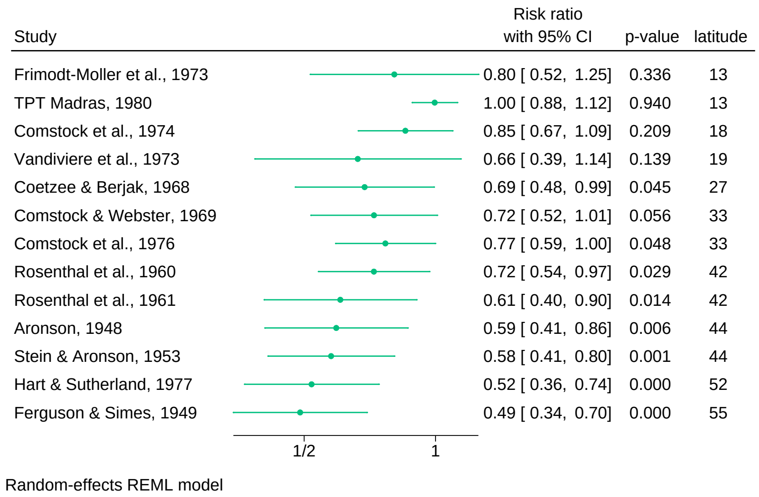
◁

▷ Example 3: Cumulative forest plot

Continuing with example 1, we now perform a cumulative meta-analysis in the ascending order of variable latitude. You can specify suboption descending within the cumulative() option to request a descending order.

We also specify rr, which is a synonym of the eform option we used in example 2, to display the RRs instead of the default log risk-ratios.

```
. meta forestplot, cumulative(latitude) rr
  Effect-size label: Log risk-ratio
        Effect size: _meta_es
          Std. err.: _meta_se
        Study label: studylbl
```



Study	Risk ratio with 95% CI	p-value	latitude
Frimodt-Moller et al., 1973	0.80 [0.52, 1.25]	0.336	13
TPT Madras, 1980	1.00 [0.88, 1.12]	0.940	13
Comstock et al., 1974	0.85 [0.67, 1.09]	0.209	18
Vandiviere et al., 1973	0.66 [0.39, 1.14]	0.139	19
Coetzee & Berjak, 1968	0.69 [0.48, 0.99]	0.045	27
Comstock & Webster, 1969	0.72 [0.52, 1.01]	0.056	33
Comstock et al., 1976	0.77 [0.59, 1.00]	0.048	33
Rosenthal et al., 1960	0.72 [0.54, 0.97]	0.029	42
Rosenthal et al., 1961	0.61 [0.40, 0.90]	0.014	42
Aronson, 1948	0.59 [0.41, 0.86]	0.006	44
Stein & Aronson, 1953	0.58 [0.41, 0.80]	0.001	44
Hart & Sutherland, 1977	0.52 [0.36, 0.74]	0.000	52
Ferguson & Simes, 1949	0.49 [0.34, 0.70]	0.000	55

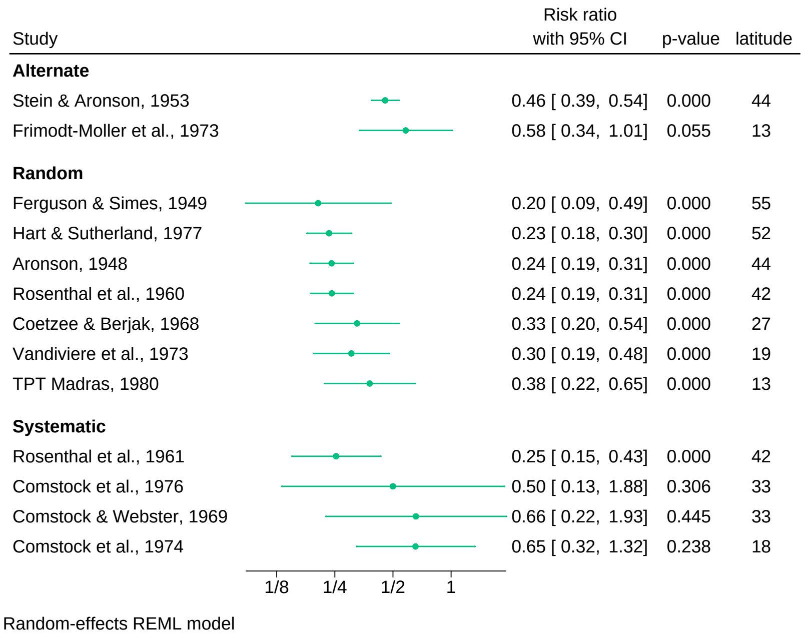
Random-effects REML model

By default, the cumulative meta-analysis forest plot displays the study labels (_id), the plot of effect sizes and their CIs (_plot), the values of effect sizes and their CIs (_esci), the p-values (_pvalue) of the corresponding significance tests of the effect sizes, and the values of the order variable (_order).

The displayed effect sizes correspond to cumulative overall effect sizes or the overall effect sizes computed for each set of accumulated studies. To distinguish them from study-specific effect sizes, we plot them as unweighted circles using the same color, green, as the overall effect size in a standard meta-analysis forest plot. You can change the default style and color of the markers by specifying the omarkeropts() option. The corresponding CIs of the cumulative effect sizes are plotted as CI lines.

We may construct a cumulative forest plot stratified by a covariate by specifying by() within cumulative(). For example, let's stratify our cumulative analysis by the method of treatment allocation recorded in variable alloc.

```
. meta forestplot, cumulative(latitude, by(alloc) descending) rr
  Effect-size label: Log risk-ratio
        Effect size: _meta_es
          Std. err.: _meta_se
        Study label: studylbl
```



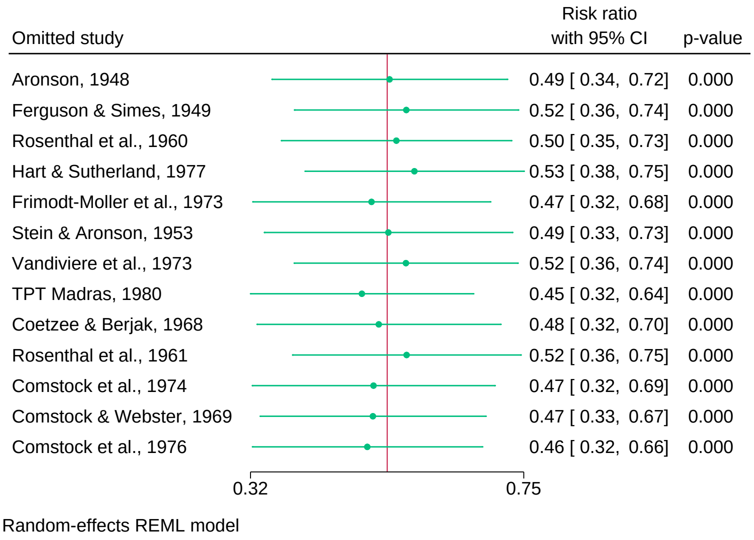
We specified that the analysis be conducted in the descending order of the `latitude` variable. The stratified forest plot shows the same columns as before but the cumulative analysis is performed separately for each group of `alloc`. A consistent pattern is observed across all three groups—RRs tend to increase as latitude decreases.

◁

▷ Example 4: Leave-one-out forest plot

Continuing with example 1, we now perform a leave-one-out meta-analysis by specifying the `leaveoneout` option.

```
    . meta forestplot, leaveoneout rr
      Effect-size label: Log risk-ratio
            Effect size: _meta_es
              Std. err.: _meta_se
            Study label: studylbl
```



By default, the leave-one-out meta-analysis forest plot displays the study labels (`_id`), the plot of effect sizes and their CIs (`_plot`), the values of effect sizes and their CIs (`_esci`), and the *p*-values (`_pvalue`) of the corresponding significance tests of the effect sizes.

For each study, the displayed effect size corresponds to an overall effect size computed from a meta-analysis excluding that study. Similarly to the case with cumulative forest plots, we will distinguish the overall effect sizes from study-specific effect sizes by plotting them as unweighted circles using the same color, green, as the overall effect size in a standard meta-analysis forest plot. You can change the default style and color of the markers by specifying the `omarkeropts()` option. The corresponding CIs of the overall effect sizes are plotted as CI lines.

By default, the leave-one-out forest plot displays a vertical line at the overall effect size based on the complete set of studies (with no omission) to facilitate the detection of influential studies. You may suppress this line by specifying option `noesrefline`.

All the overall effect sizes from the leave-one-out meta-analysis are close to the overall effect-size vertical line, and their CI lines intersect with the vertical red line based on all the studies, which means that there are no studies that substantially influence the results of our meta-analysis.

◁

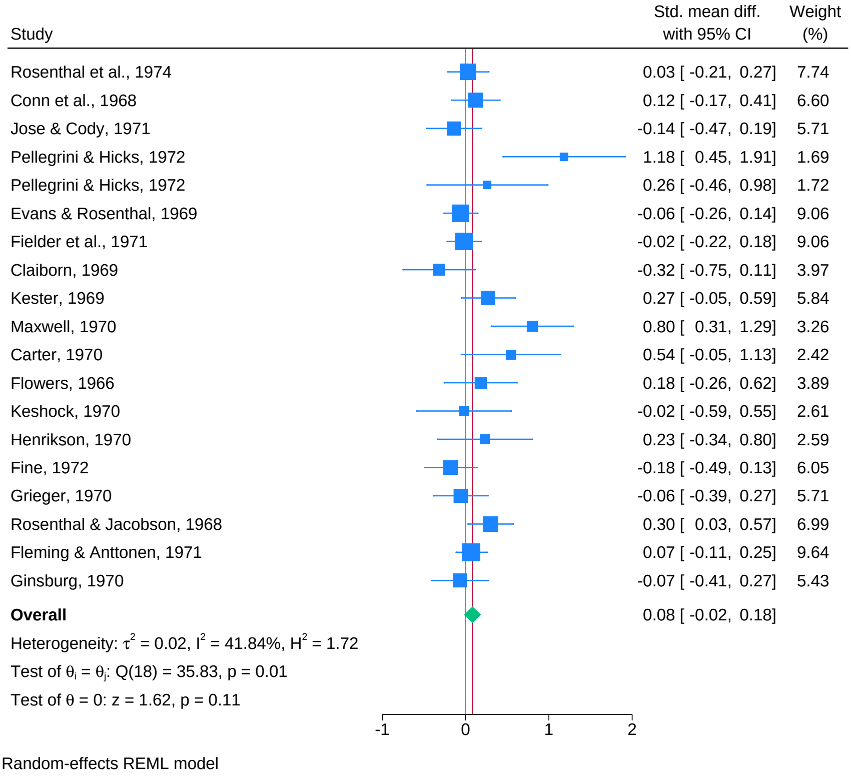
▷ Example 5: Forest plot for precomputed effect sizes

Recall the pupil IQ data (Raudenbush and Bryk 1985; Raudenbush 1984) described in *Effects of teacher expectancy on pupil IQ (pupiliq.dta)* of [META] **meta**. Here we will use its declared version (declared with `meta set`) to construct a forest plot of precomputed effect sizes.

```
. use https://www.stata-press.com/data/r18/pupiliqset, clear
(Effects of teacher expectancy on pupil IQ; set with -meta set-)
```

We specify the `nullrefline` option to show the no-effect line at 0. Effect sizes with corresponding CIs that cross this line are not statistically significant at the 5% level. We also specify the `esrefline` option to draw a vertical line at the overall effect-size value. The default look of both lines may be modified by specifying options `nullrefline(`*line_options*`)` and `esrefline(`*line_options*`)`. See [G-3] ***line_options***.

```
. meta forestplot, nullrefline esrefline
  Effect-size label: Std. mean diff.
        Effect size: stdmdiff
          Std. err.: se
        Study label: studylbl
```



When `meta` data are declared by using `meta set` (that is, when we are working with precomputed effect sizes), the `_data` column is not available. If desired, you may plot the values of effect sizes and their standard errors by specifying the `_esse` column. Other components of the graph are interpreted as in example 1.

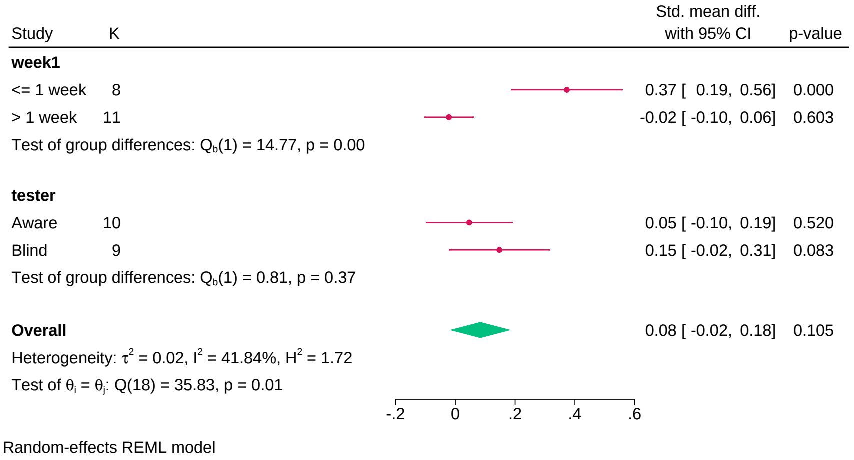
◁

▷ Example 6: Multiple subgroup-analyses forest plot

Continuing with example 5, we will conduct multiple subgroup analyses and summarize their results on a forest plot. We specify variables tester and week1 in subgroup() as follows:

```
. meta forestplot, subgroup(week1 tester)

  Effect-size label: Std. mean diff.
        Effect size: stdmdiff
          Std. err.: se
        Study label: studylbl
```



By default, the forest plot displays the study labels (_id), the number of studies within each group (_K), the plot of effect sizes and their CIs (_plot), the values of effect sizes and their CIs (_esci), and the p-values (_pvalue) of the corresponding significance tests.

To keep the output compact, the forest plot does not report individual studies, only the number of studies in each group. The between-group homogeneity test based on the Q_b is reported for each subgroup analysis. For example, for subgroup analysis based on variable week1, there are two groups, <= 1 week and > 1 week. The test investigates whether the overall effect sizes corresponding to these two groups are the same. The results of this test are identical to those we would have obtained if we had specified subgroup(week1). You may specify option nogbhomtests to suppress these tests. Alternatively, you may modify the default text for the between-group homogeneity tests using option gbhomtest#text() (# can be equal to 1 or 2 in this example); see example 16.

Just like with cumulative meta-analysis in example 3, meta forestplot uses unweighted circles and CI lines to display the overall group-specific effect sizes and their CIs. But here the circles are displayed in red—the same color used to display the group-specific diamonds in a single-variable subgroup analysis (see example 2).

◁

▷ Example 7: Modifying columns' order and cropping confidence intervals

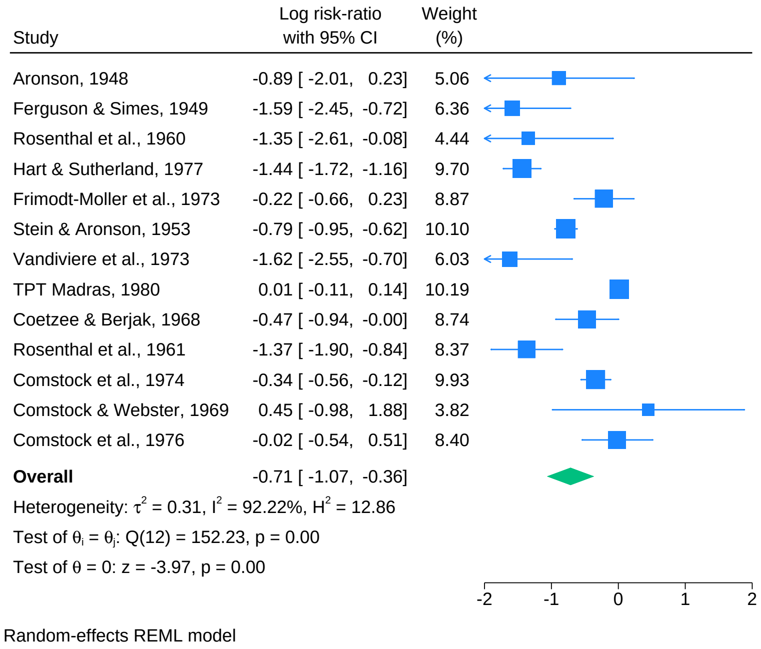
For this and the following examples, let's return to our BCG dataset from example 1.

```
. use https://www.stata-press.com/data/r18/bcgset, clear
(Efficacy of BCG vaccine against tuberculosis; set with -meta esize-)
. meta update, nometashow
```

We used `meta update` to suppress the meta setting information displayed by `meta forest` for the rest of our meta-analysis.

We can choose which columns to display and the order in which to display them in the forest plot by specifying the corresponding column names in the desired order. In the code below, we display the study labels first, followed by the effect sizes and their CIs, then weights, and finally the plot. We also use the `crop(-2 .)` option to restrict the range of the CIs at a lower limit of −2.

```
. meta forestplot _id _esci _weight _plot, crop(-2 .)
```



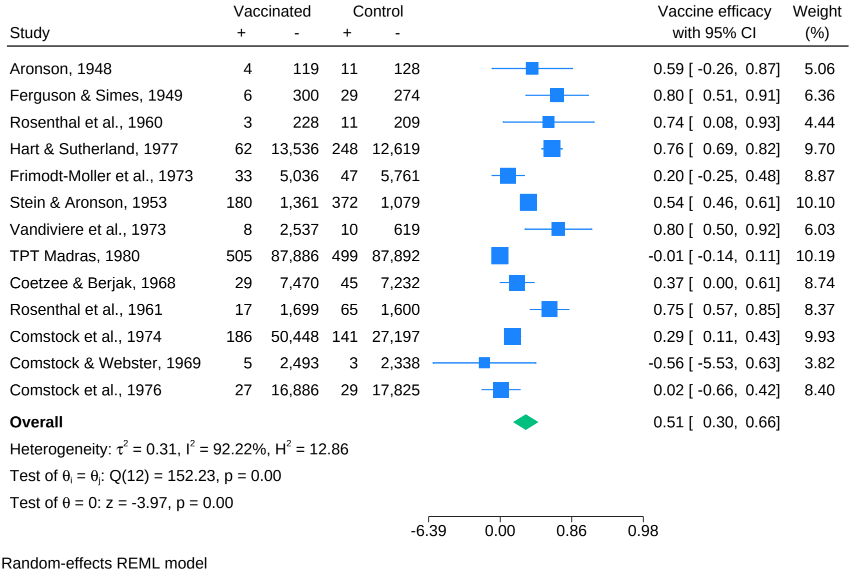
CIs that extend beyond the lower limit of −2 are identified with an arrow head at the cropped endpoint. ◁

▷ Example 8: Applying transformations and changing titles and supertitles

Continuing with the BCG dataset from example 7, we demonstrate how to override the default title and supertitle for the _data column. The summary data we have correspond to a 2 × 2 table with cells _a, _b, _c, and _d. Cells _a and _b may be referred to as _data1, and cells _c and _d may be referred to as _data2.

We override the supertitle for the _data1 column to display "Vaccinated" and the titles for each cell to display either a "+" or a "−" as follows. We also use the transform() option to report vaccine efficacies instead of log risk-ratios. Vaccine efficacy is defined as 1 − RR and may be requested by specifying transform(efficacy).

```
. meta forestplot, transform(Vaccine efficacy: efficacy)
> columnopts(_data1, supertitle(Vaccinated))
> columnopts(_a _c, title(+)) columnopts(_b _d, title(-))
```



Study	Vaccinated		Control		Vaccine efficacy	Weight
	+	-	+	-	with 95% CI	(%)
Aronson, 1948	4	119	11	128	0.59 [-0.26, 0.87]	5.06
Ferguson & Simes, 1949	6	300	29	274	0.80 [0.51, 0.91]	6.36
Rosenthal et al., 1960	3	228	11	209	0.74 [0.08, 0.93]	4.44
Hart & Sutherland, 1977	62	13,536	248	12,619	0.76 [0.69, 0.82]	9.70
Frimodt-Moller et al., 1973	33	5,036	47	5,761	0.20 [-0.25, 0.48]	8.87
Stein & Aronson, 1953	180	1,361	372	1,079	0.54 [0.46, 0.61]	10.10
Vandiviere et al., 1973	8	2,537	10	619	0.80 [0.50, 0.92]	6.03
TPT Madras, 1980	505	87,886	499	87,892	-0.01 [-0.14, 0.11]	10.19
Coetzee & Berjak, 1968	29	7,470	45	7,232	0.37 [0.00, 0.61]	8.74
Rosenthal et al., 1961	17	1,699	65	1,600	0.75 [0.57, 0.85]	8.37
Comstock et al., 1974	186	50,448	141	27,197	0.29 [0.11, 0.43]	9.93
Comstock & Webster, 1969	5	2,493	3	2,338	-0.56 [-5.53, 0.63]	3.82
Comstock et al., 1976	27	16,886	29	17,825	0.02 [-0.66, 0.42]	8.40
Overall					0.51 [0.30, 0.66]	

Heterogeneity: $\tau^2 = 0.31$, $I^2 = 92.22\%$, $H^2 = 12.86$

Test of $\theta_i = \theta_j$: Q(12) = 152.23, p = 0.00

Test of $\theta = 0$: z = -3.97, p = 0.00

Random-effects REML model

By specifying transform(Vaccine efficacy: efficacy), we also provided a meaningful label, "Vaccine efficacy", to be used for the transformed effect sizes. The overall vaccine efficacy is 0.51, which can be interpreted as a reduction of 51% in the risk of having tuberculosis among the vaccinated group.

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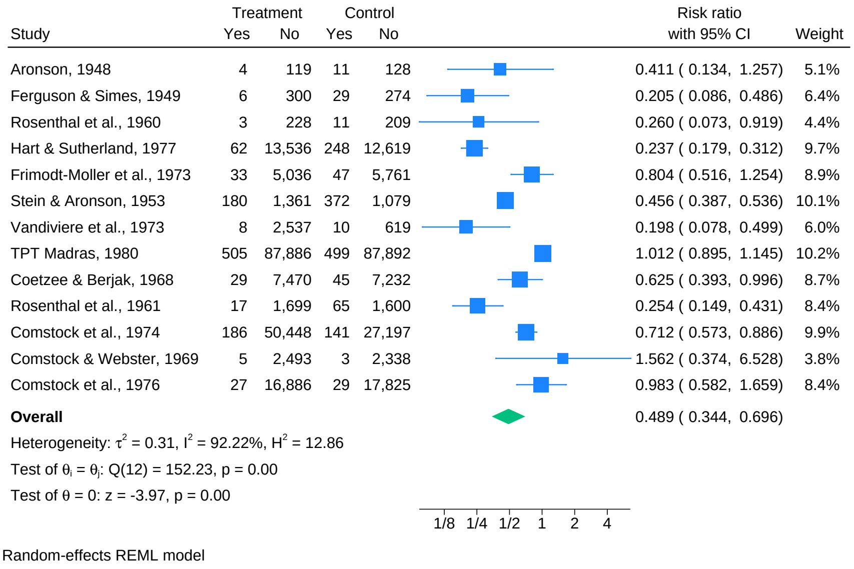
▷ Example 9: Changing columns’ formatting

Following example 8, we now demonstrate how to override the default formats for the `_esci` and `_weight` columns. For the `_esci` column, we also specify that the CIs be displayed inside parentheses instead of the default brackets. For the `_weight` column, we specify that the plotted weights be adorned with a % sign and modify the title and supertitle accordingly.

```
. meta forestplot, eform cibind(parentheses)
> columnopts(_esci, format(%6.3f))
> columnopts(_weight, mask(%6.1f%%) title(Weight) supertitle(""))
```



Study	Treatment Yes	 No	Control Yes	 No	Risk ratio with 95% CI	Weight
Aronson, 1948	4	119	11	128	0.411 (0.134, 1.257)	5.1%
Ferguson & Simes, 1949	6	300	29	274	0.205 (0.086, 0.486)	6.4%
Rosenthal et al., 1960	3	228	11	209	0.260 (0.073, 0.919)	4.4%
Hart & Sutherland, 1977	62	13,536	248	12,619	0.237 (0.179, 0.312)	9.7%
Frimodt-Moller et al., 1973	33	5,036	47	5,761	0.804 (0.516, 1.254)	8.9%
Stein & Aronson, 1953	180	1,361	372	1,079	0.456 (0.387, 0.536)	10.1%
Vandiviere et al., 1973	8	2,537	10	619	0.198 (0.078, 0.499)	6.0%
TPT Madras, 1980	505	87,886	499	87,892	1.012 (0.895, 1.145)	10.2%
Coetzee & Berjak, 1968	29	7,470	45	7,232	0.625 (0.393, 0.996)	8.7%
Rosenthal et al., 1961	17	1,699	65	1,600	0.254 (0.149, 0.431)	8.4%
Comstock et al., 1974	186	50,448	141	27,197	0.712 (0.573, 0.886)	9.9%
Comstock & Webster, 1969	5	2,493	3	2,338	1.562 (0.374, 6.528)	3.8%
Comstock et al., 1976	27	16,886	29	17,825	0.983 (0.582, 1.659)	8.4%
Overall					0.489 (0.344, 0.696)	

Heterogeneity: $\tau^2 = 0.31$, $I^2 = 92.22\%$, $H^2 = 12.86$

Test of $\theta_i = \theta_j$: Q(12) = 152.23, p = 0.00

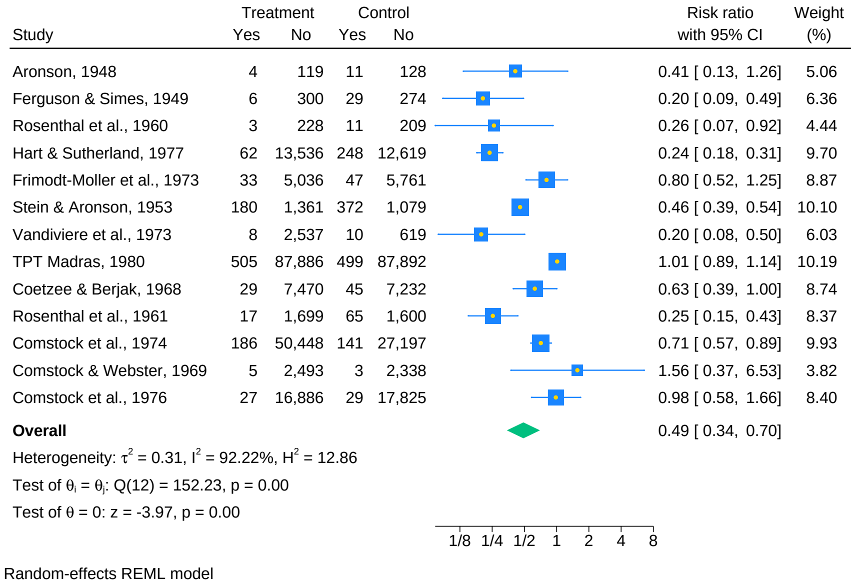
Test of $\theta = 0$: z = -3.97, p = 0.00

Random-effects REML model

▷ Example 10: Changing axis range and adding center study markers

In this example, we specify the `xscale(range(.125 8))` and `xlabel(#7)` options to specify that the x-axis range be symmetric (on the risk-ratio scale) about the no-effect value of 1 and that 7 tick marks be shown on the axis.

```
. meta forest, eform xscale(range(.125 8)) xlabel(#7) insidemarker
```



Study	Treatment Yes	Treatment No	Control Yes	Control No	Risk ratio with 95% CI	Weight (%)
Aronson, 1948	4	119	11	128	0.41 [0.13, 1.26]	5.06
Ferguson & Simes, 1949	6	300	29	274	0.20 [0.09, 0.49]	6.36
Rosenthal et al., 1960	3	228	11	209	0.26 [0.07, 0.92]	4.44
Hart & Sutherland, 1977	62	13,536	248	12,619	0.24 [0.18, 0.31]	9.70
Frimodt-Moller et al., 1973	33	5,036	47	5,761	0.80 [0.52, 1.25]	8.87
Stein & Aronson, 1953	180	1,361	372	1,079	0.46 [0.39, 0.54]	10.10
Vandiviere et al., 1973	8	2,537	10	619	0.20 [0.08, 0.50]	6.03
TPT Madras, 1980	505	87,886	499	87,892	1.01 [0.89, 1.14]	10.19
Coetzee & Berjak, 1968	29	7,470	45	7,232	0.63 [0.39, 1.00]	8.74
Rosenthal et al., 1961	17	1,699	65	1,600	0.25 [0.15, 0.43]	8.37
Comstock et al., 1974	186	50,448	141	27,197	0.71 [0.57, 0.89]	9.93
Comstock & Webster, 1969	5	2,493	3	2,338	1.56 [0.37, 6.53]	3.82
Comstock et al., 1976	27	16,886	29	17,825	0.98 [0.58, 1.66]	8.40
Overall					0.49 [0.34, 0.70]	

Heterogeneity: $\tau^2 = 0.31$, $I^2 = 92.22\%$, $H^2 = 12.86$

Test of $\theta_i = \theta_j$: Q(12) = 152.23, p = 0.00

Test of $\theta = 0$: z = -3.97, p = 0.00

Random-effects REML model

We also used the `insidemarker` option to insert a marker (yellow circle) at the center of the study markers (blue squares) to indicate the study-specific effect sizes. The default attributes of the inserted markers may be modified by specifying `insidemarker(`*marker_options*`)`; see [G-3] ***marker_options***.

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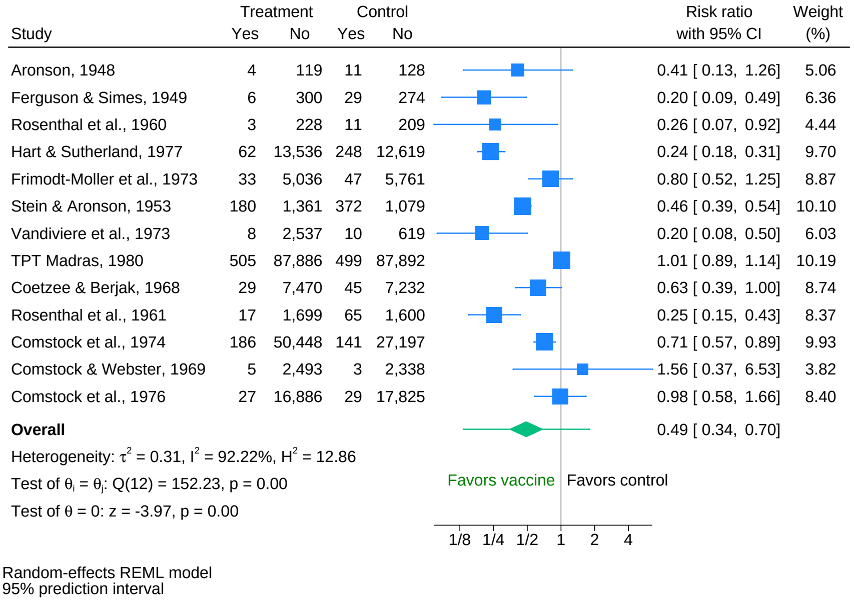
▷ Example 11: Prediction intervals and sides favoring control or treatment

Below, we specify the `favorsleft()` and `favorsright()` suboptions of the `nullrefline()` option to annotate the sides of the plot (with respect to the no-effect line) favoring the treatment or control. We will also specify the `predinterval` option to draw the prediction interval for the overall effect size.

```
. meta forest, eform predinterval
> nullrefline(
> favorsleft("Favors vaccine", color(green))
> favorsright("Favors control")
> )
```



	Treatment		Control		Risk ratio	Weight
Study	Yes	No	Yes	No	with 95% CI	(%)
Aronson, 1948	4	119	11	128	0.41 [0.13, 1.26]	5.06
Ferguson & Simes, 1949	6	300	29	274	0.20 [0.09, 0.49]	6.36
Rosenthal et al., 1960	3	228	11	209	0.26 [0.07, 0.92]	4.44
Hart & Sutherland, 1977	62	13,536	248	12,619	0.24 [0.18, 0.31]	9.70
Frimodt-Moller et al., 1973	33	5,036	47	5,761	0.80 [0.52, 1.25]	8.87
Stein & Aronson, 1953	180	1,361	372	1,079	0.46 [0.39, 0.54]	10.10
Vandiviere et al., 1973	8	2,537	10	619	0.20 [0.08, 0.50]	6.03
TPT Madras, 1980	505	87,886	499	87,892	1.01 [0.89, 1.14]	10.19
Coetzee & Berjak, 1968	29	7,470	45	7,232	0.63 [0.39, 1.00]	8.74
Rosenthal et al., 1961	17	1,699	65	1,600	0.25 [0.15, 0.43]	8.37
Comstock et al., 1974	186	50,448	141	27,197	0.71 [0.57, 0.89]	9.93
Comstock & Webster, 1969	5	2,493	3	2,338	1.56 [0.37, 6.53]	3.82
Comstock et al., 1976	27	16,886	29	17,825	0.98 [0.58, 1.66]	8.40
Overall					0.49 [0.34, 0.70]	

Heterogeneity: $\tau^2 = 0.31$, $I^2 = 92.22\%$, $H^2 = 12.86$

Test of $\theta_i = \theta_j$: Q(12) = 152.23, p = 0.00

Test of $\theta = 0$: z = -3.97, p = 0.00

Random-effects REML model
95% prediction interval

In our example, the effect sizes that are falling on the "Favors vaccine" side (left side) reported that the treatment (vaccine) reduced the risk of tuberculosis. The default placement of the labels may be modified using the Graph Editor; see [G-1] **Graph Editor**.

The prediction interval, represented by the green whiskers extending from the overall diamond, provides a plausible range for the effect size in a future, new study.

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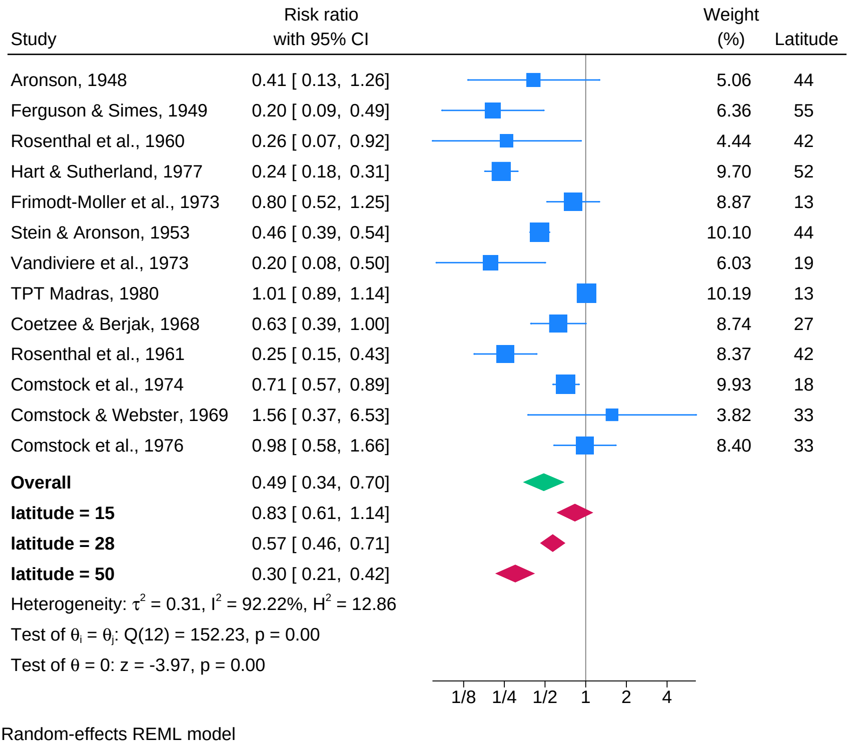
▷ Example 12: Adding custom columns and overall effect sizes

Consider example 2 of [META] **meta regress postestimation**. We will use the results of the `margins` command from that example to display overall effect sizes at the specified latitudes on the forest plot. This may be done by specifying multiple `customoverall()` options, as we show below.

We also add the `latitude` variable to the forest plot (as the last column) to show study effect sizes as a function of that variable. And we swap the `_esci` and `_plot` columns compared with the default forest plot.

```
. local col mcolor("stred")
. meta forest _id _esci _plot _weight latitude, nullrefline
> columnopts(latitude, title("Latitude"))
> customoverall(-.184 -.495  .127, label("{bf:latitude = 15}") ‘col’)
> customoverall(-.562 -.776 -.348, label("{bf:latitude = 28}") ‘col’)
> customoverall(-1.20 -1.54 -.867, label("{bf:latitude = 50}") ‘col’)
> rr
```



The latitude-specific overall effect sizes from the meta-regression model are shown as red diamonds (`stred` is the red associated with the `stcolor` scheme). In the `customoverall()` options, we specified the values of log risk-ratios, effect sizes in the estimation metric. But because we used the `rr` option, `meta forestplot` displayed the overall diamonds as risk ratios. For example, the mean risk ratio for studies conducted at `latitude` $= 50$ is roughly 0.30 with a CI of $[0.2, 0.4]$.

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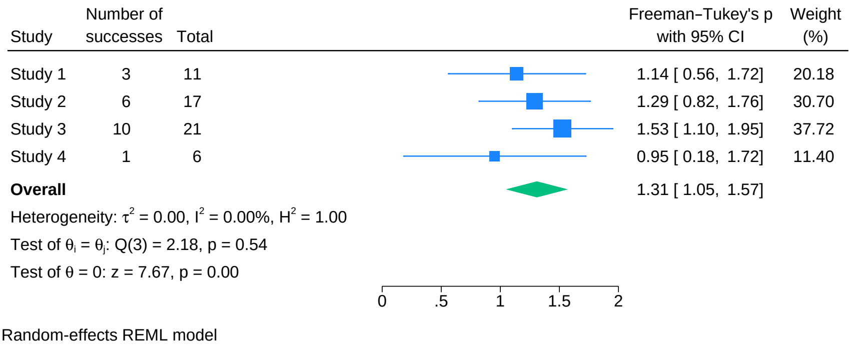
▷ Example 13: Forest plot for meta-analysis of a single proportion

Continuing from the meta esize ndeaths pensize setting in example 4 of [META] **meta data**, we will construct a forest plot to summarize our meta-analysis.

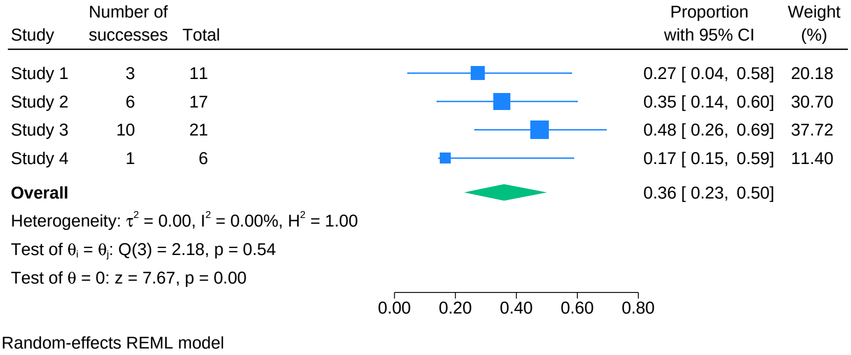
```
. meta forestplot
```



By default, the data displayed on the forest plot for pooling proportions are very similar to those displayed on a forest plot for two-sample binary data; see example 1. The only difference here is the summary data columns. Here _data corresponds to the number of events/successes (column _e, labeled as Number of successes on the forest plot) and the study sample size (column _n, labeled as Total). The displayed effect sizes are Freeman–Tukey-transformed proportions.

Below, we report our results as proportions using the proportion option. When the effect sizes are the Freeman–Tukey-transformed proportions, this option is equivalent to specifying option transform(invftukey, hmean).

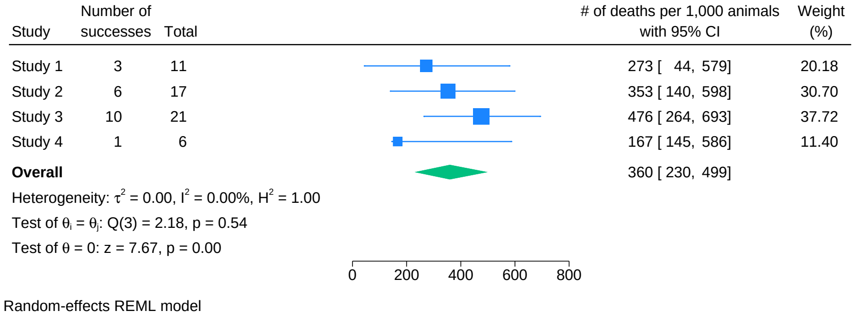
```
. meta forestplot, proportion
```



One unique characteristic of forest plots based on Freeman–Tukey-transformed proportions is that when you back-transform the effect sizes and their CIs (to report proportions), the back-transformed CIs are no longer symmetric. This is different from two-sample binary data with log odds-ratios or log risk-ratios as effect sizes. When you back-transform (exponentiate) these effect sizes to report odds ratios or risk ratios, the axis labels are also exponentiated to maintain the graphical representation of the CIs as symmetric. This is not possible for the one-sample case when the effect size is ftukeyprop because the back-transformation (the inverse Freeman–Tukey function) depends on sample size n; see *Inverse Freeman–Tukey transformation* in *Methods and formulas* in [META] **meta summarize**. The sample size varies between the studies, making it impossible to apply one transformation to the axis labels to make all study CIs symmetric. Therefore, if option proportion or transform(invftukey) is specified, no transformation is applied to the x-axis labels, and the plotted CIs for proportions will no longer be symmetric.

Next, we will use the scale(1000) suboption of transform(invftukey) to report our results as the number of deaths per 1,000 animals. We will also report the effect sizes and their CIs as integers using the format(%3.0f) suboption of columnopts(_esci).

```
. meta forestplot,
> transform("# of deaths per 1,000 animals": invftukey, scale(1000))
> xlabel(, format(%3.0f)) columnopts(_esci, format(%3.0f))
```



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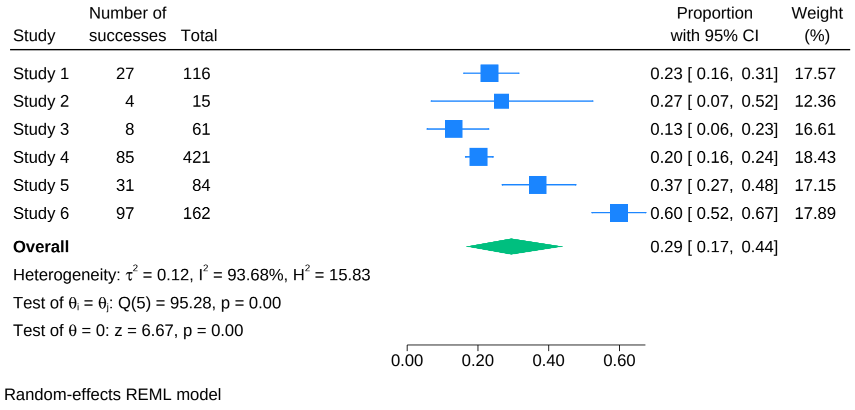
▷ Example 14: Increasing plot-region margin

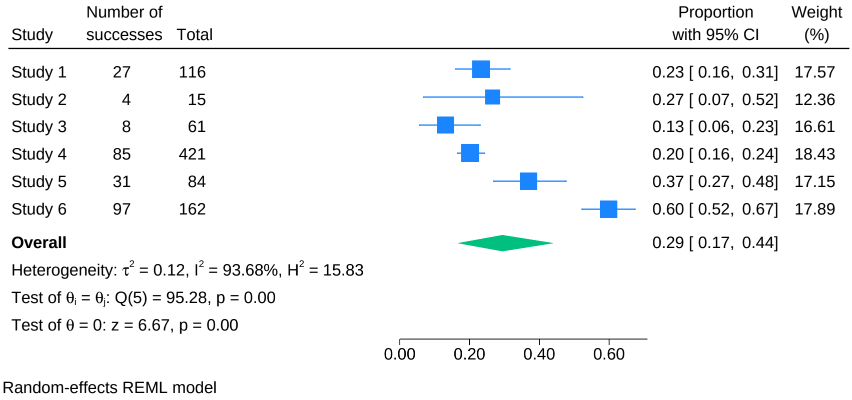
Continuing with example 8 of [META] **meta esize**, we will construct a forest plot to summarize our meta-analysis. It is quite common with forest plots of proportions for some study CIs in the _plot column to be very close to the _esci column (see Study 6 in our example).

```
. meta forestplot, proportion
```



Below, we increase the margin between the plot region of column _plot and that of column _esci using the columnopts(_plot, plotregion(margin(right))) option.

```
. meta forestplot, proportion columnopts(_plot, plotregion(margin(right)))
```



Study	Number of successes	Total	Proportion with 95% CI	Weight (%)
Study 1	27	116	0.23 [0.16, 0.31]	17.57
Study 2	4	15	0.27 [0.07, 0.52]	12.36
Study 3	8	61	0.13 [0.06, 0.23]	16.61
Study 4	85	421	0.20 [0.16, 0.24]	18.43
Study 5	31	84	0.37 [0.27, 0.48]	17.15
Study 6	97	162	0.60 [0.52, 0.67]	17.89
Overall			0.29 [0.17, 0.44]	

Heterogeneity: $\tau^2 = 0.12$, $I^2 = 93.68\%$, $H^2 = 15.83$

Test of $\theta_i = \theta_j$: Q(5) = 95.28, p = 0.00

Test of $\theta = 0$: z = 6.67, p = 0.00

Random-effects REML model

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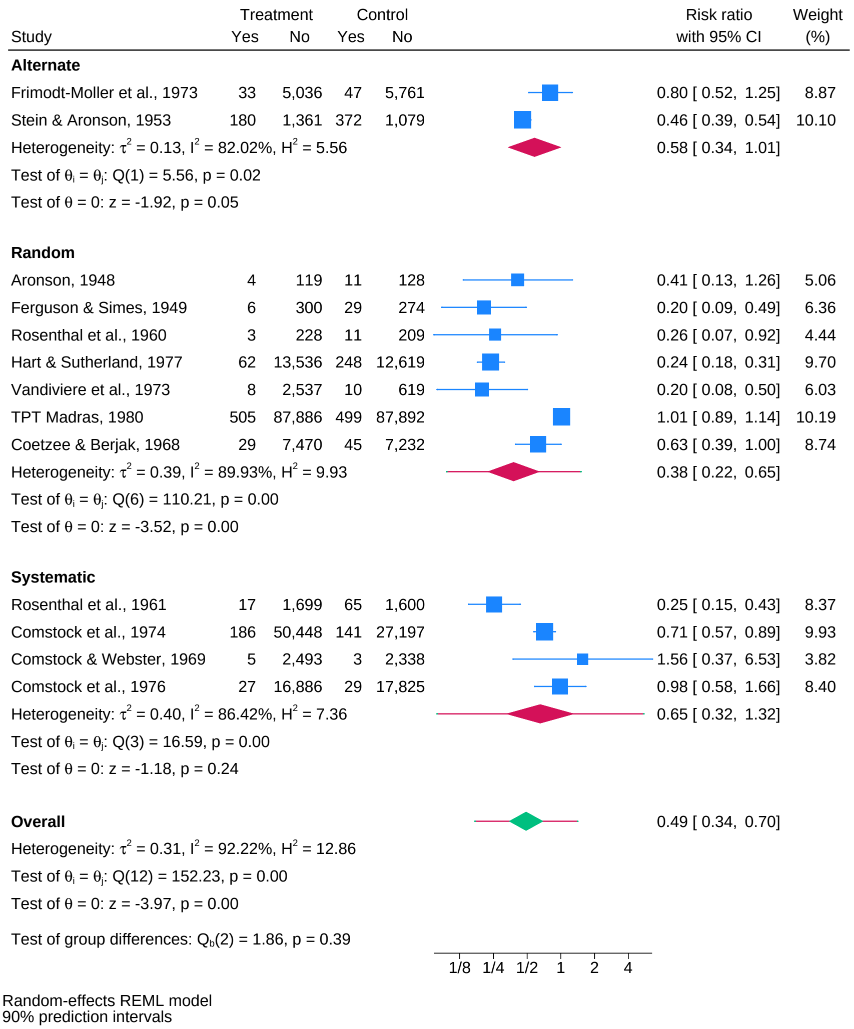
▷ Example 15: Prediction intervals with subgroup analysis and eliminating space in the _esci column

Continuing with example 2, we will add a 90% prediction interval within each subgroup. Notice that a predication interval is defined only when there are at least three studies; therefore, it is not computable for the first subgroup (`Alternate`).

```
. meta forest, subgroup(alloc) rr predinterval(90, lcolor(stred))
```

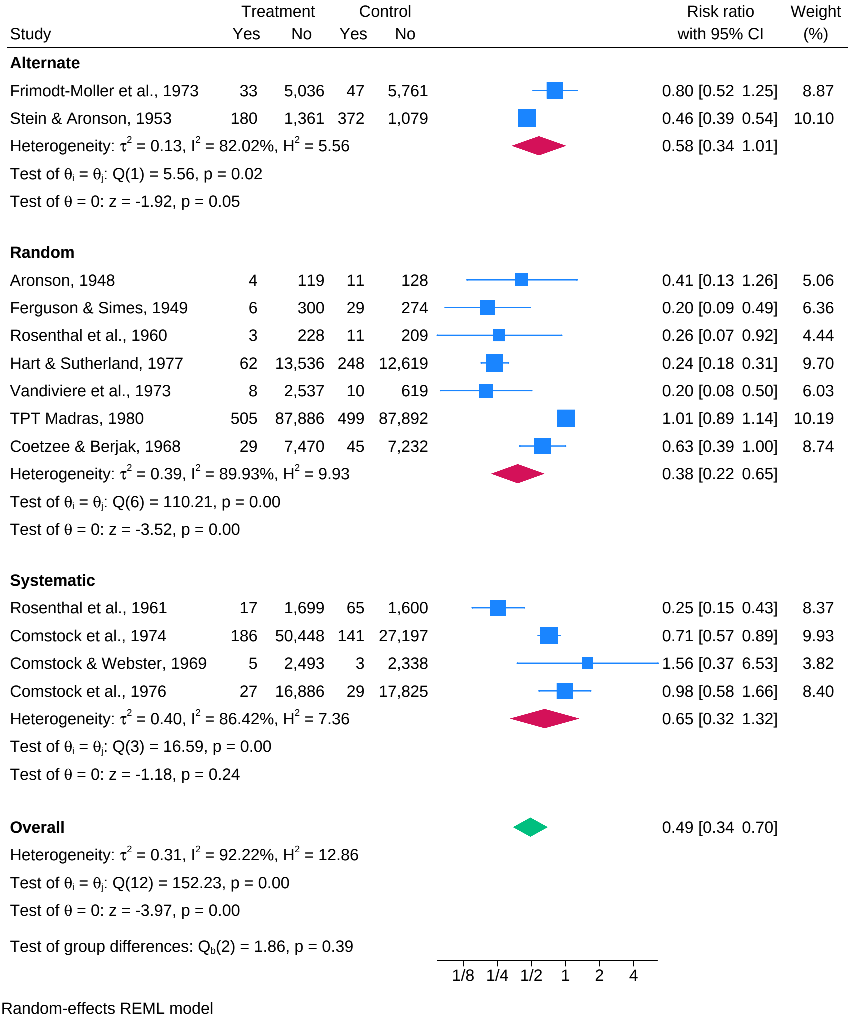


	Treatment		Control		Risk ratio	Weight
Study	Yes	No	Yes	No	with 95% CI	(%)
Alternate						
Frimodt-Moller et al., 1973	33	5,036	47	5,761	0.80 [0.52, 1.25]	8.87
Stein & Aronson, 1953	180	1,361	372	1,079	0.46 [0.39, 0.54]	10.10
Heterogeneity: $\tau^2 = 0.13$, $I^2 = 82.02\%$, $H^2 = 5.56$					0.58 [0.34, 1.01]	
Test of $\theta_i = \theta_j$: Q(1) = 5.56, p = 0.02						
Test of $\theta = 0$: z = -1.92, p = 0.05						
Random						
Aronson, 1948	4	119	11	128	0.41 [0.13, 1.26]	5.06
Ferguson & Simes, 1949	6	300	29	274	0.20 [0.09, 0.49]	6.36
Rosenthal et al., 1960	3	228	11	209	0.26 [0.07, 0.92]	4.44
Hart & Sutherland, 1977	62	13,536	248	12,619	0.24 [0.18, 0.31]	9.70
Vandiviere et al., 1973	8	2,537	10	619	0.20 [0.08, 0.50]	6.03
TPT Madras, 1980	505	87,886	499	87,892	1.01 [0.89, 1.14]	10.19
Coetzee & Berjak, 1968	29	7,470	45	7,232	0.63 [0.39, 1.00]	8.74
Heterogeneity: $\tau^2 = 0.39$, $I^2 = 89.93\%$, $H^2 = 9.93$					0.38 [0.22, 0.65]	
Test of $\theta_i = \theta_j$: Q(6) = 110.21, p = 0.00						
Test of $\theta = 0$: z = -3.52, p = 0.00						
Systematic						
Rosenthal et al., 1961	17	1,699	65	1,600	0.25 [0.15, 0.43]	8.37
Comstock et al., 1974	186	50,448	141	27,197	0.71 [0.57, 0.89]	9.93
Comstock & Webster, 1969	5	2,493	3	2,338	1.56 [0.37, 6.53]	3.82
Comstock et al., 1976	27	16,886	29	17,825	0.98 [0.58, 1.66]	8.40
Heterogeneity: $\tau^2 = 0.40$, $I^2 = 86.42\%$, $H^2 = 7.36$					0.65 [0.32, 1.32]	
Test of $\theta_i = \theta_j$: Q(3) = 16.59, p = 0.00						
Test of $\theta = 0$: z = -1.18, p = 0.24						
Overall					0.49 [0.34, 0.70]	
Heterogeneity: $\tau^2 = 0.31$, $I^2 = 92.22\%$, $H^2 = 12.86$						
Test of $\theta_i = \theta_j$: Q(12) = 152.23, p = 0.00						
Test of $\theta = 0$: z = -3.97, p = 0.00						
Test of group differences: $Q_b(2) = 1.86$, p = 0.39						

Random-effects REML model
90% prediction intervals

Next, we will eliminate the space in the _esci column right after the left bracket of the effect-size CI. This is done by removing the default binding of the CIs using option cibind(none) and specifying our own custom binding for columns _lb and _ub as follows:

```
. meta forest, subgroup(alloc) rr
> columnopts(_lb, mask("[%4.2f"))
> columnopts(_ub, mask("%4.2f]")) cibind(none)
```



Study	Treatment Yes	Treatment No	Control Yes	Control No	Risk ratio with 95% CI	Weight (%)
Alternate						
Frimodt-Moller et al., 1973	33	5,036	47	5,761	0.80 [0.52 1.25]	8.87
Stein & Aronson, 1953	180	1,361	372	1,079	0.46 [0.39 0.54]	10.10
Heterogeneity: $\tau^2 = 0.13$, $I^2 = 82.02\%$, $H^2 = 5.56$					0.58 [0.34 1.01]	
Test of $\theta_i = \theta_j$: Q(1) = 5.56, p = 0.02						
Test of $\theta = 0$: z = -1.92, p = 0.05						
Random						
Aronson, 1948	4	119	11	128	0.41 [0.13 1.26]	5.06
Ferguson & Simes, 1949	6	300	29	274	0.20 [0.09 0.49]	6.36
Rosenthal et al., 1960	3	228	11	209	0.26 [0.07 0.92]	4.44
Hart & Sutherland, 1977	62	13,536	248	12,619	0.24 [0.18 0.31]	9.70
Vandiviere et al., 1973	8	2,537	10	619	0.20 [0.08 0.50]	6.03
TPT Madras, 1980	505	87,886	499	87,892	1.01 [0.89 1.14]	10.19
Coetzee & Berjak, 1968	29	7,470	45	7,232	0.63 [0.39 1.00]	8.74
Heterogeneity: $\tau^2 = 0.39$, $I^2 = 89.93\%$, $H^2 = 9.93$					0.38 [0.22 0.65]	
Test of $\theta_i = \theta_j$: Q(6) = 110.21, p = 0.00						
Test of $\theta = 0$: z = -3.52, p = 0.00						
Systematic						
Rosenthal et al., 1961	17	1,699	65	1,600	0.25 [0.15 0.43]	8.37
Comstock et al., 1974	186	50,448	141	27,197	0.71 [0.57 0.89]	9.93
Comstock & Webster, 1969	5	2,493	3	2,338	1.56 [0.37 6.53]	3.82
Comstock et al., 1976	27	16,886	29	17,825	0.98 [0.58 1.66]	8.40
Heterogeneity: $\tau^2 = 0.40$, $I^2 = 86.42\%$, $H^2 = 7.36$					0.65 [0.32 1.32]	
Test of $\theta_i = \theta_j$: Q(3) = 16.59, p = 0.00						
Test of $\theta = 0$: z = -1.18, p = 0.24						
Overall					0.49 [0.34 0.70]	
Heterogeneity: $\tau^2 = 0.31$, $I^2 = 92.22\%$, $H^2 = 12.86$						
Test of $\theta_i = \theta_j$: Q(12) = 152.23, p = 0.00						
Test of $\theta = 0$: z = -3.97, p = 0.00						
Test of group differences: $Q_b(2) = 1.86$, p = 0.39						

Random-effects REML model

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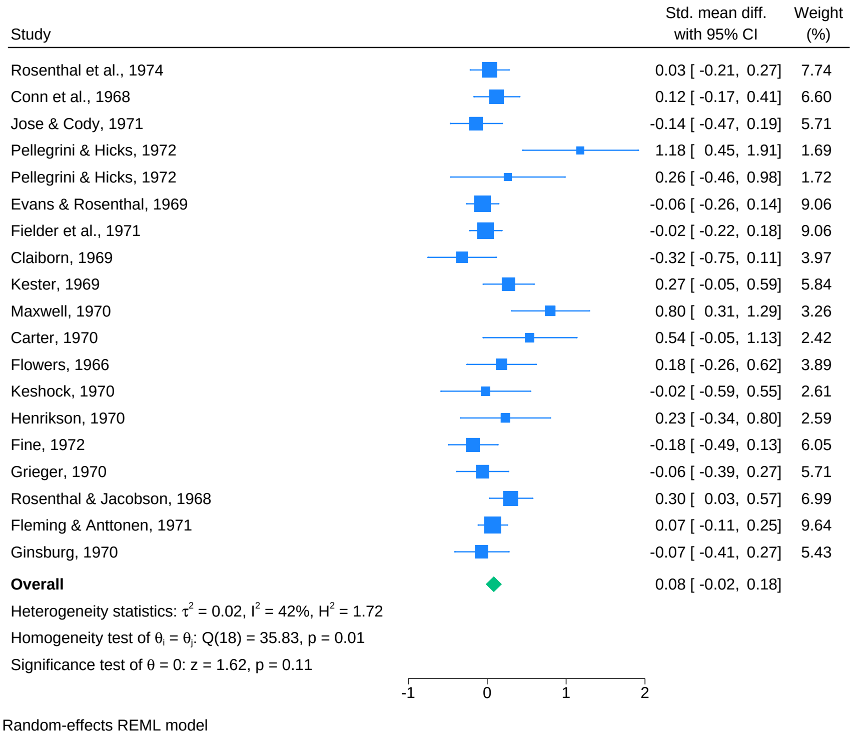
▷ Example 16: Modifying default text for heterogeneity statistics and statistical tests

Continuing with example 5, we will modify the default text reported in the three lines under `Overall` using options `ohetstatstext()` (for the first line), `ohomtesttext()` (for the second line), and `osigtesttext()` (for the third line). We will be slightly more descriptive about the type of information reported in each line and report the I^2 statistic without decimal points.

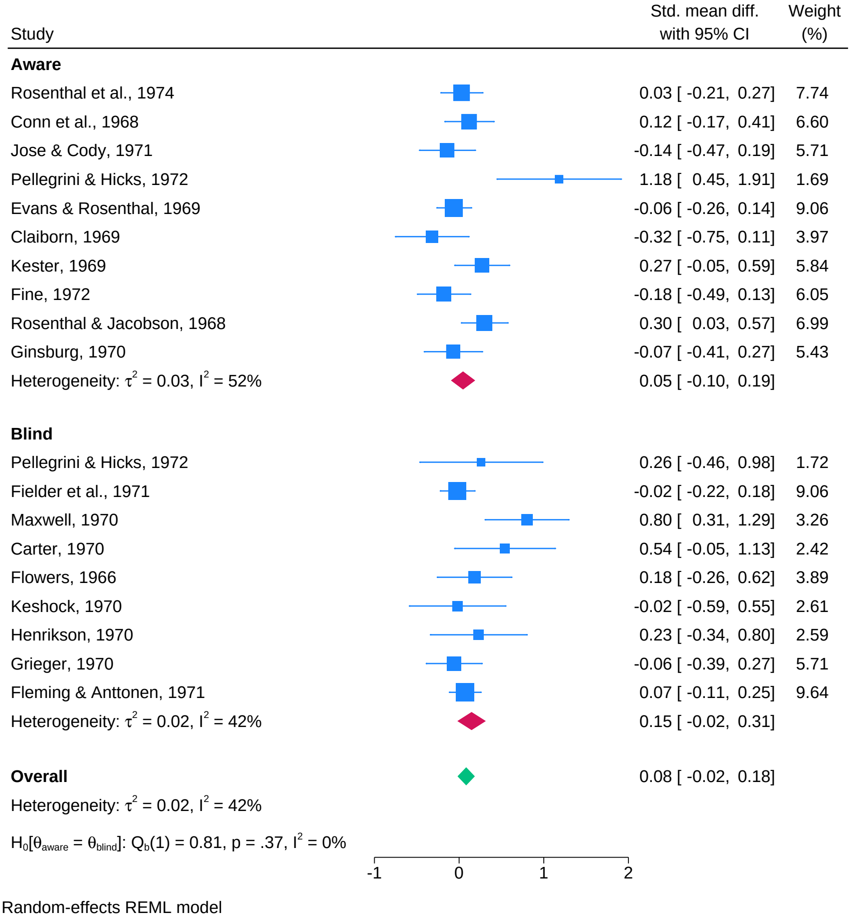
```
. use https://www.stata-press.com/data/r18/pupiliqset, clear
(Effects of teacher expectancy on pupil IQ; set with -meta set-)

. local hstats "Heterogeneity statistics:"

. local htest "Homogeneity test of {&theta}{sub:i} = {&theta}{sub:j}:"

. local stest "Significance test of {&theta} = 0:"

. meta forest,
> ohetstatstext("‘hstats’ {&tau}{sup:2} = 0.02, I{sup:2} = 42%, H{sup:2} = 1.72")
> ohomtesttext("‘htest’ Q(18) = 35.83, p = 0.01")
> osigtesttext("‘stest’ z = 1.62, p = 0.11")
```



Next, we will construct a subgroup forest plot based on variable `tester` (`aware` versus `blind`). See example 2 for a detailed description of the subgroup forest plot.

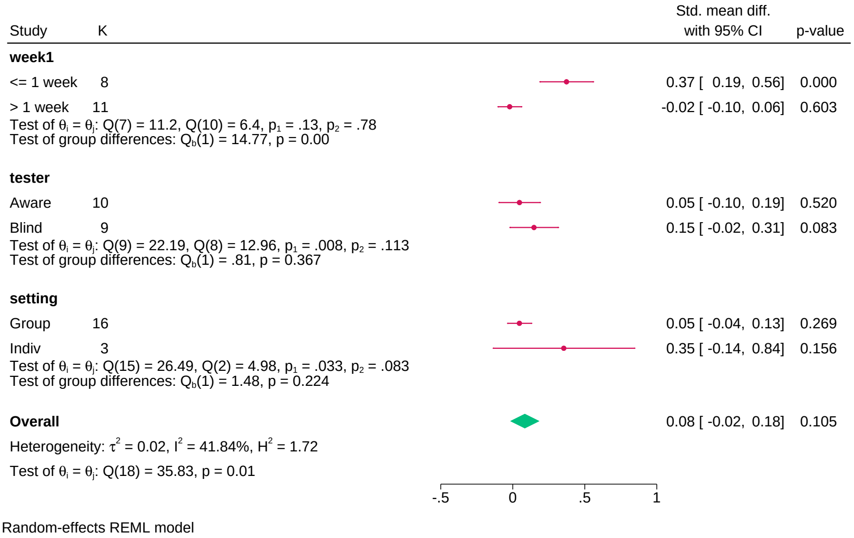
We will suppress the within-group homogeneity tests (option `nogwhomtests`) and the tests of significance for the group-specific overall effect sizes (option `nogsigtests`). We also use options `noohomtest` and `noosigtest` to suppress the same information for the overall analysis. We will report only τ^2 and I^2 in the overall heterogeneity statistics (option `ohetstatstext()`) and in the group-specific heterogeneity statistics (by repeating the `ghetstats#text()` option for each subgroup). Finally, we use option `gbhomtest1text()` to modify the description of the between-group homogeneity test and label it as $H_0 : \theta_{\text{aware}} = \theta_{\text{blind}}$ and report the I^2 statistic corresponding to the Q_b test statistic. The I^2 statistic is computed as follows: $I^2 = 100 \times \max\{0, 1 - (L-1)/Q_b\}$, where L is the number of subgroups ($L = 2$ in this example).

```
. local H0txt "H{sub:0}[{&theta}{sub:aware} = {&theta}{sub:blind}]:"
. local H0stats "Q{sub:b}(1) = 0.81, p = .37, I{sup:2} = 0% "
. meta forest, subgroup(tester) nogsigtests noosigtest nogwhomtests noohomtest
> ghetstats1text("Heterogeneity: {&tau}{sup:2} = 0.03, I{sup:2} = 52%")
> ghetstats2text("Heterogeneity: {&tau}{sup:2} = 0.02, I{sup:2} = 42%")
> ohetstatstext("Heterogeneity: {&tau}{sup:2} = 0.02, I{sup:2} = 42%")
> gbhomtest1text("‘H0txt’ ‘H0stats’")
```



Finally, we will construct a multiple subgroup-analyses forest plot based on variables `week1`, `tester`, and `setting`. See example 6 for the interpretation of this type of forest plot. By default, only information regarding the between-group homogeneity tests is reported for each variable. We will use option `gbhomtest#text()` (corresponding to the #th variable in `subgroup()`) to display the same default information regarding the between-group homogeneity test, but we now add an additional line reporting the within-group homogeneity tests for the groups defined by each variable. This is done by specifying two strings within the `gbhomtest#text()` option, one for each line. The within-group homogeneity test information may be obtained from the second table in the output of `meta summarize, subgroup(week1 tester setting)`.

```
. local Qdesc "Test of {&theta}{sub:i} = {&theta}{sub:j}:"
. local Qbdesc "Test of group differences: Q{sub:b}(1) ="
. meta forest, subgroup(week1 tester setting)
> gbhomtest1text( "‘Qdesc’ Q(7) = 11.2, Q(10) = 6.4, p{sub:1} = .13, p{sub:2} = .78"
>     "‘Qbdesc’ 14.77, p = 0.00")
> gbhomtest2text("‘Qdesc’ Q(9) = 22.19, Q(8) = 12.96, p{sub:1} = .008, p{sub:2} = .113"
>     "‘Qbdesc’ .81, p = 0.367")
> gbhomtest3text("‘Qdesc’ Q(15) = 26.49, Q(2) = 4.98, p{sub:1} = .033, p{sub:2} = .083"
>     "‘Qbdesc’ 1.48, p = 0.224")
```



◁

Methods and formulas

Methods and formulas for the statistics reported by `meta forestplot` are given in *Methods and formulas* of [META] **meta summarize**.

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Also see

[META] **meta data** — Declare meta-analysis data

[META] **meta galbraithplot** — Galbraith plots

[META] **meta labbeplot** — L’Abbé plots

[META] **meta summarize** — Summarize meta-analysis data+

[META] **meta** — Introduction to meta

[META] **Glossary**

[META] **Intro** — Introduction to meta-analysis