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Description

`meta labbeplot` produces L'Abbé plots for a meta-analysis that compares the binary outcomes of two groups. These plots are useful for assessing heterogeneity and comparing study-specific event rates in the two groups.

Quick start

Construct a L'Abbé plot based on the effect size for two-sample binary data computed by `meta esize`

```
meta labbeplot
```

Same as above, but request that the overall effect size be computed using a random-effects REML method instead of the default common-effect inverse-variance method

```
meta labbeplot, random(reml)
```

Same as above, but specify that study-marker sizes be proportional to weights from a random-effects model instead of the default common-effect model

```
meta labbeplot, random(reml) reweighted
```

Modify the default looks of the reference line and the overall effect-size line

```
meta labbeplot, rlopts(lcolor(red)) esopts(lpattern(solid))
```

Menu

Statistics > Meta-analysis

Syntax

```
meta labbeplot [ if ] [ in ] [ , options ]
```

options	Description
Main	
random[(<i>remethod</i>)]	random-effects meta-analysis
common[(<i>cefemethod</i>)]	common-effect meta-analysis
fixed[(<i>cefemethod</i>)]	fixed-effects meta-analysis
reweighted	make bubble size depend on random-effects weights
[no]metashow	display or suppress meta settings in the output
<i>graph_options</i>	affect rendition of overall L'Abbé plot
collect is allowed; see [U] 11.1.10 Prefix commands.	
<i>remethod</i>	Description
reml	restricted maximum likelihood; the default
mle	maximum likelihood
ebayes	empirical Bayes
dlaird	DerSimonian–Laird
sjonkman	Sidik–Jonkman
hedges	Hedges
hschmidt	Hunter–Schmidt
<i>cefemethod</i>	Description
mhaenszel	Mantel–Haenszel
invvariance	inverse variance
ivariance	synonym for invvariance
<i>graph_options</i>	Description
RL options	
rlopts(<i>line_options</i>)	affect rendition of the plotted reference line indicating no effect
ES options	
esopts(<i>line_options</i>)	affect rendition of the plotted estimated effect-size line
Add plots	
addplot(<i>plot</i>)	add other plots to the contour plot
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than by() documented in [G-3] <i>twoway_options</i>

Options

Main

Options `random()`, `common()`, and `fixed()` specify a meta-analysis model to use when estimating the overall effect size. For historical reasons, the default is `common(invvariance)`, regardless of the global model declared by `meta esize`. Specify one of these options with `meta labbeplot` to override this default. Options `random()`, `common()`, and `fixed()` may not be combined. Also see [Meta-analysis models](#) in [META] [Intro](#).

`random` and `random(remethod)` specify that a random-effects model be assumed for meta-analysis; see [Random-effects model](#) in [META] [Intro](#).

remethod specifies the type of estimator for the between-study variance τ^2 . *remethod* is one of `reml`, `mle`, `ebayes`, `dlaire`, `sjonkman`, `hedges`, or `hschmidt`. `random` is a synonym for `random(reml)`. See [Options](#) in [META] [meta esize](#) for more information.

`common` and `common(cefemethod)` specify that a common-effect model be assumed for meta-analysis; see [Common-effect \(“fixed-effect”\) model](#) in [META] [Intro](#). Also see the [discussion](#) in [META] [meta data](#) about common-effect versus fixed-effects models.

`common` implies `common(mhaenszel)`.

cefemethod is one of `mhaenszel` or `invvariance` (synonym `ivariance`). See [Options](#) in [META] [meta esize](#) for more information.

`fixed` and `fixed(cefemethod)` specify that a fixed-effects model be assumed for meta-analysis; see [Fixed-effects model](#) in [META] [Intro](#). Also see the [discussion](#) in [META] [meta data](#) about fixed-effects versus common-effect models.

`fixed` implies `fixed(mhaenszel)`.

cefemethod is one of `mhaenszel` or `invvariance` (synonym `ivariance`); see [Options](#) in [META] [meta esize](#) for more information.

`reweighted` is used with random-effects meta-analysis. It specifies that the sizes of the bubbles be proportional to the weights from the random-effects meta-analysis, $w_j^* = 1/(\hat{\sigma}_j^2 + \hat{\tau}^2)$. By default, the sizes are proportional to the precision of each study, $w_j = 1/\hat{\sigma}_j^2$.

`metashow` and `nometashow` display or suppress the meta setting information. By default, this information is displayed at the top of the output. You can also specify `nometashow` with `meta update` to suppress the meta setting output for the entire meta-analysis session.

RL options

`rlopts(line_options)` affects the rendition of the plotted reference (diagonal) line that indicates no effect of the intervention or treatment; see [G-3] [line_options](#).

ES options

`esopts(line_options)` affects the rendition of the dashed line that plots the estimated overall effect size; see [G-3] [line_options](#).

Add plots

`addplot(plot)` allows adding more graph twoway plots to the graph; see [G-3] [addplot_option](#).

Y axis, X axis, Titles, Legend, Overall

`twoway_options` are any of the options documented in [G-3] [twoway_options](#), excluding `by()`. These include options for titling the graph (see [G-3] [title_options](#)) and for saving the graph to disk (see [G-3] [saving_option](#)).

Remarks and examples

The L'Abbé plot (L'Abbé, Detsky, and O'Rourke 1987) is a scatterplot of the summary outcome measure such as log odds in the control group on the x axis and of that in the treatment group on the y axis. This plot is used with two-sample binary data declared by `meta esize`. The plotted summary outcome measure depends on the chosen effect size. It is log odds when the effect size is log odds-ratio, log risk when the effect size is log risk-ratio, and risk when the effect size is risk difference. The summary outcome measures are plotted as circles with their sizes (areas) proportional to study precisions. The plot also contains a reference (diagonal) line, which indicates identical outcomes in the two groups and thus represents no effect, and the estimated overall effect-size line.

The L'Abbé plot explores between-study heterogeneity by comparing group-level summary outcome measures across studies. It can also be used to determine which type of effect size is more homogeneous across studies. Compared with other meta-analysis graphs, one important advantage of the L'Abbé plot is that it displays the data on individual studies for each of the two groups. Thus, in addition to identifying outlying studies, it can also identify the outlying groups within studies. Also see Anzures-Cabrera and Higgins (2010) for more detail.

`meta labbeplot` produces L'Abbé plots. The plotted summary outcome measure is determined automatically based on the declared effect size. Unlike other `meta` commands, for historical reasons, `meta labbeplot` assumes a common-effect model with the inverse-variance method when computing the overall effect size to be plotted. You can use `random()`, `common()`, or `fixed()` to specify a different meta-analysis model or method. By default, `meta labbeplot` uses the precision weights, $1/\hat{\sigma}_j^2$, but, with a random-effects model, you can instead choose to use the random-effects weights, $1/(\hat{\sigma}_j^2 + \hat{\tau}^2)$. You can also control the look of the plotted reference and effect-size lines by specifying the `rlopts()` and `esopts()` options.

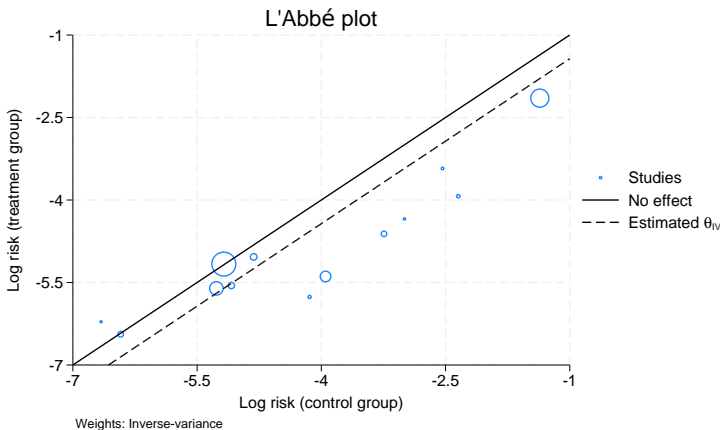
► Example 1: Basic L'Abbé plot

Consider the declared version of the BCG dataset, `bcgset.dta`, which we used in, for instance, [example 1](#) of [\[META\] meta regress](#). Let's produce the L'Abbé plot for these data.

```
. use https://www.stata-press.com/data/r19/bcgset
(Efficacy of BCG vaccine against tuberculosis; set with -meta esize-)

. meta labbeplot

Effect-size label: Log risk-ratio
  Effect size: _meta_es
   Std. err.: _meta_se
Summary data: npost nnegt nposc nnegc
      Model: Common effect
      Method: Inverse-variance
```



From the displayed meta settings, the declared effect size is a log risk-ratio. Thus, `meta labbeplot` plots the log risks on the scatterplot. The treatment-group log risk is on the y axis, and the control-group log risk is on the x axis. The sizes of the plotted markers (circles) are proportional to the precision of the trials. Large circles represent more precise, larger trials, whereas small circles represent less precise, smaller trials.

The solid reference line ($y = x$) represents the “no-effect” line. That is, the log risks (or risks) in the two groups for the trials on the line are either the same or very similar. There are two trials that are on the line in our example: one is a large trial, the other one is a small trial. The log risks for these trials are very similar in the two groups, and the corresponding log risk-ratios are close to zero.

If a circle is above the reference line, the risk in the treatment group is higher than the risk in the control group for that study. Conversely, if a circle is below the line, the risk in the treatment group is lower than the risk in the control group. In our example, one trial is above the reference line, suggesting that the risk in the treatment group is higher, but this is a very small trial. The remaining trials are below the line, suggesting that the risk is lower in the treatment group. However, the trials demonstrating large differences between the groups are also smaller (less precise) trials.

The dashed line is the overall effect-size line. The intercept of this line equals the estimate of the overall effect size, which is the overall log risk-ratio in our example. The actual estimate of the overall effect size is not important in the L'Abbé plot. What is important is whether the circles follow the effect-size line or deviate from it. When the circles deviate from the effect-size line greatly, this may be a sign of study heterogeneity. In our example, there are at least five trials that are far away from the effect-size

line. We should suspect the presence of heterogeneity in these data. In fact, we did establish in [example 1](#) of [\[META\] meta regress](#) that there is at least one moderator, the distance from the equator, that explains some of the variation in the trial effect sizes.

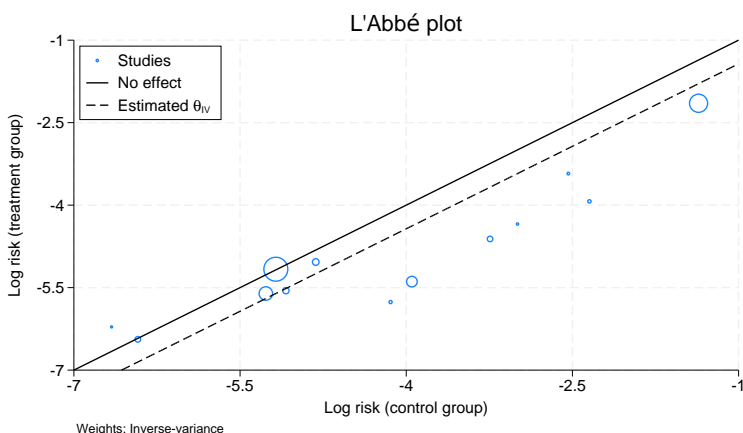


► Example 2: Custom legend

Continuing with [example 1](#), let's demonstrate how we can customize the look of the legend produced by default.

```
. meta labbeplot, legend(symxsize(*0.6) position(10) ring(0)
> region(lcolor(black)))
```

```
Effect-size label: Log risk-ratio
Effect size: _meta_es
Std. err.: _meta_se
Summary data: npost nnegt nposc nnegc
Model: Common effect
Method: Inverse-variance
```



We customized the legend with a few suboptions specified in `legend()`. We used `symxsize(*0.6)` to set the width of the key symbols to 60% of their default width. We used `position(10)` to position the label at 10 o'clock and `ring(0)` to place the legend inside the plot region. We used `region(lcolor(black))` to add a black border around the legend region.

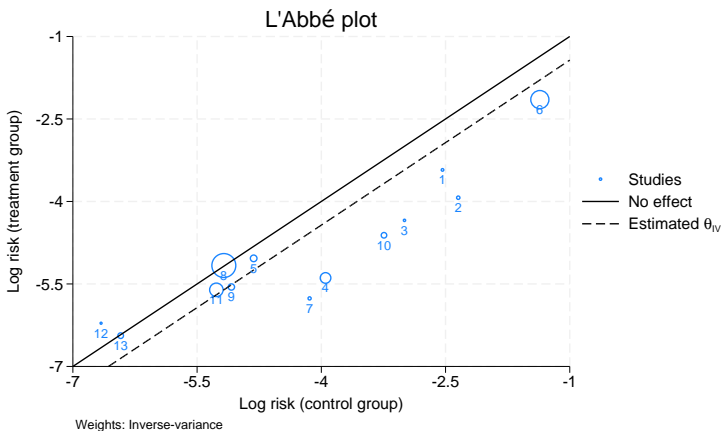


► Example 3: Labeling trials

Continuing with [example 1](#), let's say it would be nice to mark the circles with the trial labels. We use the `addplot()` option and follow similar steps to those described in [example 3](#) of [\[META\] estat bubbleplot](#), except here we generate new variables for the added scatterplot.

```
. generate double lnriskt = ln(npost/(npost + nnegt))
. generate double lnriskc = ln(nposc/(nposc + nnegc))
. local opts msymbol(none) mlabel(trial) mlabpos(6) mlabcolor(stblue)
. meta labbeplot, addplot(scatter lnriskt lnriskc, 'opts' legend(order(1 2 3)))

Effect-size label: Log risk-ratio
  Effect size: _meta_es
    Std. err.: _meta_se
Summary data: npost nnegt nposc nnegc
      Model: Common effect
      Method: Inverse-variance
```



First, we generated two new variables, `lnriskt` and `lnriskc`, that contain the log risks in the treatment and control groups. Then, we used `addplot()` to overlay the same scatterplot as produced by `meta labbeplot` but without the markers and with marker labels. We specified other options to improve the look of the graph; see [example 3](#) of [\[META\] estat bubbleplot](#) for details. Also see [example 4](#) of [\[META\] estat bubbleplot](#) for how to further improve the positioning of the labels.



Stored results

meta labbeplot stores the following in `r()`:

Scalars

<code>r(theta)</code>	estimated overall effect size
<code>r(xmin)</code>	minimum value in the control group (x axis)
<code>r(xmax)</code>	maximum value in the control group
<code>r(ymin)</code>	minimum value in the treatment group (y axis)
<code>r(ymax)</code>	maximum value in the treatment group

Macros

<code>r(model)</code>	meta-analysis model
<code>r(method)</code>	meta-analysis estimation method

Methods and formulas

Let a_j , b_j , c_j , and d_j define cell counts of a 2×2 table for study j ; see [Effect sizes for two-group comparison of binary outcomes](#) in [META] **meta esize**. Let y_j and x_j be the summary measures such as log odds for study j in the treatment and control groups. The L'Abbé plot produces a scatterplot of (y_j, x_j) with the sizes of markers (areas of circles) proportional to the weights $w_j = 1/\hat{\sigma}_j^2$ or, if `reweighted` is specified with a random-effects model, $w_j = 1/(\hat{\sigma}_j^2 + \hat{\tau}^2)$.

When the effect size is risk difference, y_j and x_j are the risks given by

$$y_j = \frac{a_j}{a_j + b_j} \quad \text{and} \quad x_j = \frac{c_j}{c_j + d_j}$$

When the effect size is log risk-ratio, y_j and x_j are the log risks given by

$$y_j = \log\left(\frac{a_j}{a_j + b_j}\right) \quad \text{and} \quad x_j = \log\left(\frac{c_j}{c_j + d_j}\right)$$

When the effect size is log odds-ratio, y_j and x_j are the log odds given by

$$y_j = \log\left(\frac{a_j}{b_j}\right) \quad \text{and} \quad x_j = \log\left(\frac{c_j}{d_j}\right)$$

The plotted reference line is the diagonal line. Studies that have the same values of the summary outcome measures in the two groups will have $y_j = x_j$ and thus will fall on the reference line.

The effect-size (dashed) line is a 45-degree line with an intercept equal to the estimated overall effect size. By default, the overall effect-size is estimated assuming a common-effect model with the inverse-variance method, but this can be changed by specifying one of `random()`, `common()`, or `fixed()`.

References

- Anzures-Cabrera, J., and J. P. T. Higgins. 2010. Graphical displays for meta-analysis: An overview with suggestions for practice. *Research Synthesis Methods* 1: 66–80. <https://doi.org/10.1002/jrsm.6>.
- L'Abbé, K. A., A. S. Detsky, and K. O'Rourke. 1987. Meta-analysis in clinical research. *Annals of Internal Medicine* Journal 107: 224–233. <https://doi.org/10.7326/0003-4819-107-2-224>.

Also see

- [META] **meta data** — Declare meta-analysis data
- [META] **meta esize** — Compute effect sizes and declare meta-analysis data
- [META] **meta forestplot** — Forest plots
- [META] **meta galbraithplot** — Galbraith plots
- [META] **meta regress** — Meta-analysis regression
- [META] **meta** — Introduction to meta
- [META] **Glossary**
- [META] **Intro** — Introduction to meta-analysis

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