

**meta esize** — Compute effect sizes and declare meta-analysis data

<a href="#">Description</a>	<a href="#">Quick start</a>	<a href="#">Menu</a>	<a href="#">Syntax</a>
<a href="#">Options</a>	<a href="#">Remarks and examples</a>	<a href="#">Stored results</a>	<a href="#">Methods and formulas</a>
<a href="#">References</a>	<a href="#">Also see</a>		

## Description

`meta esize` computes effect sizes from study summary data and uses the results to declare the data in memory to be `meta` data, informing Stata of key variables and their roles in a meta-analysis. It computes various effect sizes and their respective standard errors for two-group comparisons of continuous and binary outcomes. It then uses the computed effect sizes and standard errors to declare the data in memory to be `meta` data. If you do not have the summary data from individual studies and, instead, you have precalculated effect sizes, you can use `meta set` to declare your meta-analysis data. You must use `meta esize` or `meta set` to perform meta-analysis using the `meta` command; see [\[META\] meta data](#).

If you need to update some of the meta settings after the data declaration, see [\[META\] meta update](#). To display current meta settings, use `meta query`; see [\[META\] meta update](#).

## Quick start

Compute Hedges's  $g$  standardized mean differences and their standard errors from variables `nt` (sample size in treatment group), `meant` (mean of treatment group), `sdt` (standard deviation in treatment group), and their counterparts in the control group: `nc`, `meanc`, and `sd`

```
meta esize nt meant sdt nc meanc sdc
```

As above, but compute Cohen's  $d$  instead of the default Hedges's  $g$ , and use the DerSimonian–Laird estimation method instead of the default REML method

```
meta esize nt meant sdt nc meanc sdc, esize(cohend) random(dlaird)
```

Compute log odds-ratios and their standard errors from variables `nst` (number of successes in treatment group), `nft` (number of failures in treatment group), and their respective counterparts in control group: `nsc` and `nfc`

```
meta esize nst nft nsc nfc
```

As above, but compute the log risk-ratios instead of the default log odds-ratios

```
meta esize nst nft nsc nfc, esize(lnrratio)
```

As above, but request a common-effect meta-analysis

```
meta esize nst nft nsc nfc, esize(lnrratio) common
```

## Menu

Statistics > Meta-analysis

## Syntax

Compute and declare effect sizes for two-group comparison of continuous outcomes

```
meta esize n1 mean1 sd1 n2 mean2 sd2 [if] [in] [, options_continuous options]
```

Compute and declare effect sizes for two-group comparison of binary outcomes

```
meta esize n11 n12 n21 n22 [if] [in] [, options_binary options]
```

Variables *n1*, *mean1*, and *sd1* contain sample sizes, means, and standard deviations from individual studies for group 1 (treatment), and variables *n2*, *mean2*, and *sd2* contain the respective summaries for group 2 (control).

Variables *n11* and *n12* contain numbers of successes and numbers of failures from individual studies for group 1 (treatment), and variables *n21* and *n22* contain the respective numbers for group 2 (control). A single observation defined by variables *n11*, *n12*, *n21*, and *n22* represents a  $2 \times 2$  table from an individual study. Therefore, variables *n11*, *n12*, *n21*, and *n22* represent a sample of  $2 \times 2$  tables from all studies. We will thus refer to observations on these variables as  $2 \times 2$  tables and to values of these variables as cells.

<i>options_continuous</i>	Description
Main	
<b>esize</b> ( <i>esspecct</i> )	specify effect size for continuous outcome to be used in the meta-analysis

Model	
<b>random</b> [ ( <i>remethod</i> ) ]	random-effects meta-analysis; default is <b>random</b> ( <b>rem1</b> )
<b>common</b>	common-effect meta-analysis; implies inverse-variance method
<b>fixed</b>	fixed-effects meta-analysis; implies inverse-variance method

<i>options_binary</i>	Description
Main	
<b>esize</b> ( <i>estypebin</i> )	specify effect size for binary outcome to be used in the meta-analysis

Model	
<b>random</b> [ ( <i>remethod</i> ) ]	random-effects meta-analysis; default is <b>random</b> ( <b>rem1</b> )
<b>common</b> [ ( <i>cefemethod</i> ) ]	common-effect meta-analysis
<b>fixed</b> [ ( <i>cefemethod</i> ) ]	fixed-effects meta-analysis

Options	
<b>zerocells</b> ( <i>zcspec</i> )	adjust for zero cells during computation; default is to add 0.5 to all cells of those $2 \times 2$ tables that contain zero cells

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<i>options</i>	Description
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Options

<u>studylabel</u> ( <i>varname</i> )	variable to be used to label studies in all meta-analysis output
<u>eslabel</u> ( <i>string</i> )	effect-size label to be used in all meta-analysis output; default is <code>eslabel(Effect Size)</code>
<u>level</u> (#)	confidence level for all subsequent meta-analysis commands
[ <u>no</u> ] <u>metashow</u>	display or suppress meta settings with other meta commands

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The syntax of *esspecnt* is
$$estypecnt \left[ , esopts \right]$$

<i>estypecnt</i>	Description
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<u>hedgesg</u>	Hedges's $g$ standardized mean difference; the default
<u>cohend</u>	Cohen's $d$ standardized mean difference
<u>glassdelta2</u>	Glass's $\Delta$ mean difference standardized by group 2 (control) standard deviation; more common than <code>glassdelta1</code>
<u>glassdelta1</u>	Glass's $\Delta$ mean difference standardized by group 1 (treatment) standard deviation
<u>mdiff</u>	(unstandardized) mean difference

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<i>estypebin</i>	Description
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<u>lnoratio</u>	log odds-ratio; the default
<u>lnrratio</u>	log risk-ratio (also known as log rate-ratio and log relative-risk)
<u>rdiff</u>	risk difference
<u>lnorpeto</u>	Peto's log odds-ratio

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<i>remethod</i>	Description
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<u>reml</u>	restricted maximum likelihood; the default
<u>mle</u>	maximum likelihood
<u>ebayes</u>	empirical Bayes
<u>dlaird</u>	DerSimonian–Laird
<u>sjonkman</u>	Sidik–Jonkman
<u>hedges</u>	Hedges
<u>hschmidt</u>	Hunter–Schmidt

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<i>cefemethod</i>	Description
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<u>mhaenszel</u>	Mantel–Haenszel
<u>invvariance</u>	inverse variance
<u>ivariance</u>	synonym for <code>invvariance</code>

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## Options

### Main

`esize(esspec)` specifies the effect size to be used in the meta-analysis. For continuous outcomes, *esspec* is `estypecnt` [ , `esopts` ]. For binary outcomes, *esspec* is `estypebin`.

For continuous outcomes, *estypecnt* is one of the following: `hedgesg`, `cohend`, `glassdelta2`, `glassdelta1`, or `mdiff`. Below, we describe each type with its specific options, *esopts*.

`hedgesg` [ , `exact` `holkinse` ] computes the effect size as the Hedges's *g* (1981) standardized mean difference. This is the default for continuous outcomes. For consistency with meta-analysis literature, `hedgesg` uses an approximation to compute *g* rather than the exact computation (see *Methods and formulas*), as provided by `esize`'s option `hedgesg`. You can use the `exact` suboption to match the results from `esize` (see [R] `esize`).

`cohend` [ , `holkinse` ] computes the effect size as the Cohen's *d* (1969, 1988) standardized mean difference.

`glassdelta2` computes the effect size as the Glass's  $\Delta$  standardized mean difference, where the standardization uses the standard deviation of the group 2 (control group). `glassdelta2` is more common in practice than `glassdelta1`.

`glassdelta1` computes the effect size as the Glass's  $\Delta$  standardized mean difference, where the standardization uses the standard deviation of the group 1 (treatment group). `glassdelta2` is more common in practice than `glassdelta1`.

`mdiff` [ , `unequal` ] computes the effect size as the unstandardized or raw mean difference.

*esopts* are `exact`, `holkinse`, and `unequal`.

`exact` specifies that the exact computation be used for the bias-correction factor in Hedges's *g* instead of an approximation used by default.

`holkinse` specifies that the standard error of Hedges's *g* and Cohen's *d* be computed as described in Hedges and Olkin (1985). This is another approximation to the standard error of these effect sizes sometimes used in practice.

`unequal` specifies that the computation of the standard error of the mean difference (`esize(mdiff)`) assume unequal group variances.

For binary outcomes, *estypebin* is one of the following: `lnoratio`, `lnrratio`, `rdiff`, or `lnorpeto`.

`lnoratio` specifies that the effect size be the log odds-ratio. This is the default for binary outcomes.

`lnrratio` specifies that the effect size be the log risk-ratio, also known as a log relative-risk and a log risk-rate.

`rdiff` specifies that the effect size be the risk difference.

`lnorpeto` specifies that the effect size be the log odds-ratio as defined by Peto et al. (1977). This effect size is preferable with rare events.

For effect sizes in the log metric such as log odds-ratios, the results by default are displayed in the log metric. You can use *eform\_option* to obtain exponentiated results such as odds ratios.

### Model

Options `random()`, `common()`, and `fixed()` declare the meta-analysis model globally throughout the entire meta-analysis; see *Declaring a meta-analysis model* in [META] `meta data`. In other words, once you set your meta-analysis model using `meta esize`, all subsequent `meta` commands will assume

that same model. You can update the declared model by using `meta update` or change it temporarily by specifying the corresponding option with the `meta` commands. Options `random()`, `common()`, and `fixed()` may not be combined. If these options are omitted, `random(reml)` is assumed; see *Default meta-analysis model and method* in [META] **meta data**. 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  $\tau^2$ . *remethod* is one of `reml`, `mle`, `ebayes`, `dlaird`, `sjonkman`, `hedges`, or `hschmidt`. `random` is a synonym for `random(reml)`. Below, we provide a short description for each method based on Veroniki et al. (2016). Also see *Declaring a meta-analysis estimation method* in [META] **meta data**.

`reml`, the default, specifies that the REML method (Raudenbush 2009) be used to estimate  $\tau^2$ .

This method produces an unbiased, nonnegative estimate of the between-study variance and is commonly used in practice. Method `reml` requires iteration.

`mle` specifies that the ML method (Hardy and Thompson 1996) be used to estimate  $\tau^2$ . It produces a nonnegative estimate of the between-study variance. With a few studies or small studies, this method may produce biased estimates. With many studies, the ML method is more efficient than the REML method. Method `mle` requires iteration.

`ebayes` specifies that the empirical Bayes estimator (Berkey et al. 1995), also known as the Paule–Mandel estimator (Paule and Mandel 1982), be used to estimate  $\tau^2$ . From simulations, this method, in general, tends to be less biased than other random-effects methods, but it is also less efficient than `reml` or `dlaird`. Method `ebayes` produces a nonnegative estimate of  $\tau^2$  and requires iteration.

`dlaird` specifies that the DerSimonian–Laird method (DerSimonian and Laird 1986) be used to estimate  $\tau^2$ . This method, historically, is one of the most popular estimation methods because it does not make any assumptions about the distribution of random effects and does not require iteration. But it may underestimate the true between-study variance, especially when the variability is large and the number of studies is small. This method may produce a negative value of  $\tau^2$  and is thus truncated at zero in that case.

`sjonkman` specifies that the Sidik–Jonkman method (Sidik and Jonkman 2005) be used to estimate  $\tau^2$ . This method always produces a nonnegative estimate of the between-study variance and thus does not need truncating at 0, unlike the other noniterative methods. Method `sjonkman` does not require iteration.

`hedges` specifies that the Hedges method (Hedges 1983) be used to estimate  $\tau^2$ . When the sampling variances of effect-size estimates can be estimated without bias, this estimator is exactly unbiased (before truncation), but it is not widely used in practice (Veroniki et al. 2016). Method `hedges` does not require iteration.

`hschmidt` specifies that the Hunter–Schmidt method (Schmidt and Hunter 2015) be used to estimate  $\tau^2$ . Although this estimator achieves a lower MSE than other methods, except ML, it is known to be negatively biased. Method `hschmidt` does not require iteration.

`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)` for effect sizes `lnoratio`, `lnrratio`, and `rdiff` and `common(invvariance)` for all other effect sizes.

*cefemethod* is one of `mhaenszel` or `invvariance` (synonym `ivariance`). Below, we provide a short description for each method. Also see [Declaring a meta-analysis estimation method in \[META\] meta data](#).

`mhaenszel` is available only for binary outcomes. It specifies a meta-analysis using the Mantel–Haenszel method to estimate the overall effect size for binary outcomes. This method is the default for effect sizes `lnoratio`, `lnrratio`, and `rdiff` but is not available for effect size `lnorpeto`.

`invvariance` specifies a meta-analysis using the inverse-variance method to estimate the overall effect size. This method is available for all types of outcomes and effect sizes and is the default for continuous outcomes and for binary outcomes using effect size `lnorpeto`.

`ivariance` is a synonym for `invvariance`.

`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)` for effect sizes `lnoratio`, `lnrratio`, and `rdiff` and `fixed(invvariance)` for all other effect sizes.

*cefemethod* is one of `mhaenszel` or `invvariance` (synonym `ivariance`); see descriptions [above](#).

#### Options

`zerocells(zcspec)` is for use with binary outcomes when the effect size is either `lnoratio` or `lnrratio`. It specifies the adjustment to be used for the cells, the values of variables `n11`, `n12`, `n21`, and `n22`, when there are zero cells. The adjustment is applied during computation—the original data are not modified. The default is `zerocells(0.5, only0)`; it adds 0.5 to all cells of  $2 \times 2$  tables that contain at least one zero cell. To request no adjustment, specify `zerocells(none)`. More generally, the syntax of *zcspec* is

```
# [ , zcadj ]
```

where `#` is the adjustment value, also known as the continuity-correction value in the meta-analysis literature, and *zcadj* is `only0` or `allif0`.

`only0` specifies that `#` be added to all cells of only those  $2 \times 2$  tables that contain at least one zero cell. That is, during computation, `#` is added to each observation defined by variables `n11`, `n12`, `n21`, and `n22` if that observation contains a value of zero in any of those variables.

`allif0` specifies that `#` be added to all cells of all  $2 \times 2$  tables but only if there is at least one  $2 \times 2$  table with a zero cell. That is, during computation, `#` is added to all values of variables `n11`, `n12`, `n21`, and `n22` but only if there is a zero value in one of the four variables.

For the effect size `lnoratio`, *zcspec* may also be `tacc`, which implements the treatment-arm continuity correction of [Sweeting, Sutton, and Lambert \(2004\)](#). This method estimates the group-specific adjustment values from the data to minimize the bias of the overall odds-ratio estimator in the presence of zero cells. This method is recommended when the groups are unbalanced.

`studylabel(varname)` specifies a string variable containing labels for the individual studies to be used in all applicable meta-analysis output. The default study labels are `Study 1`, `Study 2`, ..., `Study K`, where *K* is the total number of studies in the meta-analysis.

`eslabel(string)` specifies that *string* be used as the effect-size label in all relevant meta-analysis output. The default label is `Effect Size`.

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. It will be used by all subsequent meta-analysis commands when computing confidence intervals. The default is

level(95) or as set by set level; see [R] level. After the declaration, you can specify level() with meta update to update the confidence level to be used throughout the rest of the meta-analysis session. You can also specify level() directly with the meta commands to modify the confidence level, temporarily, during the execution of the command.

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

## Remarks and examples

[stata.com](http://www.stata.com)

Remarks are presented under the following headings:

*Meta-analysis of binary data*

*Meta-analysis of continuous data*

meta esize computes various effect sizes, their standard errors, and CIs for two-group comparisons of continuous and binary outcomes from the summary data provided for each study. It then declares the computed effect-size data as the meta data; see [META] meta data. Different types of effect sizes may be specified in the esize() option. They depend on the data type, so we describe them separately for binary and continuous data below, together with other data-specific options. Also see *Declaring meta-analysis information* in [META] meta data.

### Meta-analysis of binary data

Meta-analysis primarily compares two groups. The first group is commonly referred to as the experimental or treatment group. The second group is commonly referred to as the control group.

For a binary outcome, each study typically reports cell counts from the following  $2 \times 2$  table.

group	success	failure	size
treatment	$n_{11}$	$n_{12}$	$n_1 = n_{11} + n_{12}$
control	$n_{21}$	$n_{22}$	$n_2 = n_{21} + n_{22}$

The cells of the table are composed of the numbers of “successes” and “failures” within each of the comparison groups. If a subject experiences an event of interest, it is a success; otherwise, it is a failure. Thus, the summary data for binary outcomes include the above  $2 \times 2$  table for each study.

For binary data, meta esize requires that four variables be specified containing the numbers of successes and failures in the treatment and control groups.

The goal of each study is to compare the probabilities of a success between the two groups. Various effect-size measures can be used for the comparison. For binary outcomes, meta esize provides the following effect sizes: log odds-ratios (including Peto’s log odds-ratios), the default; log risk-ratios; and risk differences. These are specified as lnoratio, lnorpeto, lnrratio, and rdiff in the esize() option.

As described in *Declaring a meta-analysis model* in [META] meta data, you can choose between a random-effects, a fixed-effects, or a common-effect model. You can also choose from a number of estimation methods that are specific to the chosen model. For fixed-effects and common-effect models, in addition to the inverse-variance method, the Mantel–Haenszel method is available (and is the default) with effect sizes lnoratio, lnrratio, and rdiff; see *Declaring a meta-analysis estimation method* in [META] meta data and *Meta-analysis estimation methods* in [META] Intro for details.

Zero cell counts are known to create computational difficulties for odds ratios and risk ratios. A common solution is to add a small number, say, 0.5, to all cells of tables containing zero cells. This and other zero-cells adjustments are available in the `zeros` option.

Let's now look at several examples. Consider the following fictional meta-analysis dataset:

```
. use https://www.stata-press.com/data/r16/metaesbin
(Fictional data for binary outcomes)
. describe
Contains data from https://www.stata-press.com/data/r16/metaesbin.dta
  obs:          4          Fictional data for binary
                           outcomes
  vars:         5          23 Apr 2019 12:14
```

---

variable name	storage type	display format	value label	variable label
study	str7	%9s		Study label
tdead	byte	%9.0g		Deaths in treatment group
tsurv	int	%9.0g		Survivors in treatment group
cdead	byte	%9.0g		Deaths in control group
csurv	int	%9.0g		Survivors in control group

---

Sorted by:

We will use this dataset to demonstrate how to compute effect sizes, specify different meta-analysis models, and adjust for zero cells with binary outcome meta-analysis data.

### ► Example 1: A simple case

When working with meta-analysis data that do not have precomputed effect sizes, we can choose to compute effect sizes in a few different ways such as odds ratios and risk ratios. Using the simplest syntactical specification, we can compute the effect sizes, their standard errors, and the corresponding confidence intervals by specifying the number of successes and failures for one group, as well as the successes and failures for the second group, in that order.

```
. meta esize tdead tsurv cdead csurv
Meta-analysis setting information
Study information
  No. of studies: 4
  Study label: Generic
  Study size: _meta_studysize
  Summary data: tdead tsurv cdead csurv
Effect size
  Type: lnoratio
  Label: Log Odds-Ratio
  Variable: _meta_es
Zero-cells adj.: 0.5, only0
Precision
  Std. Err.: _meta_se
  CI: [_meta_cil, _meta_ciu]
  CI level: 95%
Model and method
  Model: Random-effects
  Method: REML
```

The output indicates that there are 4 studies in the meta-analysis and, by default, a random-effects meta-analysis is to be assumed, where the heterogeneity parameter  $\tau^2$  is estimated via the REML



method. The default computed effect size is the log odds-ratio. `meta esize` creates multiple system variables (see *System variables* in [META] `meta data`) that store the effect-size values, their standard errors, and the upper and lower limits of the CIs for the effect sizes.

We can now use, for example, `meta summarize` to list the individual log odds-ratios and the overall log odds-ratio, which is denoted as `theta`.

```
. meta summarize
      Effect-size label:  Log Odds-Ratio
           Effect size:  _meta_es
           Std. Err.:    _meta_se

Meta-analysis summary          Number of studies =      4
Random-effects model          Heterogeneity:
Method: REML                   tau2 = 1.4417
                                I2 (%) = 69.33
                                H2 = 3.26
```

Study	Log Odds-Ratio	[95% Conf. Interval]		% Weight
Study 1	-0.600	-2.079	0.879	27.80
Study 2	0.351	-2.510	3.212	15.65
Study 3	0.778	-0.031	1.586	34.69
Study 4	-2.567	-4.638	-0.495	21.85
theta	-0.403	-1.869	1.063	

```
Test of theta = 0: z = -0.54          Prob > |z| = 0.5899
Test of homogeneity: Q = chi2(3) = 9.93  Prob > Q = 0.0192
```

See [META] `meta summarize` for details.

If we have a variable that stores the labels for each study, perhaps noting the study authors or journal, we can specify it in the `studylabel()` option with `meta esize`. Because we do not have such a variable in this dataset, each study is denoted generically by `Study #`. See [example 4](#) in [META] `meta set` for an example of how to specify the study label and effect-size label. ◀

## ► Example 2: Specify the effect size

The default is to compute the log odds-ratio for the effect size. To specify another metric, we can use the `esize()` option. For example, below we use the risk ratio (on the log scale) as our effect size by specifying `esize(lnrratio)`:

```
. meta esize tdead tsurv cdead csurv, esize(lnrratio)
Meta-analysis setting information
Study information
  No. of studies: 4
  Study label: Generic
  Study size: _meta_studysize
  Summary data: tdead tsurv cdead csurv
  Effect size
    Type: lnrratio
    Label: Log Risk-Ratio
    Variable: _meta_es
  Zero-cells adj.: 0.5, only0
  Precision
    Std. Err.: _meta_se
    CI: [_meta_cil, _meta_ciu]
    CI level: 95%
Model and method
  Model: Random-effects
  Method: REML
```

◀

### ► Example 3: Sparse data and adjustments for zero cells

Note that when we list the data, one of the studies has zero deaths.

```
. list tdead tsurv cdead csurv
```

	tdead	tsurv	cdead	csurv
1.	2	116	17	541
2.	0	15	15	682
3.	8	61	37	614
4.	1	421	9	291

By default, `meta esize` adds a constant value of 0.5 (that is, option `zerocells(0.5, only0)` is assumed) to each cell of a study that has a zero cell; see `Zero-cells adj.:` in the output of `meta set` in [example 1](#). We can modify this adjustment by specifying a different constant factor. For example, we might add 0.003 to each zero cell:

```
. meta esize tdead tsurv cdead csurv, zerocells(.003)
Meta-analysis setting information
Study information
  No. of studies: 4
  Study label: Generic
  Study size: _meta_studysize
  Summary data: tdead tsurv cdead csurv
  Effect size
    Type: lnoratio
    Label: Log Odds-Ratio
    Variable: _meta_es
  Zero-cells adj.: .003, only0
  Precision
    Std. Err.: _meta_se
    CI: [_meta_cil, _meta_ciu]
    CI level: 95%
Model and method
  Model: Random-effects
  Method: REML
```

Or we may instead choose a different type of continuity correction, for example, the treatment-arm continuity correction (TACC), which we specify as `zerocells(tacc)`:

```
. meta esize tdead tsurv cdead csurv, zerocells(tacc)
Meta-analysis setting information
Study information
  No. of studies: 4
  Study label: Generic
  Study size: _meta_studysize
  Summary data: tdead tsurv cdead csurv
  Effect size
    Type: lnoratio
    Label: Log Odds-Ratio
    Variable: _meta_es
  Zero-cells adj.: tacc
  Precision
    Std. Err.: _meta_se
    CI: [_meta_cil, _meta_ciu]
    CI level: 95%
Model and method
  Model: Random-effects
  Method: REML
```

Note that this option can be specified only when using the log odds-ratio as the effect size.

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#### ► Example 4: Specify the meta-analysis model

In the examples above, we have been using the default random-effects model, but we could specify a different model. For example, we can use a common-effect model using the Mantel–Haenszel method to estimate the overall effect size:

```
. meta esize tdead tsurv cdead csurv, common(mhaenszel)
Meta-analysis setting information
Study information
  No. of studies: 4
  Study label: Generic
  Study size: _meta_studysize
  Summary data: tdead tsurv cdead csurv
  Effect size
    Type: lnoratio
    Label: Log Odds-Ratio
    Variable: _meta_es
  Zero-cells adj.: 0.5, only0
  Precision
    Std. Err.: _meta_se
    CI: [_meta_cil, _meta_ciu]
    CI level: 95%
Model and method
  Model: Common-effect
  Method: Mantel-Haenszel
```

In the above, we could have specified simply `common` because the Mantel–Haenszel method is the default for a common-effect model with log odds-ratios.

◀

## Meta-analysis of continuous data

As with binary outcomes, meta-analysis of continuous outcomes also compares two groups. As before, the first group is commonly referred to as the experimental or treatment group, and the second group is commonly referred to as the control group.

For a continuous outcome, each study often reports the numbers of observations, means, and standard deviations in the two groups. Various effect sizes are then computed from these summary data for each study. Thus, to compute effect sizes for continuous data, `meta esize` requires that six variables be specified containing the numbers of observations, means, and standard deviations of the treatment and control groups. The supported effect sizes are the raw mean difference, `esize(mdif)`, and standardized mean differences: Hedges's  $g$ , `esize(hedgesg)` (the default); Cohen's  $d$ , `esize(cohend)`; and Glass's  $\Delta$ s, `esize(glassdelta2)` and `esize(glassdelta1)`; see [Methods and formulas](#) for their definitions.

As described in [Declaring a meta-analysis model](#) in [META] [meta data](#), you can choose between a random-effects, a fixed-effects, or a common-effect model. You can also choose from several [estimation methods](#) for random-effects models. Fixed-effects and common-effect models assume the inverse-variance estimation method. Also see [Declaring a meta-analysis estimation method](#) in [META] [meta data](#) and [Meta-analysis estimation methods](#) in [META] [Intro](#) for details.

Let's now demonstrate several usages of `meta esize` for continuous outcomes. Consider the following fictional meta-analysis dataset:

```
. use https://www.stata-press.com/data/r16/metaescnt, clear
(Fictional summary data for continuous outcomes)
. describe
Contains data from https://www.stata-press.com/data/r16/metaescnt.dta
  obs:                10                Fictional summary data for
                                         continuous outcomes
  vars:                6                19 Apr 2019 14:00
```

variable name	storage type	display format	value label	variable label
n1	byte	%9.0g		Study sizes of group 1
m1	float	%9.0g		Means of group 1
sd1	float	%9.0g		Std. Dev. of group 1
n2	byte	%9.0g		Study sizes of group 2
m2	float	%9.0g		Means of group 2
sd2	float	%9.0g		Std. Dev. of group 2

Sorted by:

We will use this dataset to demonstrate different usages of the `meta esize` command with continuous-outcomes meta-analysis data.

## ► Example 5: The assumed model

In the simplest specification, `meta esize` requires that we specify the sample sizes, means, and standard deviations for each group in the meta-analysis.

```
. meta esize n1 m1 sd1 n2 m2 sd2
Meta-analysis setting information
Study information
  No. of studies: 10
  Study label: Generic
  Study size: _meta_studysize
  Summary data: n1 m1 sd1 n2 m2 sd2
  Effect size
    Type: hedgesg
    Label: Hedges's g
    Variable: _meta_es
  Bias correction: Approximate
  Precision
    Std. Err.: _meta_se
  Std. Err. adj.: None
    CI: [_meta_cil, _meta_ciu]
  CI level: 95%
Model and method
  Model: Random-effects
  Method: REML
```

We see from the output that the Hedges's  $g$  standardized mean difference is used for the effect size, and, as for binary outcomes, a random-effects REML model is assumed. See [Meta settings with meta esize](#) in [META] [meta data](#) for a detailed description of all settings for this dataset.

◀

## ► Example 6: Selecting an effect size

If we do not feel the need to standardize the mean differences, we could instead use the raw mean difference as the effect size by specifying `esize(mdif)`.

```
. meta esize n1 m1 sd1 n2 m2 sd2, esize(mdif)
Meta-analysis setting information
Study information
  No. of studies: 10
  Study label: Generic
  Study size: _meta_studysize
  Summary data: n1 m1 sd1 n2 m2 sd2
  Effect size
    Type: mdif
    Label: Mean Diff.
    Variable: _meta_es
  Precision
    Std. Err.: _meta_se
  Std. Err. adj.: None
    CI: [_meta_cil, _meta_ciu]
  CI level: 95%
Model and method
  Model: Random-effects
  Method: REML
```

◀

### ► Example 7: Specifying different meta-analysis models and methods

Rather than using the default REML estimation method, we may want to use a different method, such as the DerSimonian–Laird method. We can specify this method in the `random()` option.

```
. meta esize n1 m1 sd1 n2 m2 sd2, random(dlaird)
Meta-analysis setting information
Study information
  No. of studies: 10
  Study label: Generic
  Study size: _meta_studysize
  Summary data: n1 m1 sd1 n2 m2 sd2
  Effect size
    Type: hedgesg
    Label: Hedges's g
    Variable: _meta_es
  Bias correction: Approximate
  Precision
    Std. Err.: _meta_se
  Std. Err. adj.: None
    CI: [_meta_cil, _meta_ciu]
  CI level: 95%
Model and method
  Model: Random-effects
  Method: DerSimonian-Laird
```

Or, instead of the random-effects model, we may specify a fixed-effects model, which implies the inverse-variance estimation method.

```
. meta esize n1 m1 sd1 n2 m2 sd2, fixed
Meta-analysis setting information
Study information
  No. of studies: 10
  Study label: Generic
  Study size: _meta_studysize
  Summary data: n1 m1 sd1 n2 m2 sd2
  Effect size
    Type: hedgesg
    Label: Hedges's g
    Variable: _meta_es
  Bias correction: Approximate
  Precision
    Std. Err.: _meta_se
  Std. Err. adj.: None
    CI: [_meta_cil, _meta_ciu]
  CI level: 95%
Model and method
  Model: Fixed-effects
  Method: Inverse-variance
```

## Stored results

meta esize stores the following characteristics and system variables:

### Characteristics

<code>_dta[_meta_marker]</code>	“_meta_ds_1”
<code>_dta[_meta_K]</code>	number of studies in the meta-analysis
<code>_dta[_meta_studylabel]</code>	name of string variable containing study labels or Generic
<code>_dta[_meta_estype]</code>	type of effect size; varies
<code>_dta[_meta_eslabelopt]</code>	eslabel( <i>eslab</i> ), if specified
<code>_dta[_meta_eslabel]</code>	effect-size label from eslabel(); default varies
<code>_dta[_meta_eslabeldb]</code>	effect-size label for dialog box
<code>_dta[_meta_esvardb]</code>	_meta_es
<code>_dta[_meta_level]</code>	default confidence level for meta-analysis
<code>_dta[_meta_esizeopt]</code>	esize( <i>estype</i> ), if specified
<code>_dta[_meta_esopt_exact]</code>	exact, if esize(, exact) is specified
<code>_dta[_meta_esopt_holkinse]</code>	holkinse, if esize(, holkinse) is specified
<code>_dta[_meta_esopt_unequal]</code>	unequal, if esize(, unequal) is specified
<code>_dta[_meta_modellabel]</code>	meta-analysis model label: Random-effects, Common-effect, or Fixed-effects
<code>_dta[_meta_model]</code>	meta-analysis model: random, common, or fixed
<code>_dta[_meta_methodlabel]</code>	meta-analysis method label; varies by meta-analysis model
<code>_dta[_meta_method]</code>	meta-analysis method; varies by meta-analysis model
<code>_dta[_meta_randomopt]</code>	random( <i>remethod</i> ), if specified
<code>_dta[_meta_zcopt]</code>	zerocells( <i>zcspec</i> ), if specified
<code>_dta[_meta_zcadj]</code>	type of adjustment for zero cells, if zerocells() specified
<code>_dta[_meta_zcvalue]</code>	value added to cells to adjust for zero cells, if specified
<code>_dta[_meta_show]</code>	empty or nometashow
<code>_dta[_meta_n1var]</code>	name of group 1 sample-size variable; for continuous data
<code>_dta[_meta_mean1var]</code>	name of group 1 mean variable; for continuous data
<code>_dta[_meta_sd1var]</code>	name of group 1 std. dev. variable; for continuous data
<code>_dta[_meta_n2var]</code>	name of group 2 sample-size variable; for continuous data
<code>_dta[_meta_mean2var]</code>	name of group 2 mean variable; for continuous data
<code>_dta[_meta_sd2var]</code>	name of group 2 std. dev. variable; for continuous data
<code>_dta[_meta_n11var]</code>	name of <i>n11</i> variable; for binary data
<code>_dta[_meta_n12var]</code>	name of <i>n12</i> variable; for binary data
<code>_dta[_meta_n21var]</code>	name of <i>n21</i> variable; for binary data
<code>_dta[_meta_n22var]</code>	name of <i>n22</i> variable; for binary data
<code>_dta[_meta_datatype]</code>	data type; continuous or binary
<code>_dta[_meta_datavars]</code>	variables specified with meta esize
<code>_dta[_meta_setcmdline]</code>	meta esize command line
<code>_dta[_meta_ifexp]</code>	<i>if</i> specification
<code>_dta[_meta_inexp]</code>	<i>in</i> specification

### System variables

<code>_meta_id</code>	study ID variable
<code>_meta_es</code>	variable containing effect sizes
<code>_meta_se</code>	variable containing effect-size standard errors
<code>_meta_cil</code>	variable containing lower bounds of CIs for effect sizes
<code>_meta_ciu</code>	variable containing upper bounds of CIs for effect sizes
<code>_meta_studylabel</code>	string variable containing study labels
<code>_meta_studysize</code>	variable containing total sample size per study

## Methods and formulas

Methods and formulas are presented under the following headings:

- Effect sizes for continuous outcomes*
  - Unstandardized mean difference*
  - Standardized mean difference*
- Effect sizes for binary outcomes*
  - Odds ratio*
  - Risk ratio (rate ratio)*
  - Risk difference*
  - Zero-cells adjustments*
- Confidence intervals for effect sizes*

## Effect sizes for continuous outcomes

As we described in *Meta-analysis of continuous data*, meta-analysis often compares two groups: experimental (or treated) group and control group.

When the response (measurement) is continuous, studies typically report a mean and standard deviation for each group. For a given study, the following table denotes the underlying population parameters and the reported summary statistics (data) for each group.

group	population		sample		
	mean	sd	mean	sd	size
treatment	$\mu_1$	$\sigma_1$	$\bar{x}_1$	$s_1$	$n_1$
control	$\mu_2$	$\sigma_2$	$\bar{x}_2$	$s_2$	$n_2$

The majority of this section is based on [Borenstein \(2009\)](#).

### Unstandardized mean difference

Consider the population mean difference

$$\theta = \mu_1 - \mu_2$$

For each study in the meta-analysis, `meta esize` with option `esize(mdif)` estimates  $\theta$  using the difference in sample means,

$$D = \bar{x}_1 - \bar{x}_2$$

The variance of  $D$ , assuming that the two population standard deviations are equal, is estimated by

$$\widehat{\text{Var}}(D) = \left( \frac{1}{n_1} + \frac{1}{n_2} \right) s^2$$

where  $s$  is the pooled sample standard deviation

$$s = \sqrt{\frac{(n_1 - 1) s_1^2 + (n_2 - 1) s_2^2}{n_1 + n_2 - 2}}$$

For unequal population standard deviations, use option `esize(mdif, unequal)`; then the variance of  $D$  is estimated by

$$\widehat{\text{Var}}(D) = \frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}$$

Unstandardized (raw) mean differences are not comparable across studies if the underlying means are measured on different scales.



## Standardized mean difference

The standardized mean difference is

$$\theta = \frac{\mu_1 - \mu_2}{\sigma}$$

Note that  $\theta$  does not depend on the scale of measurement. The definition of the standardized mean difference implicitly assumes that the population standard deviations,  $\sigma_1$  and  $\sigma_2$ , are the same:  $\sigma_1 = \sigma_2 = \sigma$ .

`meta esize` with option `esize(cohend)` estimates  $\theta$  using Cohen's  $d$  statistic (Cohen 1969, 1988),

$$d = \frac{\bar{x}_1 - \bar{x}_2}{s}$$

The estimated variance of  $d$  is given by

$$\widehat{\text{Var}}(d) = \frac{n_1 + n_2}{n_1 n_2} + \frac{d^2}{2(n_1 + n_2)}$$

Hedges (1981) introduced an adjustment to Cohen's  $d$  for small samples that accounts for a small upward bias in the absolute value of  $\theta$ . `meta esize` with option `esize(hedgesg, exact)` computes Hedges's  $g$  as

$$g = c(m) \times d$$

where  $m = n_1 + n_2 - 2$  is the degrees of freedom used to estimate  $s$  and

$$c(m) = \frac{\Gamma\left(\frac{m}{2}\right)}{\sqrt{\frac{m}{2}} \Gamma\left(\frac{m-1}{2}\right)}$$

The adjustment  $c(m)$  is less than 1 and approaches 1 as  $m$  gets large. The variance estimate of Hedges's  $g$  is

$$\widehat{\text{Var}}(g) = c(m)^2 \times \widehat{\text{Var}}(d)$$

Hedges (1981) also introduced an accurate approximation for  $c(m)$  that has been traditionally used in meta-analysis. The approximation for  $c(m)$  is

$$J = 1 - \frac{3}{4m - 1}$$

`meta esize` with option `esize(hedgesg)` computes Hedges's  $g$  using  $J$  for  $c(m)$ ; thus,

$$g = J \times d$$

and

$$\widehat{\text{Var}}(g) = J^2 \times \widehat{\text{Var}}(d)$$

`meta esize` with option `esize(glassdelta2)` estimates  $\theta$  using Glass's  $\Delta$  (Smith and Glass 1977),

$$\Delta = \frac{\bar{x}_1 - \bar{x}_2}{s_2}$$

Notice that the standard deviation in the denominator is  $s_2$ , the sample standard deviation from the control group, which is considered to be a more reliable estimate of the common variance. The estimated variance of  $\Delta$  is given by

$$\widehat{\text{Var}}(\Delta) = \frac{n_1 + n_2}{n_1 n_2} + \frac{\Delta^2}{2(n_2 - 1)}$$

In the absence of the control group, such as in observational studies, [Kline \(2013\)](#), among others, suggests providing statistics standardized by the standard deviation of each group. Glass's  $\Delta$  where standardization is based on the treatment group may be computed via option `esize(glassdelta1)`.

Alternative standard-error estimators are available for Hedges's  $g$  and Cohen's  $d$  effect sizes.

[Hedges and Olkin \(1985, eq. 8, 80\)](#) provide another commonly used estimator for the variance of Hedges's  $g$ .

$$\widehat{\text{Var}}(g) = \frac{n_1 + n_2}{n_1 n_2} + \frac{g^2}{2(m - 1.94)}$$

`meta esize` uses this formula when option `esize(hedgesg, holkinse)` is specified.

The alternative variance estimator of  $d$  is given by

$$\widehat{\text{Var}}(d) = \frac{n_1 + n_2}{n_1 n_2} + \frac{d^2}{2(n_1 + n_2 - 2)}$$

This variance estimator may be requested via option `esize(cohend, holkinse)`.

## Effect sizes for binary outcomes

As we described in [Meta-analysis of binary data](#), meta-analysis often compares two groups: experimental (or treated) group and control group. When the response (measurement) is binary, each study typically reports cell counts from the following  $2 \times 2$  table.

group	success	failure	size
treatment	$a$	$b$	$n_1 = a + b$
control	$c$	$d$	$n_2 = c + d$

Here, for simplicity, we use a different notation for the cell counts ( $a$ ,  $b$ ,  $c$ , and  $d$ ) compared with the similar table in [Meta-analysis of binary data](#).

For the treatment group,  $n_1$  is assumed fixed,  $a \sim \text{binomial}(n_1, \pi_1)$ , and  $\pi_1$  is the probability of a success. For the control group,  $n_2$  is assumed fixed,  $c \sim \text{binomial}(n_2, \pi_2)$ , and  $\pi_2$  is the probability of a success. The goal of each study is to compare the two success probabilities,  $\pi_1$  and  $\pi_2$ .

Estimates of the success probabilities are  $\hat{\pi}_1 = a/n_1$  for the treatment group and  $\hat{\pi}_2 = c/n_2$  for the control group.

## Odds ratio

`meta esize` with option `esize(lnoratio)` computes estimates of the log odds-ratios. Odds ratio is the ratio of the odds of a success in the treatment group over the odds of a success in the control group.

$$\text{OR} = \frac{\pi_1 / (1 - \pi_1)}{\pi_2 / (1 - \pi_2)}$$

The odds ratio is estimated by

$$\widehat{\text{OR}} = \frac{ad}{bc}$$

The distribution of  $\widehat{\text{OR}}$  is typically skewed, but the natural logarithm of  $\widehat{\text{OR}}$ ,  $\ln(\widehat{\text{OR}})$ , is asymptotically normally distributed. The estimate of the variance of  $\ln(\widehat{\text{OR}})$  is

$$\widehat{\text{Var}} \{ \ln(\widehat{\text{OR}}) \} = \frac{1}{a} + \frac{1}{b} + \frac{1}{c} + \frac{1}{d}$$

`meta esize` with option `esize(lnorpeto)` computes estimates of effect size using Peto's log odds-ratio (Peto et al. 1977; Yusuf et al. 1985). Peto's odds ratio and log odds-ratio are

$$\widehat{\text{OR}}^{\text{Peto}} = \exp \left\{ \frac{a - E(a)}{\text{Var}(a)} \right\}$$

$$\ln \left( \widehat{\text{OR}}^{\text{Peto}} \right) = \frac{a - E(a)}{\text{Var}(a)}$$

where the expectation and variance of  $a$  are estimated assuming a hypergeometric distribution:

$$E(a) = \frac{(a+c)n_1}{n}$$

$$\text{Var}(a) = \frac{n_1 n_2 (a+c)(b+d)}{n^2 (n-1)}$$

The variance estimate of  $\ln \left( \widehat{\text{OR}}^{\text{Peto}} \right)$  is

$$\widehat{\text{Var}} \left\{ \ln \left( \widehat{\text{OR}}^{\text{Peto}} \right) \right\} = \frac{1}{\text{Var}(a)}$$

See, for instance, Fleiss 1993, Fleiss, Levin, and Paik 2003, and Bradburn et al. (2007) for a discussion of potential bias of Peto's odds ratio and its performance in sparse data.

## Risk ratio (rate ratio)

`meta esize` with option `esize(lnrratio)` computes estimates of the log risk-ratios. The risk ratio (RR), also known as the rate ratio or relative risk in the health sciences, is

$$\text{RR} = \frac{\pi_1}{\pi_2}$$

RR is estimated by

$$\widehat{\text{RR}} = \frac{a/n_1}{c/n_2}$$

Similarly to odds ratios,  $\widehat{\text{RR}}$  typically has a skewed distribution, but the natural logarithm of  $\widehat{\text{RR}}$ ,  $\ln(\widehat{\text{RR}})$ , is asymptotically normally distributed. The estimate of the variance of  $\ln(\widehat{\text{RR}})$  is

$$\widehat{\text{Var}} \{ \ln(\widehat{\text{RR}}) \} = \frac{1}{a} + \frac{1}{c} - \frac{1}{a+b} - \frac{1}{c+d}$$

## Risk difference

`meta esize` with option `esize(rdif)` computes estimates of the risk differences. The risk difference is

$$RD = \pi_1 - \pi_2$$

and is estimated by

$$\widehat{RD} = \frac{a}{n_1} - \frac{c}{n_2}$$

$\widehat{RD}$  is asymptotically normally distributed and is thus typically used without a transformation in meta-analysis.

The estimated variance of  $\widehat{RD}$  is

$$\widehat{\text{Var}}(\widehat{RD}) = \frac{ab}{n_1^3} + \frac{cd}{n_2^3}$$

## Zero-cells adjustments

The variance estimates of  $\ln(\widehat{OR})$  and  $\ln(\widehat{RR})$  are not defined if there are any empty (zero count) cells in a  $2 \times 2$  table. In this case, it is customary to add a small value, often referred to as “continuity correction”, to each cell prior to computing the log odds- or risk-ratio.

By default, `meta esize` adds 0.5 to each cell of  $2 \times 2$  tables containing empty cells (Gart and Zweifel 1967 and Gart, Pettigrew, and Thomas 1985). Alternatively, you can add a different number or add a number to each cell of all  $2 \times 2$  tables, as long as there is at least one  $2 \times 2$  table with zero cells; see option `zerocells()`.

For odds ratios, Sweeting, Sutton, and Lambert (2004) proposed the treatment-arm continuity correction (TACC) method, which estimates the continuity-correction values from the data separately for each group; see `zerocells(tacc)`.

## Confidence intervals for effect sizes

For the  $j$ th study in a given meta-analysis, let  $\widehat{\theta}_j$  be one of the effect-size estimators described above; then the asymptotic  $100(1 - \alpha)\%$  confidence interval computed by `meta esize` is

$$\widehat{\theta}_j \pm z_{1-\alpha/2} \sqrt{\widehat{\text{Var}}(\widehat{\theta}_j)}$$

where  $z_{1-\alpha/2}$  is the usual critical value from the standard normal distribution.

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## Also see

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

[META] **meta set** — Declare meta-analysis data using generic effect sizes

[META] **meta update** — Update, describe, and clear meta-analysis settings

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

[META] **Glossary**

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

[R] **esize** — Effect size based on mean comparison