Description

`meta update` updates certain components of the meta-analysis after it was declared by `meta set` or `meta esize`. This command is useful for updating some of the meta settings without having to fully respecify your meta-analysis variables. The updated settings will be used throughout the rest of your meta-analysis session.

`meta query` reports whether the data in memory are `meta` data and, if they are, displays the current meta setting information identical to that produced by `meta set` or `meta esize`.

`meta clear` clears meta settings, including meta data characteristics and system variables. The original data remain unchanged. You do not need to use `meta clear` before doing another `meta set` or `meta esize`.

Quick start

Check whether data are declared as `meta` data, and, if they are, describe their current meta-analysis setting information

```
meta query
```

Keep the same meta-analysis setting (specified earlier using `meta set` or `meta esize), but use a DerSimonian–Laird random-effects model

```
meta update, random(dlaird)
```

Keep the same meta-analysis setting (specified earlier using `meta esize`), but use the log risk-ratio as the effect size

```
meta update, esize(lnrratio)
```

Clear meta-analysis declaration

```
meta clear
```
Syntax

Update meta-analysis settings declared using meta esize for continuous outcomes

```bash
meta_update [, options_continuous options]
```

Update meta-analysis settings declared using meta esize for binary outcomes

```bash
meta_update [, options_binary options]
```

Update meta-analysis settings declared using meta set

```bash
meta_update [, options_generic options]
```

Describe meta data

```bash
meta_query [, short]
```

Clear meta data

```bash
meta_clear
```

<table>
<thead>
<tr>
<th>options_continuous</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>esize(esspeccnt)</td>
<td>specify effect size for continuous outcome to be used in the meta-analysis</td>
</tr>
<tr>
<td>random(remethod)</td>
<td>random-effects meta-analysis</td>
</tr>
<tr>
<td>common</td>
<td>common-effect meta-analysis; implies inverse-variance method</td>
</tr>
<tr>
<td>fixed</td>
<td>fixed-effects meta-analysis; implies inverse-variance method</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>options_binary</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>esize(estypebin)</td>
<td>specify effect size for binary outcome to be used in the meta-analysis</td>
</tr>
<tr>
<td>random(remethod)</td>
<td>random-effects meta-analysis</td>
</tr>
<tr>
<td>common(cefemethod)</td>
<td>common-effect meta-analysis</td>
</tr>
<tr>
<td>fixed(cefemethod)</td>
<td>fixed-effects meta-analysis</td>
</tr>
<tr>
<td>zerocells(zcspec)</td>
<td>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</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>options_generic</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>random(remethod)</td>
<td>random-effects meta-analysis</td>
</tr>
<tr>
<td>common</td>
<td>common-effect meta-analysis; implies inverse-variance method</td>
</tr>
<tr>
<td>fixed</td>
<td>fixed-effects meta-analysis; implies inverse-variance method</td>
</tr>
<tr>
<td>studysize(varname)</td>
<td>total sample size per study</td>
</tr>
</tbody>
</table>
### Options

For `meta update` options, see *Options of [META] meta set* and *Options of [META] meta esize*. `short` is used with `meta query`. It displays a short summary of the meta settings containing the information about the declared type of the effect size, effect-size and standard-error variables, and meta-analysis model and estimation method. This option does not appear on the dialog box.

### Remarks and examples

When conducting a meta-analysis, you may wish to explore how your results are affected by modifying certain characteristics of your model. For example, suppose you are using log odds-ratios as your effect sizes and the DerSimonian–Laird random-effects model. You want to investigate how your results would change if you were to use log risk-ratios instead. You could use `meta esize`, but you would need to respecify all four of your summary-data variables.

```
.meta esize summary'data, esize(lnrratio) random(dlaird)
```

Instead, you can use `meta update` to simply update the effect sizes.

```
.meta update, esize(lnrratio)
```

`meta update` will run `meta esize` keeping all the model components unchanged except for those you specified.

You can use `meta query` to describe the current meta-analysis settings. With `meta` data in memory, `meta query` produces the same output as `meta set` and `meta esize`. If the data in memory are not declared to be `meta` data, `meta query` will report the following:

```
.meta query
   (data not meta set; use meta set or meta esize to declare as meta data)
```

To clear meta settings, use `meta clear`.

For more details and examples, see *Modifying default meta settings* and *Displaying and updating meta settings* in [META] `meta data`.

### Stored results

`meta update` updates characteristics and contents of system variables described in *Stored results of [META] meta set* and *Stored results of [META] meta esize*. 

---

<table>
<thead>
<tr>
<th>options</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>studylabel(varname)</td>
<td>variable to be used to label studies in all meta-analysis output</td>
</tr>
<tr>
<td>eslabel(string)</td>
<td>effect-size label to be used in all meta-analysis output; default is <code>eslabel(Effect Size)</code></td>
</tr>
<tr>
<td>level(#)</td>
<td>confidence level for all subsequent meta-analysis commands</td>
</tr>
<tr>
<td>[no]metashow</td>
<td>display or suppress meta settings in the output</td>
</tr>
</tbody>
</table>
Also see

[META] meta data — Declare meta-analysis data

[META] meta esize — Compute effect sizes and declare meta-analysis data

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

[META] meta — Introduction to meta

[META] Glossary

[META] Intro — Introduction to meta-analysis