meta update — Update, describe, and clear meta-analysis settings

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

Menu

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Syntax

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

```
meta update [, options_continuous options]
```

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

```
meta update [, options_binary options]
```

Update meta-analysis settings declared using meta set

```
meta update [, options_generic options]
```

Describe meta data

```
meta query [, short]
```

Clear meta data

```
meta clear
```

<table>
<thead>
<tr>
<th>options_continuous</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>esize(esspecent)</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[ celemethod ]</td>
<td>common-effect meta-analysis</td>
</tr>
<tr>
<td>fixed[ celemethod ]</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 x 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`. 
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