Creating graphs of meta-analyses with R

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Meta-analysis is a type of research aiming at statistically summarising information from several previous studies. It is becoming increasingly important in the medical field as the amount of information available increases [1, 2]. Commercially available computer programmes for meta-analysis usually offer limited flexibility, and the quality of graphs is sometimes poor. R offers almost unlimited flexibility in creating high-quality graphs.
I show how I used R to create a meta-analysis graph [3] that, while presenting information in a fairly standard way, had some idiosyncratic features that would have been impossible to deal with when using standard meta-analysis software (such as Comprehensive Meta-Analysis [4], but also Thomas Lumley's new R package rmeta). A major drawback of our procedure is that as high as its flexibility is, as low is its user-friendliness – it would have to be re-programmed for every new study or even update of this study.
I conclude that R is an excellent tool for creating the type of high-quality individualised graphs that are needed when submitting completed research to a scientific journal. However, there is room for improvement concerning ease of use, and there is a gap to fill between readymade, easy-to-use but relatively inflexible software and pure programming language. The package rmeta is a very welcome step in this process, but there is also a need for more generalised packages or functions that combine flexibility with ease of use.

References:
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