

## **Abstract**

Combining everything, all at once – Considerations for preclinical meta-analysis of animal data

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Quantitatively synthesizing and meta-analyzing data from published literature to produce an overall summary estimate of effects across studies is currently regarded as the highest level of evidence. While the method is well established in the clinical field, uptake in the preclinical domain of animal data is still underrepresented.

The methods for preclinical systematic review are based on those used in the clinical field but adapted to accommodate the differences found between these study types. Preclinical systematic reviews are characterized by higher variability in study design elements and a larger number of included studies that have a smaller sample size. This variability enables researchers to investigate factors contributing to heterogeneity using meta-regression models. Another important aspect of preclinical meta-analysis is that data are often nested (e.g., in research groups), requiring multilevel models to account for non-independence. Meta-analyses of animal data not only foster identification of promising interventions for translation but can also inform the design of future primary experiments, supporting ethical research in line with the three R's (Replacement, Reduction and Refinement).

In this talk, we will provide an overview of the differences between clinical and preclinical meta-analyses and highlight considerations for animal data. More specifically, we will give examples of meta-analyses exploring factors explaining between-study heterogeneity and discuss the nested data structure of primary experiments. We then will go into detail on multilevel meta-regression. Our presentation aims to give an overview of preclinical meta-analysis methodology and how to apply multilevel models to animal data.