

ARPAS Symposium: Understanding Meta-Analysis

316 Unsophisticated “cowboy” methods used traditionally to merge results from multiple experiments. F. N. Owens* and A. Hassan, *Pioneer Hi-Bred Int'l, Johnston, IA.*

Meta-analysis, initially used in 1904, is one statistical method for combining results from qualitative studies to develop and test relationships among multiple factors. Most concepts in nutrition and biology preceded or evolved without sophisticated meta-analysis. By checking the consistency of relationships across multiple experiments, often by within-trial regressions weighted by animal numbers in the mean, consensus opinions were reached to be substantiated or refuted by subsequent experiments. Scientific giants of the past (S. Brody, J. T. Reid) observed trends and relationships within masses of data and developed our basic concepts of growth and development. Similarly, the “equivalent body weight” concept presumably was developed by unweighted curvilinear regression. Mean energy values and nutrient analyses for 1,088 feeds in texts by F. B. Morrison were generated manually from 8,981 experiments after “outliers” were removed. Concepts in energy metabolism (the California Net Energy system) and amino acid requirements for growth (the Ideal Protein system) involved compilation of masses of measurements cleverly interpreted and merged by simplistic methods. The field of epidemiology is based on correlations across multiple data sets; its blunders illustrate that that correlations need not reflect cause-effect relationships. Meta-analyses helps to detect the statistical consistency of treatment effects among experiments, to reduce the cost of and need for animals or subjects in future experiments, and to define response curve shapes across diverse genetic and environmental conditions. Most granting agencies now require both α and β errors to be predicted. Though pre-packaged programs are widely available for complex statistical manipulations, scientists must understand both the upsides and the pitfalls involved with complex analyses. By including meta-analysis within publica-

tions of original research, misinterpretations by authors, readers, and the public could be reduced.

Key words: merged experiments, meta-analysis, statistical methods

317 Meta-analysis: The good, the bad and the ugly. I. J. Lean* and A. R. Rabiee, *SBScibus, Camden, NSW, Australia.*

Meta-analysis can be a powerful tool to provide a more precise estimate of the effect of treatment or risk factor for disease, or other outcomes, than any individual study contributing to a pooled analysis. It is also possible, and desirable, to examine new hypotheses using the pooled data that could not be readily tested using other forms of study. However, the confidence with which a user can apply these results depends on the conduct of the meta-analysis, the basal data that contribute to a meta-analysis and the biological responses of the treatments and responses under consideration. The role of publication bias and the value of unpublished results are explored. This presentation considers the base data that contribute to a meta-analysis and provides guidelines for presentation of results. Examples of meta-analyses will be used to examine sources of variability or heterogeneity in study results and strengths and weaknesses of different approaches to pooling data. Tools for assessing heterogeneity including the I^2 statistic and use of different funnel plots to assess publication bias are evaluated. The value and limitations of meta-regressions approaches to address causal relationships, especially in nutritional studies is addressed. Flaws in some approaches to the pooling of data will be explored with a view to achieving a greater consistency in approach to meta-analytical studies.

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