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Calibration of Disease Simulation Model Using an Engineering Approach

To the Editor—In a recent study, Kong et al. [1] addressed the important question of how to calibrate complex models. Kong et al. compared two parameter search algorithms to calibrate the lung cancer policy microsimulation model. We believe that the article is an important contribution to the literature for comparing the performance of the two calibration algorithms and highlighting the importance of calibration in disease modeling and the lack of standard calibration procedures.

The authors take the position that the only way to estimate unobservable model parameters is using model calibration and that the primary purpose of calibration is to estimate unobservable natural history parameters (p. 521, paragraph 2). Nevertheless, unobserved parameters can be estimated using other methods besides model calibration and, perhaps more importantly, the benefits of model calibration go far beyond estimation of unobserved natural history parameters.

Alternative methods to estimate unobservable parameters include Parmigiani, who solved an integral equation for the unobservable incidence rate of preclinical tumors that included previously developed theories of the growth rate of breast tumors [2,3]. Another commonly used approach is elicitation of expert opinions [2]. The microsimulation screening analysis (MISCAN) colorectal model was populated over the course of a 2-day expert meeting at which all input parameters were defined [4]. Expert opinion elicitation can also be integrated with calibration methods to define the ranges of allowable parameter values, as Kong et al. raised as an issue of concern in the discussion of their study [1].

Besides allowing the estimation of unobserved parameters, model calibration is also a way to evaluate and adjust the consistency of model structural and parameter assumptions [5,6]. Given that a model should be based on the best current scientific understanding of the disease (that is likely to change over time), and simplifying assumptions and input parameters from different sources will have been used, it is sensible to explore how consistent this combination of assumptions (the model) really is. This can be done by comparing the model output to empirical data (e.g., disease prevalence rates or mortality rates) and, if the model does not provide a good fit to the data, by exploring variation (within a prior plausible bounds) in the structural or parameter assumptions to identify combinations that provide a better fit to the data. Commonly, only parameters are varied to achieve an improved fit [2], but variation of other components including health states and pathways (structural assumptions) can also be explored during calibration within the known uncertainty associated with these assumptions [7–9]. Another advantage of using model calibration to estimate the parameters of the model is that the estimation process will induce correlation between the parameter estimates. This is particularly beneficial given that it is often difficult to identify and establish correlation between parameters in disease models [10].

The calibration of disease models is an important and active area of methodological research and this article is a welcome addition. The search for the parameter sets that minimize the discrepancy between model output and multiple calibration targets is just one area that should be explored in future research. Others include the selection of the weights to be used in the global goodness-of-fit statistic, the methods used to assess goodness of fit (least squares, chi-square, maximum likelihood, etc.), and, perhaps of critical importance for economic evaluation analysis, the methods used to integrate the results of model calibration and economic parameters.—Tazio Vanni, MD, MSc, Rosa Legood, PhD, Department of Public Health and Policy, London School of Hygiene and Tropical Medicine, London, UK; and Richard G. White, PhD, Department of Epidemiology and Population Health, London School of Hygiene and Tropical Medicine, London, UK.

No conflicts of interest to declare.

References

1 Kong CY, Pamela MM, Gazelle GS. Calibration of disease simulation model using an engineering approach. Value Health 2009;12:521–9.
2 Karnon J, Goyder E, Tappenden P, et al. A review and critique of modelling in prioritising and designing screening programmes. Health Technol Assess 2007;11:iii–iv, ix–xi, 1–145.
3 Parmigiani G. Modeling in Medical Decision Making. A Bayesian Approach. New York: Wiley, 2002.
4 Loeve F, Boer R, van Oortmarssen GJ, et al. The MISCAN-COLON simulation model for the evaluation of colorectal cancer screening. Comput Biomed Res 1999;32:13–33.
5 Philips Z, Ginnelly L, Sculpher M, et al. Review of guidelines for good practice in decision-analytic modelling in health technology assessment. Health Technol Assess 2004;8:iii–iv, ix–xi, 1–158.
6 Cooper BS. Confronting models with data. J Hosp Infect 2007;65(Suppl. 2):S88–92.
7 Jit M, Choi YH, Edmunds WJ. Economic evaluation of human papillomavirus vaccination in the United Kingdom. BMJ 2008;337:a769.
8 Weinstein MC. Recent developments in decision-analytic modelling for economic evaluation. Pharmacoeconomics 2006;24:1043–53.
9 Bojke L, Claxton K, Sculpher M, et al. Characterizing structural uncertainty in decision analytic models: a review and application of methods. Value Health 2009;12:739–49.
10 Ades AE, Claxton K, Sculpher M Evidence synthesis, parameter correlation and probabilistic sensitivity analysis. Health Econ 2006;15:373–81.

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