In a recent article, Kim et al. (1) addressed the important question of how best to estimate parameters in complex models of human papillomavirus. Unfortunately, in their paper they make a number of incorrect claims about the advantages of their method and the disadvantages of more established methods. First, they wrongly claim that Bayesian techniques for identifying model parameters require informative prior distributions (2). They also claim that their technique of identifying multiple discrete parameter sets to fit curves is superior to the approach of finding a joint probability density of the parameters in a model, partly because the former uses common measures of effect produced in cross-sectional, case-control, and cohort studies as part of the approach to model calibration. In fact, more rigorous Bayesian inference procedures regularly incorporate meta-analysis with these common measures, projecting the results of this analysis directly from prior data onto the inference used to construct posterior parameter distributions (3). The software and techniques for implementing these analyses have been made simple, free, and open-source (4).

Kim et al. claim that their estimation method is novel for providing a range of results to allow a more complete representation of model uncertainty. The Bayesian approach inherently accounts for uncertainty in a probabilistic manner and would be superior to the authors’ approach, which would not find a probability distribution but simply produce more discrete parameter estimates with more sampling. The approach described by Kim et al. is not capable of discriminating among “good-fitting” parameter sets. Perhaps most importantly, the Bayesian approach offers specific criteria for determining when estimation has converged onto posterior distributions of parameter estimates (5, 6) and for distinguishing among alternative model structures (7, 8). The authors’ output appears to be heavily oriented towards their baseline precalibrated parameter set, and their model was unable to fit the available data, unless they assumed that natural immunity exceeded 50 percent for high-risk types of human papillomavirus. This suggests a basic underlying problem with the model used. The model adopted by Kim et al. violates principles of identifiability (9), given its large negative degrees of freedom, and the authors could benefit from becoming more familiar with such identifiability issues if they intend to make bold claims about parameter estimation.

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REFERENCES

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