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Comment on Article by Craigmile et al.

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I would first like to congratulate the authors for taking on a very ambitious modeling project. It is increasingly the case in a broad variety of application areas that there is interest in combining data collected on different measurement scales, while accounting for complications such as censoring, missingness and spatial misalignment. Bayesian hierarchical modeling provides a natural paradigm for addressing such problems. However, difficulties in specifying the model and implementing the analysis provide a significant hurdle to many statisticians, limiting the use of Bayesian hierarchical models in applications such as exposure assessment. It is too often the case that ad hoc methods are used for combining information from different sources, with the results then used to make important regulatory decisions. For example, it is standard practice to summarize data from a particular source using a point estimate, which is then included without accounting for estimation uncertainty in a model for data from a different source. This type of exercise leads to a modeling house of cards, which can certainly produce highly misleading inferences and predictions. The Craigmile et al. article is a step in the right direction toward shifting the current standard practice.

All that said, I feel it necessary in my role as a discussant to raise a number of issues with their analysis. First, the primary goal of the article is to provide a behind-the-scenes look at the practical details involved in implementing a Bayesian hierarchical analysis in a complex setting. However, the authors focus on an arsenic exposure pathways application, which has been considered in a number of previous Bayesian analyses. The authors rely heavily on the models chosen in these previous analyses without much justification, allowing them to essentially bypass the challenging issue of model uncertainty. This luxury will be unavailable in most applications, and it is typically necessary to properly account for model uncertainty to obtain reasonable inferences and predictions, particularly in exposure pathway modeling.

I found the author's assessment of the Clayton et al. (2002) model insufficient. Even an eyeball analysis of the correlation table in Figure 4 showed a number of discrepancies, and it seems much more appealing to formally account for the obvious fact that the Clayton et al. (2002) model may not hold exactly. This can be done by allowing uncertainty in the directed acyclic graph (DAG), while using a prior centered on the Clayton et al. (2002) structure. There are many more modeling assumptions made, and it seems insufficient to simply rely on graphs of model fit and posterior predictive checks, because it is unlikely that the sparse data will provide evidence against even a poor model. In the authors' defense, accommodating model uncertainty does complicate the analysis, and one must make some pragmatic decisions to simplify the process.

A second major issue is the widespread use of diffuse but proper normal and gamma priors. Because data are sparse and there are many parameters to estimate, high variance priors seem to be a very bad idea. The first issue is that one does not want

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