

A Hierarchical Model for Probabilistic Dose-Response Assessment of *Bacillus anthracis*

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Project Scope:

To assess the susceptibility of unobserved species on the basis of species with observed susceptibilities, a Bayesian meta-analysis is used to analyze experimental data from three different studies. The data obtained from the studies provided four sets of host-species/organism-strain groups for analysis as combined data using a hierarchical model. Parameters describing the susceptibility of individual species are modeled as deriving from a distribution describing the variation of susceptibilities among different species. Hyperparameters defined the prior distribution of the dose-response parameters for the population of host species and strains. Markov Chain Monte Carlo (MCMC) methods were used to develop posterior distributions of exponential dose-response model parameters for each species. A sensitivity analysis on the prior distribution was conducted to evaluate its effect on the resulting posterior distributions. This is an important factor to evaluate when the sample size is small as is typical with Category A agent dose-response studies.

Recent Progress:

A Bayesian hierarchical statistical approach to fitting dose response parameters for *Bacillus anthracis* was compared to a classical, or frequentist, likelihood-based approach. The Bayesian approach uses a fully probabilistic framework to characterize parameter uncertainty. Confidence intervals for human dose-response from the Bayesian hierarchical model were much larger than for a classical approach, but the classical pooling process requires a much stronger assumption about the relatedness of humans and other species.

Future Plans:

A major challenge is to properly represent the degree of relatedness of different dose-response experiments. A framework for future research in this area is to consider two attributes for each experiment, microbial strain virulence and host species susceptibility. An autocorrelation function based on degree of difference on these attributes can then be used to represent the relatedness of different dose-response experiments in a quantitative and flexible manner.

Relevance to listed research areas:

This work is directly relevant to the Biological Threats and Countermeasures HS-STEM research area. It particularly addresses the assessment, characterization and prioritization of chemical-biological threats, and the medical response to biological threat events.

Publications:

Jade Mitchell-Blackwood, Patrick L. Gurian, and Mark Weir, “*A Bayesian statistical modeling approach for Bacillus anthracis*,” Society for Risk Analysis 2007 Annual Meeting (2007).