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Accurate Experimental Design and Model Selection Computations

In the mathematical modeling of infectious diseases, it is always a challenge to construct a good model and it is common to find multiple proposed models for the same pathogenic phenomena. Typically the models are systems of differential equations, which the authors then fit to experimental data to infer conclusions about the biological system. We consider a model selection methodology which includes models for deterministic individual dynamics and random population effects. These are combined in the stochastic complexity model selection criterion which balances goodness-of-fit with a measure of statistical sophistication. The inverse problem concerning the distinguishability of a class of models will be discussed. In particular, a previously unaddressed issue concerns the relationship between random sources and those arising from the numerical discretization. For example, when modeling *in vivo* HIV infection dynamics under therapy, log-normally distributed errors are frequently assumed in measuring the viral plasma counts. A crucial component to the computation of the model selection criteria in involves estimating the log-likelihood which changes dramatically depending upon the absolute tolerance of the ODE solver. Analytical and computational results in the context of the HIV example will be presented as well as preliminary development on a method for addressing this issue.