

LilleBror for misspecification-robust likelihood free inference in high dimensions

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Likelihood-free inference for simulator-based statistical models has recently grown rapidly from its infancy to a useful tool for practitioners. However, models with more than a very small number of parameters as the target of inference have remained an enigma, in particular for the approximate Bayesian computation (ABC) community. To advance the possibilities for performing likelihood-free inference in high-dimensional parameter spaces, here we introduce an extension of the popular Bayesian optimisation based approach to approximate discrepancy functions in a probabilistic manner which lends itself to an efficient exploration of the parameter space. Our method achieves computational scalability by using separate acquisition procedures for the discrepancies defined for different parameters. These efficient high-dimensional simulation acquisitions are combined with exponentiated loss-likelihoods to provide a misspecification-robust characterisation of the marginal posterior distribution for all model parameters. The method successfully performs computationally efficient inference in a 100-dimensional space on canonical examples and compares favourably to existing Copula-ABC methods. We further illustrate the potential of this approach by fitting a bacterial transmission dynamics model to daycare centre data, which provides biologically coherent results on the strain competition in a 30-dimensional parameter space.