



On optimality of kernels for approximate Bayesian computation using sequential Monte Carlo

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Approximate Bayesian computation (ABC) has gained popularity over the past few years for the analysis of complex models arising in population genetic, epidemiology and system biology. Sequential Monte Carlo (SMC) approaches have become work horses in ABC. Here we discuss how to construct the perturbation kernels that are required in ABC SMC approaches, in order to construct a set of distributions that start out from a suitably defined prior and converge towards the unknown posterior. We derive optimality criteria for different kernels, which are based on the Kullback-Leibler divergence between a distribution and the distribution of the perturbed particles. We will show that for many complicated posterior distributions, locally adapted kernels tend to show the best performance. In cases where it is possible to estimate the Fisher information we can construct particularly efficient perturbation kernels. We find that the added moderate cost of adapting kernel functions is easily regained in terms of the higher acceptance rate. We demonstrate the computational efficiency gains in a range of toy-examples which illustrate some of the challenges faced in real-world applications of ABC, before turning to two demanding parameter inference problem in molecular biology, which highlight the huge increases in efficiency that can be gained from choice of optimal models. We conclude with a general discussion of rational choice of perturbation kernels in ABC SMC settings.

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