

Model misspecification in population genomic

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Abstract

In likelihood-free settings, problematic effects of model misspecification can manifest themselves during computation, leading to nonsensical answers, particularly causing convergence problems in sequential algorithms. This issue has been well studied in the last 10 years, leading to a number of methods for robust inference. In practical applications, likelihood-free methods tend to be applied to the output of complex simulations where there is a choice of summary statistics that can be computed. One approach to handling misspecification is to simply not use summary statistics computed from simulations of the model under the prior that cannot be matched with those observed in the data. This presentation gives a brief review of methods for observing and handling misspecification in ABC and SBI, and then discusses approaches that we have explored in a population genomic modelling framework.