

# ABC and Bayesian Model Choice

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Approximate Bayesian computation (ABC) has been a primary tool of inference in population genetics for the past 15 years, in particular for the comparison and selection of evolution scenarios. However, in complex models, ABC algorithms need to summarise the data into small dimension summary statistics.

The choice of those summary statistics has important bearings on the validation of the resulting inference.

Those statistics are nonetheless customarily used in ABC algorithms and applied studies without consistency checks. After exposing the bases of ABC algorithms, we show why this is the case and we derive necessary and sufficient conditions on summary statistics for the corresponding Bayes factor to be convergent, namely to asymptotically select the true model. Those conditions, which amount to the expectations of the summary statistics differing asymptotically under the two models, are quite natural and can be exploited in ABC settings to infer whether or not a choice of summary statistics is appropriate, via a Monte Carlo validation.