An introduction to Approximate Bayesian Computation methods

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Many statistical applications in several areas as genetics, epidemiology or population biology, often involve stochastic models with analytically intractable likelihood functions. The rapidly growing literature on Approximate Bayesian Computation (ABC) has led to a set of methods which do not involve direct calculation of the likelihood, leading to approximate Bayesian inference. Along the talk we will introduce the type of problems and the ideas behind these approximations. Several extensions of the basics algorithms will be presented, and finally, we will show how the goodness of fit approach for this type of models could be assess in a very easy way. Along the talk we will highlight many of the open problems in this area that could be interesting for future collaborations.