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Abstract

Approximate Bayesian Computational (ABC) method, also known as the likelihood free method, has been a popular and most satisfactory approach in recent years to approximate the posterior distribution when the likelihood of data is intractable. This approximation is applied in a wealth of applications such as genetics. In this project, we study the original ABC algorithms. Three models are evaluated, including – Basic ABC model 1, Basic ABC model 2 and I.I.D. model. One application is the AR (1) model where real data example is illustrated. All models are built on two Monte Carlo Methods – rejection sampling and Markov Chain Monte Carlo (MCMC) method.