

## **Abstract**

Approximate Bayesian Computation (ABC) methods are a new class of likelihood-free techniques that deal with intractable likelihood problems in Bayesian statistics. ABC methods have proven their usefulness in many applications in which the likelihood is intractable or expensive to compute such as genetics, biology, time series. This project is a study of the developments in ABC in the recent years, divided into three parts.

Part one studies developments in Rejection ABC and MCMC ABC algorithms. Rejection ABC proves to be a simple and intuitive way to implement ABC but is hugely inefficient and three innovations are introduced and evaluated. MCMC ABC provides better efficiency by sacrificing independent samples for dependent samples.

Part two explores a new and novel approach in ABC for i.i.d models that is able to retain the probabilistic structure of the models. A naive MCMC algorithm with one auxiliary data proves to be very inefficient while an improved MCMC algorithm with multiple datasets provides us with both efficiency and an acceptable degree of accuracy. An attempt is made to validate the idea that noisy ABC results in better accuracy than MCMC with multiple datasets for larger data size.

Part three looks at how ABC can be used in applied problems, in particular particle filtering for Hidden Markov Models, acknowledging the usefulness of ABC while also noting the risk of the filter collapse.