

Approximate Bayesian Computation

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Introduction

The objective of this presentation is to give an overview of the Approximate Bayesian Computation (ABC) algorithm through the replication of the paper **Approximate Bayesian computational methods** by Marin et al. (2012).

The paper talks about different variants of ABC by estimating the posterior of Moving Average models.

ABC methods are known as likelihood-free techniques, thus are a useful approach in problems that the likelihood is intractable, e.g., likelihood not available in closed form, or likelihood too expensive to calculate.

- Coalecent models in population genetics (Tavaré et al., 1997);
- Species dynamics (Jabot and Lohier, 2016);
- Real-world model of HIV transmission (McKinley et al., 2018).

In some settings where we have latent variables, the likelihood is expressed as:

$$\ell(\boldsymbol{\theta} \mid \mathbf{y}) = \int \ell^*(\boldsymbol{\theta} \mid \mathbf{y}, \mathbf{u}) d\mathbf{u}$$

Hence, \mathbf{y} is observed and \mathbf{u} is latent and $\boldsymbol{\theta}$ is the parameter of interest.

Rubin (1984) described the ABC algorithm as a thought experiment to explain how to sample from a posterior distribution. Tavaré et al. (1997) is usually considered the paper responsible for the proposing ABC for inferring the posterior distribution.

Algorithm 1: Original ABC method

```
for  $i=1$  to  $N$  do  
  repeat  
    Sample  $\theta' \sim \pi(\cdot)$   
    Generate  $z \sim p(\cdot \mid \theta')$   
  until  $y = z$ ;  
end
```

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