Approximate Bayesian Computation

Davi Barreira

FGV - Escola de Matemtica Aplicada

Table of contents

- 1. Objective & Motivation
- 2. Original ABC Algorithm
- 3. Moving Average

Objective & Motivation

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.

Objective & Motivation

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).

Objective & Motivation

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

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

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

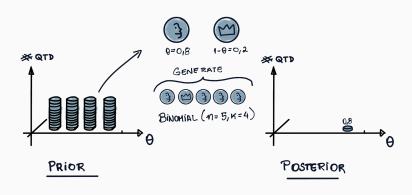
4

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 infering the posterior distribution.

Algorithm 1: Original ABC method

```
\begin{tabular}{ll} \textbf{for } i{=}1 \ to \ N \ \textbf{do} \\ & & \textbf{repeat} \\ & & \textbf{Sample } \theta' \sim \pi(\cdot) \\ & & \textbf{Generate } \textbf{z} \sim p(\cdot \mid \theta') \\ & & \textbf{until } \textbf{y} = \textbf{z}; \\ \end{tabular}
```

Below we have an schematic drawing with an example of the ABC method for Beta/Binomial model.



The proof that the algorithm indeed results in an iid sample from the posterior is shown below. Let y be the observed, θ the parameter of interest and z the generated samples.

$$p(\theta_i) \propto \sum_{\mathbf{z} \in \mathbb{D}} \pi(\theta_i) p(\mathbf{z} \mid \theta_i) \mathbb{I}_{\mathbf{y}}(\mathbf{z}) = \pi(\theta_i) p(\mathbf{y} \mid \theta_i) \propto \pi(\theta_i \mid \mathbf{y})$$

Pritchard et al. (1999) extended the original algorithm to the case of continuos sample spaces.

Algorithm 2: ABC method for discrete and continuous distributions

```
\begin{tabular}{l|l} \textbf{for } i = 1 \ to \ N \ \textbf{do} \\ \hline & \textbf{repeat} \\ & \mid \ \mathsf{Sample} \ \theta' \sim \pi(\cdot) \\ & \mid \ \mathsf{Generate} \ \textbf{z} \sim p(\cdot \mid \theta') \\ & \quad \textbf{until} \ \rho[\eta(\textbf{\textit{y}}), \eta(\textbf{\textit{z}})] \leq \epsilon; \\ \hline \end{tabular}
```

end

- $-\eta$: function defining a statistic (e.g. the mean),
- ρ : a distance function,
- $-\epsilon$: acceptance tolerance.

For this ABC algorithm, instead of the actual posterior, we get

$$\pi_{\epsilon}(\theta, \mathbf{z} \mid \mathbf{y}) = \frac{\pi(\theta)p(\mathbf{z} \mid \theta)\mathbb{I}_{A_{\epsilon, \mathbf{y}}}(\mathbf{z})}{\int_{A_{\epsilon, \mathbf{y}} \times \theta} \pi(\theta)p(\mathbf{z} \mid \theta)d\mathbf{z}d\theta}$$

Where, $A_{\epsilon, y} = \{ z \in \mathbb{D} \mid \rho[\eta(z), \eta(y) \leq \epsilon]. \}$

Hence, for a tolerance (ϵ) "small enough", we expect a good approximation.

$$\pi_{\epsilon}(oldsymbol{ heta} \mid oldsymbol{y}) = \int \pi_{\epsilon}(oldsymbol{ heta}, oldsymbol{z} \mid oldsymbol{y}) doldsymbol{z} pprox \pi(oldsymbol{ heta} \mid oldsymbol{y})$$

Moving Average

We will use the Moving Average model, also denoted as MA(q), for assessing the performance of the ABC methods. The MA(q) process is a stochastic process defined by:

$$y_k = u_k + \sum_{i=1}^q \theta_i u_{k-i}$$

Where $(u_k)_{k\in\mathbb{Z}}\stackrel{iid}{\sim} N(0,1)$. For a q=2, imposing the standard identifiability condition we obtain the following conditions:

$$-2<\theta_1<2, \qquad \theta_1+\theta_2>-1, \qquad \theta_1-\theta_2<1.$$

Hence, we use an uniform distribution over this triangular region as prior for θ . The likelihood of $\mathbf{y} \mid \theta$ is more complex because of the need to integrate \mathbf{u} .

Moving Average

We generate a synthetic sample of length 100 using $(\theta_1, \theta_2) = (0.6, 0.2)$. For q = 2 we can also numerically calculate the real posterior and the marginal distributions.

$$\pi(\theta \mid \mathbf{y}) \propto \pi(\theta) p(\mathbf{y} \mid \theta), \qquad \mathbf{y} \mid \theta \sim MVN(0, \Sigma)$$

$$\Sigma = \begin{bmatrix} 1 + \theta_1^2 + \theta_2^2 & \theta_1 + \theta_2\theta_1 & \theta_2 & 0 & 0 & 0 & \dots & 0 \\ \theta_1 + \theta_2\theta_1 & 1 + \theta_1^2 + \theta_2^2 & \theta_1 + \theta_2\theta_1 & \theta_2 & 0 & 0 & \dots & 0 \\ \theta_2 & \theta_1 + \theta_2\theta_1 & 1 + \theta_1^2 + \theta_2^2 & \theta_1 + \theta_2\theta_1 & \theta_2 & 0 & \dots & 0 \\ 0 & \theta_2 & \theta_1 + \theta_2\theta_1 & 1 + \theta_1^2 + \theta_2^2 & \theta_1 + \theta_2\theta_1 & \theta_2 & \dots & 0 \\ \vdots & \vdots \\ 0 & 0 & 0 & 0 & 0 & 0 & \theta_2 & \theta_1 + \theta_1\theta_2 & 1 + \theta_1^2 + \theta_2^2 \end{bmatrix}$$

References i

- Jabot, F. and Lohier, T. (2016). Non-random correlation of species dynamics in tropical tree communities. *Oikos*, 125(12):1733–1742.
- Marin, J.-M., Pudlo, P., Robert, C. P., and Ryder, R. J. (2012). Approximate bayesian computational methods. *Statistics and Computing*, 22(6):1167–1180.
- McKinley, T. J., Vernon, I., Andrianakis, I., McCreesh, N., Oakley, J. E., Nsubuga, R. N., Goldstein, M., and White, R. G. (2018). Approximate bayesian computation and simulation-based inference for complex stochastic epidemic models. *Statist. Sci.*, 33(1):4–18.
- Pritchard, J. K., Seielstad, M. T., Perez-Lezaun, A., and Feldman, M. W. (1999). Population growth of human Y chromosomes: a study of Y chromosome microsatellites. *Molecular Biology and Evolution*, 16(12):1791–1798.

References ii

- Rubin, D. B. (1984). Bayesianly justifiable and relevant frequency calculations for the applied statistician. *Ann. Statist.*, 12(4):1151–1172.
- Tavaré, S., Balding, D. J., Griffiths, R. C., and Donnelly, P. (1997). Inferring coalescence times from dna sequence data. *Genetics*, 145(2):505–518.