Approximate Bayesian Computation

Davi Barreira

FGV - Escola de Matemtica Aplicada

Introduction

Objective

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.

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).

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.

Original Algorithm

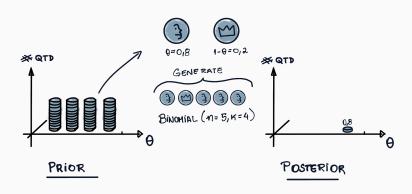
Rubin (1984) described the ABC algorithm as a thought experiment to explain how to sample from a posterior distribution. Tavaré et al. (1997) is usually considered the paper responsible for the proposing ABC for infering the posterior distribution.

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}
```

Original Algorithm

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



Original Algorithm

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

Algorithm 2: ABC method for discrete and continuous distributions

end

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

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.