

Approximate Bayesian Computation

Davi Barreira

FGV - Escola de Matematica 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.

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)

Some references to showcase `[allowframebreaks]` Marin et al. (2012)

References

- 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.

- 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.