Approximate Bayesian Computation

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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.

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.

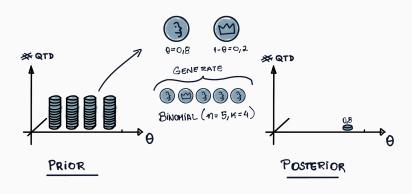
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Rubin (1984) described the ABC algorithm as a thought experiment to explain how to sample from a posterior distribution. Tavaré et al. (1997) is usually considered the paper responsible for the proposing ABC for infering the posterior distribution.

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}
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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{y}), \eta(\textbf{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.

$$\pi_{\epsilon}(heta \mid extbf{ extit{y}}) = \int \pi_{\epsilon}(heta, extbf{ extit{z}} \mid extbf{ extit{y}}) d extbf{ extit{z}} pprox \pi(heta \mid extbf{ extit{y}})$$

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.