# **K2-ABC: Approximate Bayesian Computation with Kernel Embeddings**

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### Summary

- ABC = Bayesian inference paradigm: likelihood is intractable but generating (pseudo) data given any parameter value is easy.
- Approximate posterior defined through a *measure of similarity* between pseudo data and the observed data.
- Similarity typically measured through summary statistics: difficult to define, requires domain experts and often introduces a difficult-to-quantify information loss when statistics are not sufficient.
- Contribution: Use Maximum Mean Discrepancy (MMD), a kernel-based distance between probability measures, to define this similarity.
  No information loss for a broad family of kernels.

## Maximum Mean Discrepancy (MMD) [1]

$$MMD(P,Q) = \sup_{\|f\|_{\mathcal{H}} \le 1} \mathbb{E}_{\mathbf{x} \sim P}[f(\mathbf{x})] - \mathbb{E}_{\mathbf{y} \sim Q}[f(\mathbf{y})] = \|\mu_P - \mu_Q\|_{\mathcal{H}}$$
$$\approx \left[\frac{1}{n(n-1)} \sum_{i \neq j} k(\mathbf{x}_i, \mathbf{x}_j) + \frac{1}{n(n-1)} \sum_{i \neq j} k(\mathbf{y}_i, \mathbf{y}_j) - \frac{2}{n^2} \sum_{i,j=1}^n k(\mathbf{x}_i, \mathbf{y}_j)\right]^{1/2}$$

Nonparametric distance

### **Approximate Bayesian Computation (ABC)**

• Given: Prior  $p(\theta)$ , intractable likelihood  $p(\mathbf{Y}|\theta)$ , observed set  $\mathbf{Y}$ . • Goal: Sample from  $p(\theta|\mathbf{Y}) \propto p(\theta)p(\mathbf{Y}|\theta)$ . • Problem: Cannot evaluate  $p(\mathbf{Y}|\theta)$ . Can sample  $\mathbf{X} \sim p(\cdot|\theta)$  easily.

**Example**: a complicated dynamical system for blow fly population

$$N_{t+1} = PN_{t-\tau} \exp\left(-\frac{N_{t-\tau}}{N_0}\right) e_t + N_t \exp(-\delta \varepsilon_t)$$
where  $e_t \sim \text{Gamma}\left(\frac{1}{\sigma_p^2}, \sigma_p^2\right)$  and  $\varepsilon_t \sim \text{Gamma}\left(\frac{1}{\sigma_d^2}, \sigma_d^2\right)$ .
$$\bullet \theta := \{P, N_0, \sigma_d, \sigma_p, \tau, \delta\}$$

$$\bullet \text{Given } \mathbf{Y} = \{N_1, \dots, N_T\}, \text{ want } \mathbf{y}^* \qquad \text{from prior}$$

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$$\mathsf{MMD}(P,Q) = 0 \iff P = Q$$
  
• Kernel  $k(\mathbf{x},\mathbf{y}) = \langle \phi(\mathbf{x}), \phi(\mathbf{y}) \rangle_{\mathcal{H}}$   
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Space of distributions  $E_{\mathbf{x} \sim P}[\phi(\mathbf{x})]$ 

•  $\mu_{p(\cdot|\theta)}$  is always sufficient. • Intuitively,  $\mu_{p(\cdot|\theta)}$  contains all moments of  $p(\cdot|\theta)$ .

# K2-ABC (Proposed)

**Output:** Posterior empirical distribution  $\sum_{i=1}^{M} w_i \delta_{\theta_i}$ 1: for i = 1, ..., M do 2: Sample  $\theta_i \sim p(\theta)$ 3: Sample pseudo dataset  $\mathbf{X}_i \sim p(\cdot | \theta_i)$ 4:  $\widetilde{w}_i = \kappa_{\varepsilon}(\mathbf{X}_i, \mathbf{Y}) = \exp\left(-\widehat{\mathrm{MMD}}(\mathbf{X}_i, \mathbf{Y})^2 / \varepsilon\right)$ 5: Set  $w_i = \widetilde{w}_i / \sum_{j=1}^{M} \widetilde{w}_j$  for i = 1, ..., M

**Experiments on Blow Fly Data** 

## **ABC Likelihood** $p_{\varepsilon}(\mathbf{Y}|\boldsymbol{\theta})$



κ<sub>ε</sub>(X, Y) defines similarity between X and Y.
ABC algorithms sample from p<sub>ε</sub>(θ|Y) ∝ p(θ)p<sub>ε</sub>(Y|θ)
Commonly used rejection ABC sets κ<sub>ε</sub>(X, Y) := 1[||s(X) - s(Y)||<sub>2</sub> < ε].</li>
-s : function to compute summary statistics
-1[·] ∈ {0,1}: indicator function

#### **Problems with Summary Statistics** $s(\cdot)$

- Difficult to design **sufficient statistics**.
- More statistics give high sufficiency. But, higher rejection rate. • Insufficient  $s(\cdot)$  will lead to an incorrect posterior.



K2-ABC can infer correct  $\theta$  without the need for handcrafted  $s(\cdot)$ .

### **Contribution: Kernel-Based Similarity**

• Use a kernel distance MMD to define similarity  $\kappa_{\varepsilon}$ . No need for  $s(\cdot)$ .

Rejection ABC	K2-ABC (Proposed)
$egin{aligned} & \kappa_{m{arepsilon}}(\mathbf{X},\mathbf{Y}) \ &= 1[\ s(\mathbf{X})-s(\mathbf{Y})\ _2 < m{arepsilon}] \end{aligned}$	$egin{aligned} & \kappa_{m{arepsilon}}(\mathbf{X},\mathbf{Y}) \ &= \expig(-\widehat{\mathrm{MMD}}(\mathbf{X},\mathbf{Y})^2/m{arepsilon}ig) \end{aligned}$

• MMD can detect any difference in distributions without the need of handcrafted summary statistics.

#### References

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Code: github.com/wittawatj/k2abc