



Robust Bayesian Inference for Simulator-based Models via the MMD Posterior Bootstrap

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Outline

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Motivation

- Independent sampling is possible, but the likelihood is unavailable
- Model is usually at best a rough approximation of a complex physical or biological phenomenon
- It will most likely not capture all of the key characteristics of the underlying data generating process.



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Background

• Place a nonparametric prior *directly* on the data-generating mechanism \mathbb{P}^* :

 $\mathbb{P} \sim DP(\alpha, \mathbb{F}), \quad \mathbb{P}|_{x_{1:n}} \sim DP(\alpha', \mathbb{F}')$

where

$$\alpha' = \alpha + n, \quad \mathbb{F}' := \frac{\alpha}{\alpha + n} \mathbb{F} + \frac{n}{n + \alpha} \mathbb{P}_n, \quad \mathbb{P}_n = \frac{1}{n} \sum_{i=1}^n \delta_{x_i}$$

For a loss function *I*(*x*, θ) propagate uncertainty from P* to the parameter of interest θ through

 $\theta_l^*(\mathbb{P}^*) := \operatorname{arg\,inf}_{\theta \in \Theta} \mathbb{E}_{X \sim \mathbb{P}^*}[l(X, \theta)]$

The push-forward measure $(\theta_I^*)_{\#}(\mathsf{DP}(\alpha',\mathbb{F}'))$ gives a posterior on Θ denoted by Π_{NPL} .

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Method

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$$\bigcup (\mathbb{P}_{\theta}, \mathbb{P}^{*})$$

- Use a distance-based loss between real and target distribution
- Target: $\theta_0 = \arg \inf_{\theta \in \Theta} D(\mathbb{P}^*, \mathbb{P}_{\theta})$ for some distance function $D : \mathcal{P} \times \mathcal{P} \to \mathbb{R}_+$
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Proposal: Maximum Mean Discrepancy (MMD) based loss

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- Map θ^* now corresponds to a minimum MMD estimator as in Briol et al. (2019); Chérief-Abdellatif and Alquier (2022)
- Integral Probability Metrics (IPMs), Müller (1997):

$$D(\mathbb{P},\mathbb{Q}) = \sup_{f\in\mathcal{F}} \left| \int_{\mathcal{X}} f(x)\mathbb{P}(dx) - \int_{\mathcal{X}} f(x)\mathbb{Q}(dx) \right|$$

- Maximum Mean Discrepancy (MMD): Restrict *F* to a unit *Reproducing Kernel Hilbert space* (RKHS), *H_k*, defined through a symmetric, positive definite kernel function k : X × X → ℝ, with associated norm || · ||_{H_k} and inner product ⟨·, ·⟩_{H_k} : *H_k* × *H_k* → ℝ.
- Reproducing property:

$$f(x) = \langle f, k(\cdot, x) \rangle_{\mathcal{H}_k}$$

• Functions in \mathcal{H}_k have the form $f(x) = \sum_{i=1}^d c_i k(x, x_i)$ for some $c_i \in \mathbb{R}$

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Maximum Mean Discrepancy (MMD)

• So MMD is defined as:

$$MMD(\mathbb{P},\mathbb{Q}) = \sup_{\substack{f \in \mathcal{H}_k, \\ \|f\|_{\mathcal{H}_k} \le 1}} \left| \int_{\mathcal{X}} f(x) \mathbb{P}(dx) - \int_{\mathcal{X}} f(x) \mathbb{Q}(dx) \right|$$

- The MMD between two probability measures $\mathbb P$ and $\mathbb Q$ can be expressed as

$$\begin{split} MMD^{2}(\mathbb{P},\mathbb{Q}) &:= \int_{\mathcal{X}} \int_{\mathcal{X}} k(x,y) \mathbb{P}(dx) \mathbb{P}(dy) - 2 \int_{\mathcal{X}} \int_{\mathcal{X}} k(x,y) \mathbb{P}(dx) \mathbb{Q}(dy) \\ &+ \int_{\mathcal{X}} \int_{\mathcal{X}} k(x,y) \mathbb{Q}(dx) \mathbb{Q}(dy) \end{split}$$

• It can be estimated for example using a U-statistic as in Gretton et al. (2008):

$$\begin{split} MMD_{k,U}^{2}(\mathbb{P}^{m},\mathbb{Q}^{n}) &= \frac{1}{m(m-1)} \sum_{i \neq j} k(y_{i},y_{j}) - \frac{2}{nm} \sum_{i=1}^{n} \sum_{j=1}^{m} k(x_{i},y_{j}) \\ &+ \frac{1}{n(n-1)} \sum_{i \neq j} k(x_{i},x_{j}) \end{split}$$

where $\{y_j\}_{j=1}^m \stackrel{iid}{\sim} \mathbb{P}$ and $\{x_i\}_{i=1}^n \stackrel{iid}{\sim} \mathbb{Q}$.

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 $\longrightarrow \theta^*(\mathbb{P}^*) = \operatorname{arg\,inf}_{\theta \in \Theta} \mathsf{MMD}^2_{k,U}(\mathbb{P}^*, \mathbb{P}_{\theta})$

MMD Posterior Bootstrap

• Draw
$$\mathbb{P}^{(j)} \sim \mathsf{DP}(lpha', \mathbb{F}')$$

• Obtain $\theta^{(j)} := \theta^*(\mathbb{P}^{(j)}) = \arg \min_{\theta \in \Theta} \mathsf{MMD}^2_{k,U}(\mathbb{P}^{(j)}, \mathbb{P}_{\theta})$

$$\begin{split} \tilde{x}_{1:T}^{(j)} &\stackrel{\text{iid}}{\sim} \mathbb{F}, \quad (w_{1:n}^{(j)}, \tilde{w}_{1:T}^{(j)}) \sim \text{Dir}\left(1, \dots, 1, \frac{\alpha}{T}, \dots, \frac{\alpha}{T}\right). \\ \mathbb{P}^{(j)} &= \sum_{i=1}^{n} w_{i}^{(j)} \delta_{x_{i}} + \sum_{k=1}^{T} \tilde{w}_{k}^{(j)} \delta_{\bar{x}_{k}^{(j)}} \sim \hat{\nu}. \end{split}$$
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where $\hat{
u}$ denotes the probability measure on $\mathcal P$ defined by (1).

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Algorithm 1: MMD Posterior Bootstrap

input: $\mathbf{x}_{1:n}$, T, B, α , \mathbb{F} , \mathbb{U} , G_{θ} . for $j \leftarrow 1$ to B do Sample $\tilde{\mathbf{x}}_{1:T}^{(j)} \stackrel{\text{iid}}{\sim} \mathbb{F}$ and $(w_{1:n}^{(j)}, \tilde{w}_{1:T}^{(j)}) \sim \text{Dir}(1, \dots, 1, \frac{\alpha}{T}, \dots, \frac{\alpha}{T}).$ Set $\mathbb{P}^{(j)} = \sum_{i=1}^{n} w_{i}^{(j)} \delta_{x_{i}} + \sum_{k=1}^{T} \tilde{w}_{k}^{(j)} \delta_{\tilde{x}_{k}^{(j)}}.$ Obtain $\theta^{(j)} = \theta^{*}(\mathbb{P}^{(j)})$ using numerical optimisation.

return Posterior bootstrap sample $\theta^{(1:B)}$

Theoretical Results

- Assumption: $\sup_{x,x'\in\mathcal{X}} |k(x,x')| < \infty$
- W.L.O.G. $|k(x, x')| \leq 1 \quad \forall \quad x, x' \in \mathcal{X}$
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Generalisation error

- Assumption: $\sup_{x,x'\in\mathcal{X}} |k(x,x')| < \infty$
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$$0 \leq \underbrace{\mathbb{E}}_{x_{1:n} \stackrel{\text{id}}{\sim} \mathbb{P}^*} \left[\mathbb{E}_{\mathbb{P} \sim \nu} \left[\mathsf{MMD}(\mathbb{P}^*, \mathbb{P}_{\theta^*}(\mathbb{P})) \right] \right] - \inf_{\theta \in \Theta} \mathsf{MMD}(\mathbb{P}^*, \mathbb{P}_{\theta})}_{\leq \frac{2}{\sqrt{n}} + \frac{2}{\sqrt{\alpha + n + 2}} + \frac{4\alpha}{\alpha + n}}$$



• Rate agrees with results in Chérief-Abdellatif and Alquier (2022)

• For standard Bayesian inference with posterior measure Π_n defined on Θ directly, for any $M_n \to +\infty$ such that $M_n n^{-\frac{1}{2}} \to 0$:

$$\Pi_n\left(\theta\in\Theta:\mathsf{MMD}(\mathbb{P}_{\theta},\mathbb{P}^*)>\mathsf{inf}_{\theta\in\Theta}\mathsf{MMD}(\mathbb{P}_{\theta},\mathbb{P}^*)+\tfrac{M_n}{n^{1/2}}\right)\overset{n\to\infty}{\longrightarrow}0\qquad(2)$$

• In our case:

$$\nu\left(\mathbb{P}\in\mathcal{P}:\mathsf{MMD}(\mathbb{P}_{\theta^*(\mathbb{P})},\mathbb{P}^*)>\inf_{\theta\in\Theta}\mathsf{MMD}(\mathbb{P}_{\theta},\mathbb{P}^*)+\frac{M_n}{n^{1/2}}\right)\stackrel{n\to\infty}{\longrightarrow}0.$$

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• Suppose $\mathbb{P}^* = (1 - \epsilon) \tilde{\mathbb{P}} + \epsilon \mathbb{Q}$

• Then

$$\mathbb{E}_{\substack{\mathbf{x}_{1:n} \text{ id } \mathbb{P}^{*}}} \left[\mathbb{E}_{\mathbb{P} \sim \hat{\nu}} \left[\mathsf{MMD} \left(\tilde{\mathbb{P}}, \mathbb{P}_{\theta^{*}}(\mathbb{P}) \right) \right] \right]$$

$$\leq \inf_{\theta \in \Theta} \mathsf{MMD}(\tilde{\mathbb{P}}, \mathbb{P}_{\theta}) + 4\epsilon + \frac{2}{\sqrt{n}} + \frac{2}{\sqrt{\alpha + n + 2}} + \frac{4\alpha}{\alpha + n}$$

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Applications

 $\mathbb{P}^* = (1 - \epsilon) \mathbb{P}_{\theta_0} + \epsilon \mathbb{Q} \text{ where } \mathbb{P}_{\theta_0} \text{ denotes the G-and-k distribution with } \\ \theta_0 = (3, 1, 1, -\log(2)), \text{ and } \mathbb{Q} \text{ is the shifted distribution } \mathbb{Q} = \mathbb{P}_{\theta_0} \pm 50$



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Example: Contaminated G-and-k distribution model



Figure 1: Comparison of posterior marginal distributions obtained using the MMD Posterior Bootstrap (NPL-MMD) and the Wasserstein-ABC (WABC) method in Bernton et al. (2019).

- Arising in Systems Biology (see e.g. Bonassi et al., 2011)
- A dynamic model used to study cellular networks describing the interaction of two genes over time
- For cell *i* and unknown parameters $\theta = (\alpha_1, \alpha_2, \beta_1, \beta_2, \mu, \sigma, \gamma)^\top$, the simulator input is $u_i = (u_{i,1,1}, u_{i,1,2}, \dots, u_{i,\tau,1}, u_{i,\tau,2}, u_{i,\tau+1,1})^\top \sim \text{Unif}([0, 1]^{2T+1})$ and the simulator G_{θ} is defined through:

$$G_{\theta}(u_{i}) = \Phi^{-1} \left(\Phi \left(\frac{-(\mu + v_{i,T}) v_{i,T}^{\gamma}}{\mu \sigma} \right) + u_{i,T+1,1} \left(1 - \Phi \left(\frac{-(\mu + v_{i,T}) v_{i,T}^{\gamma}}{\mu \sigma} \right) \right) \right) \frac{\mu \sigma}{v_{i,T}^{\gamma}} + (\mu + v_{i,T})$$

where for $t = 1, \ldots, T - 1$, we have

$$\begin{split} \tilde{v}_{i,t+1} &= v_{i,t} + \frac{\alpha_1}{1 + w_{i,t}^{\beta_1}} - (1 + 0.03v_{i,t}) \\ \tilde{w}_{i,t+1} &= w_{i,t} + \frac{\alpha_2}{1 + v_{i,t}^{\beta_2}} - (1 + 0.03w_{i,t}) \\ v_{i,t+1} &= \tilde{v}_{i,t+1} + 0.5\Phi^{-1} \big(\Phi(-2\tilde{v}_{i,t+1}) + u_{i,t,1}(1 - \Phi(-2\tilde{v}_{i,t+1})) \big) \\ w_{i,t+1} &= \tilde{w}_{i,t+1} + 0.5\Phi^{-1} \big(\Phi(-2\tilde{w}_{i,t+1}) + u_{i,t,2}(1 - \Phi(-2\tilde{w}_{i,t+1})) \big) \end{split}$$

- Arising in Systems Biology (see e.g. Bonassi et al., 2011)
- A dynamic model used to study cellular networks describing the interaction of two genes over time
- For cell *i* and unknown parameters $\theta = (\alpha_1, \alpha_2, \beta_1, \beta_2, \mu, \sigma, \gamma)^\top$, the simulator input is $u_i = (u_{i,1,1}, u_{i,1,2}, \dots, u_{i,\tau,1}, u_{i,\tau,2}, u_{i,\tau+1,1})^\top \sim \text{Unif}([0, 1]^{2T+1})$ and the simulator G_{θ} is defined through:

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 Inference on θ = (α₁, α₂, β₁, β₂, μ, σ, γ) for n = 2000 data points simulated from the toggle-switch model in which 10% of the data have some added Cauchy noise of location parameter 0 and scale parameter 10.



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Discussion & current work

Strengths:

- $\checkmark\,$ Posterior Bootstrap algorithm suitable for simulator-based models inducing robustness through:
 - Bayesian Nonparametric Learning (NPL) framework
 - Minimum Maximum Mean Discrepancy (MMD) estimators
- ✓ Highly parallelisable algorithm
- \checkmark Generalisation error, posterior consistency and robustness to outliers guarantees

- ✓ Optimisation; objective usually not convex
- ✓ Kernel choice and associated hyperparameters
- MMD approximation; estimators with improved sample complexity e.g. Bharti et al. (2023)

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• Measurement Error in the covariates

• Covariate X is only observed via a *noisy* proxy W such that:

 $X = W + N, \quad \mathbb{E}[N] = 0$

• Function $g: \Theta \times \mathcal{X} \to \mathbb{R}$ explains the relationship between X and Y such that:

$$Y = g(\theta_0, X) + E, \quad \mathbb{E}[E] = 0.$$

- We do **not** have observations from \mathbb{P}^* anymore!
- If our model assumes that there is no ME, how can we be robust?
- Poster later today :)

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