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## S1 Appendix. Algorithms of calibration methods.

### 1 Algorithm for Rejection ABC

A description of the Rejection ABC algorithm is found below, as described in (1).

1. Randomly sample parameter values  $\theta^*$  independently from the prior distribution  $\pi(\theta)$ .
2. Simulate data set  $y$  from the model, using sampled parameter  $\theta^*$  and obtain a summary statistic(s)  $s$ .
3. If  $d(t, s) \leq \epsilon$ , retain  $\theta^*$ , otherwise reject, where  $d$  expresses the Euclidean distance between target  $t$  and summary statistics  $s$ , with each statistic being normalized with a division by the standard deviation of the simulated set of the statistic, and  $\epsilon$  represents a tolerance level.
4. Return to 1 and repeat until desired posterior size is attained. Where posterior size is the number of parameter combinations retained.

### 2 Algorithm for Bayesian Calibration followed by Sampling Importance Resampling

A description of the BcSIR algorithm as described in (2).

1. **Sampling Stage:** Draw initial random sample of  $N$  inputs  $(\theta_i, i = 1, 2, \dots, N)$  from the prior distribution  $\pi(\theta)$ .
2. **Importance Stage:**
  - a) For each  $\theta_i$ , run model, obtain output and calculate the likelihood  $L_i$
  - b) Compute importance weights:

$$w_i = \frac{L_i}{\sum_{j=1}^N L_j}. \quad (1)$$

3. **Resampling Stage:** Resample desired posterior size from the initial  $N$  parameter inputs with replacement, using the computed weights as sampling weights.

### 3 Algorithm for AbcSmc

A description of the AbcSmc algorithm is found below, as described in (3), where  $N$  is the number of parameter combinations sampled,  $\rho$  is the fraction retained in the posterior, and  $n = \lfloor \rho * N \rfloor$  is the size of the posterior:

1. Set the SMC iterator  $l = 1$ .
  - a) For sample iterator  $i = 1, \dots, N$ :
    - i. Sample parameter vector  $\theta_i^{(1)}$  independently from prior distributions  $\pi(\theta)$
    - ii. Simulate data  $x_i^{(1)} \sim p(x_i^{(1)} | \theta_i^{(1)})$ .
2. Calculate Partial least squares regression (PLS) model for  $\theta^{(l)}$  and  $x^{(l)}$
3. Transform observed data and each  $x_i^{(l)}$  to new independent, orthogonal metrics using PLS model
4. Calculate Euclidean distance between transformed observed and transformed simulated metrics
5. Set  $\Theta^{(l)} = \text{best } \theta^{(l)}$ , the best  $n$  samples, ranked by smallest distance.
6. The user determines the convergence of the algorithm - when a desired posterior is attained. If  $l > 1$  and  $\Theta$  has converged, stop here. Otherwise:
  - a) Set  $\tau_{l+1}^2$  equal to twice the variance of  $\Theta^{(l)}$
  - b) For  $j = 1, \dots, n$ :
    - i. Set weight  $\omega_j^{(l)} \propto \begin{cases} 1/n & : l = 1 \\ \pi(\Theta_j^{(l)}) / \sum_{k=1}^n \omega_j^{(l-1)} K(\Theta_j^{(l)} | \Theta_k^{(l-1)}; \tau_l^2) & : l > 1 \end{cases}$ 

where  $K(\Theta_j^{(l)} | \Theta_k^{(l-1)}; \tau_l^2)$  is a Gaussian perturbation kernel with mean  $\Theta_k^{(l-1)}$  and variance  $\tau_l^2$ , evaluated at  $\Theta_j^{(l)}$ .
  - c) Normalize  $\omega_i^{(l)}$  to sum to 1.
  - d) Set  $l = l + 1$ 
    - i. For  $i = 1, \dots, N$ :
      - A. Choose  $\theta_i^*$  from  $\Theta^{(l-1)}$  with probabilities  $\omega^{(l-1)}$ .
      - B. Sample  $\theta_i^{(l)}$  from  $\text{Gaussian}(\theta_i^*, \tau_l^2)$
      - C. Simulate data  $x_i^{(l)} \sim p(x_i^{(l)} | \theta_i^{(l)})$ .
  - e) Go to step 2.

#### 4 Algorithm for Seq ABC

A description of the Seq ABC algorithm, as described in (4), where  $N$  is the number of parameter values sampled,  $N\alpha = \lfloor \alpha N \rfloor$  is the number of parameter values to retain at each step among the  $N$  parameter values ( $\alpha \in [0, 1]$ ) and  $Pacc_{min}$ , a positive number between 0 and 1, is the stopping criterion of the algorithm.

1. **for**  $l=1$  **do**

a) **for**  $i = 1$  to  $N$  **do**

i. Sample parameter value  $\theta_i^{(0)}$  from the prior distribution  $\pi(\theta)$  and simulate data set  $y$  from the model such that  $y \sim f(y|\theta_i^{(0)})$ .

ii. Set  $d_i^{(0)} = d(x, y)$ , that is, distance between simulated data  $y$  and observed data  $x$

iii. Set the weight,  $w_i^{(0)} = 1$

b) **end for**

c) Let  $\epsilon_1 = Q_{p^{(0)}}(\alpha)$ , the first  $\alpha$ -quantile of the set of distance  $d^{(0)}$ , where  $d^{(0)} = \{d_i^{(0)}\}_{1 \leq i \leq N}$

d) Let  $\{(\theta_i^{(1)}, w_i^{(1)}, d_i^{(1)})\} = \{(\theta_i^{(0)}, w_i^{(0)}, d_i^{(0)}) | d_i^{(0)} < \epsilon_1, 1 \leq i \leq N\}$

e) Take  $\sigma_1^2$  as twice the weighted empirical variance of  $\{(\theta_i^{(1)}, w_i^{(1)})\}_{1 \leq i \leq N\alpha}$

f) Set  $Pacc = 1$ , where  $Pacc$  is the stopping criterion for the current step.

g)  $l \leftarrow l + 1$

2. **end for**

3. **While**  $Pacc > Pacc_{min}$  **do**, where  $Pacc_{min}$  is the stopping criterion for the algorithm

a) **for**  $i = N\alpha + 1$  to  $N$  **do**

i. Pick  $\theta_i^*$  from  $\theta_j^{(l-1)}$  with probability  $\frac{w_j^{(l-1)}}{\sum_{k=1}^{N\alpha} w_k^{(l-1)}}$ ,  $1 \leq j \leq N\alpha$

- ii. Generate  $\theta_i^{(l-1)} | \theta_i^* N(\theta_i^*, \sigma_{(l-1)}^2)$  and  $x f(x | \theta_i^{(l-1)})$
- iii. Set  $d_i^{(l-1)} = d(S(x), S(y))$
- iv. Set  $w_i^{(l-1)} = \frac{\pi(\theta_i^{(l-1)})}{\sum_{j=1}^{N_\alpha} (w_j^{(l-1)} / \sum_{k=1}^{N_\alpha} w_k^{(l-1)}) \sigma_{(l-1)}^{-1} \psi(\sigma_{(l-1)}^{-1} (\theta_i^{(l-1)} - \theta_j^{(l-1)}))}$
- b) **end for**
- c) Set  $Pacc = \frac{1}{N - N_\alpha} \sum_{k=N_\alpha+1}^N 1_{d_i^{(l-1)} < \epsilon_{l-1}}$
- d) let  $\epsilon_l = Q_{d^{(l-1)}}(\alpha)$  where  $d^{(l-1)} = \{d_i^{(l-1)}\}_{1 \leq i \leq N}$
- e) Let  $\{(\theta_i^{(l)}, w_i^{(l)}, d_i^{(l)})\} = \{(\theta_i^{(l-1)}, w_i^{(l-1)}, d_i^{(l-1)}) | d_i^{(l-1)} \leq \epsilon_l, 1 \leq i \leq N\}$
- f) Take  $\sigma_l^2$  as twice the weighted empirical variance of  $\{(\theta_i^{(l)}, w_i^{(l)})\}_{1 \leq i \leq N_\alpha}$
- g)  $l \leftarrow l + 1$
- 4. **end while**

Where  $\forall u \in [0, 1]$  and  $X = \{x_1, \dots, x_n\}$ ,  $Q_X(u) = \inf\{x \in X | F_X(x) \geq u\}$  and  $F_X(x) = \frac{1}{n} \sum_{k=1}^n 1_{x_k \leq x}$ .

Where  $\psi(x) = \frac{1}{\sqrt{2\pi}} e^{-\frac{x^2}{2}}$

## 5 Algorithm for Incremental Mixture Importance Sampling

We used the BcIMIS algorithm as described in (5), where  $N_0 = B * 10$  is the initial sample size,  $B$  is the incremental sample size at each iteration of the algorithm and  $k$  is the number of iterations.

### 1. Initial stage:

- a) Sample  $N_0$  parameter values or inputs  $\theta_1, \theta_2, \dots, \theta_{N_0}$  from the prior distribution  $p(\theta)$ .
- b) For each  $\theta_i$ , run model and calculate the likelihood  $L_i$ , and form the importance weights:

$$w_i^{(0)} = \frac{L_i}{\sum_{j=1}^{N_0} L_j}. \quad (2)$$

**2. Importance Sampling Stage:** For  $k = 1, 2, \dots$ , repeat the following steps:

- a) Choose the current maximum weight input as the center  $\theta^{(k)}$ . Estimate  $\Sigma^{(k)}$  from the weighted covariance of the  $B$  inputs with the smallest Mahalanobis distances to  $\theta^{(k)}$ , where the distances are calculated with respect to the covariance of the importance weights and  $\frac{1}{N_k}$ .
- b) Sample  $B$  new inputs from a multivariate Gaussian distribution  $H_k$  with covariance matrix  $\Sigma^{(k)}$ .
- c) Calculate the likelihood of the new inputs and combine the new inputs with the previous ones. From the importance weights:

$$w_i^{(k)} = c L_i x \frac{p(\theta_i)}{q^{(k)}(\theta_i)}, \quad (3)$$

Where  $c$  is chosen so that the weights add to 1,  $q^{(k)}$  is the mixture sampling distribution  $q^{(k)} = \frac{N_0}{N_k} p + \frac{B}{N_k} \sum_{s=1}^k H_s$ ,  $H_s$  is the  $s$ -th multivariate normal distribution,  $N_0 = B * 10$  is the initial sample size and  $N_k = N_0 + Bk$  is the total number of inputs up to iteration  $k$ .

**3. Resample Stage:**

- a) The algorithm stops when the expected fraction of unique parameter combinations in resample is at least  $(1 - \frac{1}{e}) = 0.632$
- b) Once the stopping criterion is satisfied, resample  $J$  inputs with replacement from  $\theta_1, \dots, \theta_{N_k}$  with weights  $w_1, \dots, w_{N_k}$ , where  $K$  is the number of iterations at the importance sampling stage.

# List of references

- [1] Pritchard JK, Seielstad MT, Perez-Lezaun A, Feldman MW. Population growth of human Y chromosomes: a study of Y chromosome microsatellites. *Molecular biology and evolution*. 1999;16(12):1791–1798.
- [2] Menzies NA, Soeteman DI, Pandya A, Kim JJ. Bayesian methods for calibrating health policy models: a tutorial. *PharmacoEconomics*. 2017;35(6):613–624.
- [3] Hladish TJ, Pearson CA, Chao DL, Rojas DP, Recchia GL, Gómez-Dantés H, et al. Projected impact of dengue vaccination in Yucatán, Mexico. *PLoS neglected tropical diseases*. 2016;10(5).
- [4] Lenormand M, Jabot F, Deffuant G. Adaptive approximate Bayesian computation for complex models. *Computational Statistics*. 2013;28(6):2777–2796.
- [5] Raftery AE, Bao L. Estimating and projecting trends in HIV/AIDS generalized epidemics using incremental mixture importance sampling. *Biometrics*. 2010;66(4):1162–1173.