An Approximate Likelihood Perspective on ABC Methods

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Abstract: We are living in the big data era, as current technologies and networks allow for the easy and routine collection of data sets in different disciplines. Bayesian Statistics offers a flexible modeling approach which is attractive for describing the complexity of these datasets. These models often exhibit a likelihood function which is intractable due to the large sample size, high number of parameters, or functional complexity. Approximate Bayesian Computational (ABC) methods provide likelihood-free methods for performing statistical inferences with Bayesian models defined by intractable likelihood functions. The vastity of the literature on ABC methods created a need to review and relate all ABC approaches so that scientists can more readily understand and apply them for their own work. This article provides a unifying review, general representation, and classification of all ABC methods from the view of approximate likelihood theory. This clarifies how ABC methods can be characterized, related, combined, improved, and applied for future research. Possible future research in ABC is then suggested.

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1. Introduction

Bayesian models are applied for statistical inference in many scientific fields. The posterior distribution is the main object of Bayesian Statistics and it is the result of the combination of two information sources, namely the prior distribution, which reflects extra-experimental knowledge, and the likelihood function, which formalizes the information provided by the data through the use of a given statistical model.

Posterior inferences with such models can be undertaken by applying classical Monte Carlo (MC) methods, which provide iterative algorithms that can generate approximate samples from the posterior distribution, without the marginal likelihood. They include Markov chain Monte Carlo (MCMC) methods, such as Metropolis-Hastings (MH), Gibbs, slice, and adaptive rejection sampling algorithms [e.g., 227, 44]; and include population MC [PMC, e.g., 51], sequential MC [SMC, e.g., 66], and other importance sampling (IS) methods [e.g., 166]. Alternatively, variational inference (VI) optimization methods can be applied to find a tractable density function that minimizes the divergence to the exact posterior density [30].

However, modern “big data” applications require complex models and demanding computational techniques; in some of these situations, MCMC or VI methods may be extremely slow or even impossible to implement. ABC methods are useful in the general scenario where for the given Bayesian model of interest for data analysis, the likelihood is not easily evaluated or intractable, but it is still possible to either draw samples from this likelihood conditionally on the model parameters [e.g., 98, 277, 216, 23]; or to find a point-estimate of some model parameter function based on a sufficient statistic of the data [e.g., 253], on an empirical likelihood [185], or on a bootstrap method [e.g., 285].

Approximate Bayesian Computational (ABC) methods provide “likelihood-free” methods for performing statistical inferences with Bayesian models defined by intractable likelihood functions.

Since ABC was introduced [253, 216, 23], it has been applied to many scientific fields, models, and problems involving intractable likelihoods. ABC has been applied in independent and related fields of archaeology [e.g., 282, 260, 60]; astronomy and cosmology [e.g., 157, 50, 278, 4, 138]; various biology subfields including cell biology [e.g., 135, 268, 269], ecology and molecular ecology [e.g., 258, 282, 21, 122, 283, 151, 26, 91], evolutionary biology and molecular ecology [e.g., 116, 127, 86, 233, 267, 21, 87, 167, 222, 244, 85], genetics [e.g., 22, 36, 178, 255], molecular biology [e.g., 216], population biology [e.g., 83, 192, 18, 21, 28, 82, 274, 10, 75], population genetics [e.g., 23, 179, 249, 113, 251, 24, 84] and phylogeography [e.g., 21, 116], synthetic biology [e.g., 14], systematic biology [e.g., 253, 254, 17, 165], and systems biology [e.g., 252, 218, 219, 258, 21, 257, 164, 147, 155, 162]; climate science [e.g., 118]; economics including econometrics, finance, insurance [e.g., 202, 199, 49, 207, 201]; epidemiology [e.g., 241, 169, 180, 258, 21, 34, 1, 270, 173, 150, 110, 182, 232]; hydrology [e.g., 272, 193], nonlinear system identification (SID) [e.g., 148]; nuclear medicine [e.g., 89]; oncology [e.g., 238]; pharmacokinetics and pharmadynamics [e.g.,
ABC methods have been developed to estimate various Bayesian models with intractable likelihood, including alpha-stable [199], bivariate beta distribution [e.g., 204], coalescent [e.g., 253, 87], copula [106, 107, 108], differential equation [e.g., 258], ecological [e.g., 283, 91], epidemic [e.g., 180, 181, 182, 150], extreme value [81, 80], financial [e.g., 199], hidden Markov [e.g., 130], hydrological [e.g., 193], image analysis [e.g., 193, 188], network analysis [e.g., 273, 92], order-restricted [140], population evolution [e.g., 173], quantile distribution [e.g., 6, 73, 211], spatial process [239], species abundance distribution [e.g., 124], state-space [16, 265], stationary process [8], statistical relational learning [63], susceptible-infected-removed (SIR) [258], and time-series models [e.g., 129, 128]. ABC methods have also been developed for optimal Bayesian designs [76, 112], reinforcement learning [70], and the estimation of intractable integrated likelihoods [105] and for approximate maximum likelihood estimation [e.g., 235, 208]; while a few studies of ABC asymptotics have emerged [e.g., 65, 13, 158, 159]. Currently, there are at least 28 software packages and published program code for ABC analysis [23, 7, 117, 95, 54, 53, 56, 134, 250, 168, 256, 32, 40, 163, 197, 276, 120, 141, 61, 125, 206, 260, 16, 90, 4, 195, 271, 131, 186]. A recent Google Scholar search using the terms “Approximate Bayesian Computation” OR “Synthetic Likelihood” yielded 8,480 publications, and this number continues to grow rapidly.

The vastity of the literature on ABC methods created a need to review and relate all ABC approaches so that scientists can more readily understand and apply them for their own work. This article provides a unifying review, general representation, and classification of all ABC methods from the view of approximate likelihood theory. Currently, any ABC method (algorithm) can be categorized as either (1) rejection-, (2) kernel-, and (3) coupled ABC; and (4) synthetic-, (5) empirical- and (6) bootstrap-likelihood methods; and can be combined with classical MC or VI algorithms. However, given the vast ABC literature, all of these methods may appear very different to scientists. Further, all 22 reviews of ABC methods [179, 209, 177, 21, 28, 62, 114, 225, 242, 174, 263, 35, 176, 248, 12, 226, 80, 150, 165, 172, 243, 78] have covered rejection and kernel ABC methods, but only three covered synthetic likelihood, one reviewed the empirical likelihood, and none have reviewed coupled ABC and bootstrap likelihood methods.

This article provides a unifying review, general representation, and classifications of all ABC methods, from the approximate likelihood theory view [79, Ch.24]. This clarifies how these methods can be characterized, related, combined, improved, and applied for future research.

Next, Section 2 begins to set specific ideas by describing some examples of Bayesian models defined by intractable likelihoods for which ABC is known to be successful, while explaining ways in which likelihoods can be intractable. Then, Section 3 presents, for all ABC methods, the general approximate likelihood representation to unify and classify them, and a general iterative IS (and MH) MC algorithm for sampling approximate posterior distributions. On this basis, Section 4 reviews the six types of ABC methods; Section 5 itemizes ABC
methods that have been combined with either the classical MC, VI, or simulated annealing algorithms; Section 6 covers ABC model choice methods; and Section 7 summarizes the available statistical software packages for ABC. Section 8 describes some open problems in ABC. Section 9 concludes the article.

2. Examples of Bayesian Models with Intractable Likelihoods

A Bayesian model is defined by a parameter vector $\theta$, having space $\Theta \subseteq \mathbb{R}^d$, a likelihood measure $f(y_n|\theta)$ for a given data set $(y_n = (y_i)_{i=1}^n)$ of $n$ sample observations with sample space $Y_n$, and by a prior distribution (measure) with density $\pi(\theta)$ defined on the parameter space, $\Theta \subseteq \mathbb{R}^d$. The likelihood and prior densities are each a continuous p.d.f. and/or a discrete p.m.f., corresponding to c.d.f.s $F(y_n|\theta)$ and $\Pi(\theta)$, respectively.

According to Bayes theorem, a set of data $(y_n)$ updates the prior to a posterior distribution, defined by probability measure $\pi(\theta|y_n) = f(y_n|\theta)\pi(\theta)/m(y_n)$, with marginal likelihood normalizing constant $m(y_n) = \int f(y_n|\theta)\Pi(d\theta)$. Also, $f_n(y) = \int f(y|\theta)\Pi(d\theta|y_n)$ is the posterior predictive density of a future observable $y$. However, for many Bayesian models, the likelihood $f(y_n|\theta)$ is analytically and/or computationally intractable. Then, posterior inferences are infeasible using analytical, MCMC, SMC, PMC, IS, VI, or other appropriate methods.

We now proceed to describe three examples of Bayesian models defined by intractable likelihoods, each of which has a posterior distributions that can be estimated using ABC methods.

2.1. $g$-and-$k$ Distribution

The first example of an intractable likelihood is defined by the $g$-and-$k$ distribution [172]. This distribution extends the normal distribution by allowing for added skewness or heavier (lighter) tails, and can describe a wide variety distribution shapes with four interpretable parameters. The generalized $g$-and-$k$ distribution [172] is defined by the quantile function:

$$F^{-1}_{gk}(u; A, B, g, k) = A + B(1 + c \tanh([g/2]z_u))z_u(1 + z_u^2)^k,$$

(2.1)

where $z_u = N^{-1}(u | 0, 1)$ is the standard normal $N(0, 1)$ quantile function, and has parameters $\theta = (A, B, g, k)$. Here, $A \in \mathbb{R}$ is a location parameter, $B > 0$ is a scale parameter, $g \geq 0$ controls skewness, $k \geq 0$ controls kurtosis (tail size), and $c = .8$ provides a standard choice of overall asymmetry constant [224, 171].

The likelihood p.d.f. of the $g$-and-$k$ distribution has the form $f(y_n|\theta) = \prod_{i=1}^n f(y_i|\theta)$, assuming that the given set of $n$ sample observations $y_n = (y_i)_{i=1}^n$ are i.i.d. from $f(y|\theta)$. A Bayesian $g$-and-$k$ model is completed by the specification of a prior distribution $\pi(\theta)$ on the space of the model parameters $\theta = (A, B, g, k)$. However, the $g$-and-$k$ likelihood p.d.f. has no closed-form expression in general. Instead, the likelihood p.d.f. is expressible in terms of derivatives of quantile functions, and needs to be computed completely numerically.
for each of the individual data points $y_i$ [224, 211]. As a result, the computation of the $g$-and-$k$ likelihood is slow even for a moderate data sample size $n$, and hundreds of time slower than computing the normal p.d.f. [224, 211]. Then, for the inference from the posterior distribution $\pi(\theta \mid y_n) \propto f(y_n \mid \theta)\pi(\theta)$ of the Bayesian $g$-and-$k$ model, any standard MCMC approach is computationally slow because it requires making $n$ calls to numerical optimization to evaluate the likelihood p.d.f. $f(y_n \mid \theta)$ in each MCMC sampling iteration [211].

ABC can be employed for performing inferences from the approximate posterior distribution of the parameters $\theta = (A, B, g, k)$, based on the specification of a surrogate likelihood that approximates the exact $g$-and-$k$ model likelihood, but is less computationally costly. The rejection ABC (R-ABC) method (Section 4.1) has proven to be a viable ABC method for this model, which is based on finding parameter values which produce simulated (synthetic) data sets that are similar to the observed data sets $y_n$, based on summary statistics of each data set [for details, see 211].

### 2.2. Mixed-Effects Model

The second example is given by the general mixed-effect model, which for the $j$th observation within blocking factor $k$, is given by:

$$y_{jk} = x_{jk}^T \beta + b_k + \varepsilon_{jk}, \quad (2.2)$$

for $j = 1, \ldots, J_k$ and $k = 1, \ldots, K$, and $n = \sum_{k=1}^K J_k$, where the $x_{jk}$ are the fixed-effect predictor vectors, assuming $b_k \overset{iid}{\sim} F_\zeta$ and $\varepsilon_{jk} \overset{iid}{\sim} F_\sigma$ with the $b_k$ and the $\varepsilon_{jk}$ uncorrelated. The mixed-effects model (2.2) has corresponding likelihood:

$$f(y_n \mid \theta) = \int \prod_{j,k} G(y_{jk} - x_{jk}^T \beta - b_k) d\prod_{k} F_b(b_k). \quad (2.3)$$

A Bayesian mixed-effects model is completed by the specification of a prior distribution $\pi(\theta) = \pi(\beta, \zeta, \sigma)$, with corresponding posterior p.d.f. $\pi(\theta \mid y_n) \propto f(y_n \mid \theta)\pi(\theta)$. The likelihood (2.3) is intractable virtually impossible to evaluate unless $F_\zeta$ and $F_\sigma$ are standard distributions such as normal distributions. But it is well-known that empirical violations of these assumptions would cast doubt about the accuracy of the inferences from the posterior $\pi(\theta \mid y_n)$. In principle, any of the Approximate Bayesian Computational (ABC) methods (Section 4) can be implemented to perform posterior inferences of the Bayesian mixed-effects model with intractable likelihood.

### 2.3. Hidden Potts Model

The third example is provided by the Potts model, which originated in statistical physics, and is now widely used for applications in image processing, spatial
modelling, computational biology, and computational neuroscience. To explain this model, let $i \in \{1, \ldots, n\}$ denote the pixels (nodes) of an image lattice, where for each node $i$, the value $y_i \in \{1, \ldots, k\}$ denotes the node’s state among $k$ possible states. The Potts model is a Markov random field model defined in terms of its conditional probabilities:

$$\Pr(y_i | y_{i-\ell}) = \frac{\exp\{\theta \sum_{j \sim i, j \neq \ell} \delta(y_i, y_j)\}}{\sum_{k=1}^{k^n} \exp\{\theta \sum_{i \sim \ell} \delta(y_i, y_j)\}},$$

(2.4)

for $i = 1, \ldots, n$, where $\theta \geq 0$ is the inverse temperature (scale) parameter, $i \sim \ell$ are the neighboring pixels of $i$, and $\delta(\cdot, \cdot)$ is the Kronecker delta function. For example, using a first-order neighborhood, $i \sim \ell$ refer to the four pixels immediately adjacent to internal node $i$ of the image lattice, and pixels on the image boundary have less than four neighbors.

A Bayesian Potts model is completed by the specification of a prior distribution $\pi(\theta)$ on $[0, \infty)$. According to Bayes’ theorem, given the data $y_n = (y_i)_{i=1}^n$, the posterior distribution of the Potts model is given by $\pi(\theta | y_n) \propto f(y_n | \theta)\pi(\theta)$, with likelihood defined by:

$$f(y_n | \theta) = \frac{\exp\left(\theta \sum_{i \sim \ell \in \mathcal{E}} \delta(y_i, y_j)\right)}{\sum_{y_n^* \in \mathcal{I}} \exp\left(\theta \sum_{i \sim \ell \in \mathcal{E}} \delta(y_i^*, y_j^*)\right)}.$$

(2.5)

The Potts model likelihood (2.5) is intractable because its denominator involves a sum over all $k^n$ possible combinations of the labels $y_n \in \mathcal{I}$. Clearly, the likelihood computation time, and the inference of the posterior distribution $\pi(\theta | y_n)$, depends on the size $n$ of the image lattice.

For the inference of the posterior distribution $\pi(\theta | y_n)$, for large $n$, an MCMC algorithm would be virtually impossible to implement because it would require evaluating the likelihood, and rejection ABC (R-ABC) is time consuming because simulating a (synthetic) data set from the likelihood (2.5) is computationally costly. However, the synthetic likelihood (SL-ABC) and bootstrap likelihood (BL-ABC) approaches to ABC have proven to be successful in providing inference from the posterior distribution $\pi(\theta | y_n)$ of the Bayesian Potts model with relatively low computational cost [see 188, 285], the general SL-ABC and BL-ABC methods are described in Section 4.

3. Approximate Likelihoods and Sampling Algorithm

We now introduce the general unifying representation of all ABC methods. Each ABC method provides approximate inference of the posterior distribution $\pi(\theta | y_n) = f(y_n | \theta)\pi(\theta)/m(y_n)$ for a given Bayesian model defined by an intractable likelihood $f(y_n | \theta)$, and by implication, an intractable marginal likelihood $m(y_n)$. 
Specifically, ABC provides tractable posterior inference by replacing the exact likelihood with an approximate likelihood that admits the general representation:

\[ L_\eta(y_n | \theta) = \int K(t(y_n) | \hat{\eta}_{\theta,N}^{(t(z_{n(k)}))}) \prod_{k=1}^N f(z_{n(k)} | \theta) dz_{n(k)}. \]  

(3.1)

Above, \( t(y_n) \) is a vector of summary statistics of the data \( y_n \) (possibly, \( t(y_n) \equiv y_n \)), which ideally are of low dimension (dim) and sufficient as the given Bayesian model and data set permit; parameter identifiability requires \( \dim(t) \geq \dim(\theta) \).

\( K(t(y_n) | \hat{\eta}_{\theta,N}^{(t(z_{n(k)}))}) \) is the kernel density function, given a parameter estimate \( \hat{\eta}_{\theta,N}^{(t(z_{n(k)}))} \) obtained from \( N \) synthetic data set samples \( \{z_{n(k)}\}_{k=1}^N \) iid \( f(\cdot | \theta) \) of size \( n(k) \) from the exact model likelihood. ABC methods that use \( N = 1 \) set \( t(z_{n(k)}) = t(z_n) \), and methods that sample no synthetic data (\( N = 0 \)) set \( K(t(y_n) | \hat{\eta}_{\theta,N}^{(t(z_{n(k)}))}) \equiv K(t(y_n) | \hat{\eta}_{\theta,N}) \).

An unbiased estimator of the general approximate likelihood (3.1) is given by:

\[ \hat{L}_\eta^{(g)}(y_n | \theta) = \frac{1}{S} \sum_{s=1}^S K(t(y_n) | \hat{\eta}_{\theta,N}^{(t(z_{n(k)}))}), \quad \{z_{n(k)}\}_{k=1}^N \text{iid } f(\cdot | \theta). \]  

(3.2)

For discrete data, the indicator function kernel \( K(t(y_n) | \hat{\eta}_{\theta,N}^{(t(z_{n(k)}))}) = \mathbf{1}(t(y_n) = t(z_{n(k)})) \) provides an unbiased estimator of the exact model likelihood \( f(y_n | \theta) \) [234]. For realistic settings, the equality constraint is replaced by some kernel \( K \) in (3.2) that tolerates some small level of inequality.

The general likelihood (3.1) gives rise to the approximate posterior density:

\[ \pi_L(\theta | y_n) = L_\eta(y_n | \theta) \pi(\theta) / m_L(\theta), \]  

(3.3)

with \( m_L(\theta) = \int L_\eta(y_n | \theta) \Pi(d\theta) \). Theoretically, (3.3) exemplifies a limited information likelihood posterior when \( \eta_\theta \equiv \theta \) and \( t(y_n) \not\equiv y_n \) [214, 71, 284, 149, 142], and indirect inference [104, 115, 132] when \( \eta_\theta \not\equiv \theta \) [74].

Using the general approximate likelihood representation (3.1), Table 1 summarizes the six types of ABC methods proposed in the literature. They differ by the choice of kernel function \( (K) \), the number \( (N) \) and method of sampling iid synthetic data sets from the exact model likelihood \( f(y_n | \theta) \), and by whether or not it implements indirect inference.

For any one of these six types of ABC methods, a general IS algorithm can be employed for ABC inference of the posterior \( \pi_L(\theta | y_n) \) in (3.3), for any function \( g(\theta) \) of interest, using the prior \( \pi(\theta) \) as the instrumental density. For the general inference of \( \int g(\theta) \pi_L(\theta | y_n) d\theta \), this integral can be rewritten as:

\[ \frac{\int g(\theta) L_\eta(y_n | \theta) \Pi(d\theta)}{\int L_\eta(y_n | \theta) \Pi(d\theta)}. \]  

(3.4)

and estimated via IS by employing a sampling scheme of the form:

\[ \frac{\frac{1}{S} \sum_{s=1}^S g(\hat{\theta}_s) K(t(y_n) | \hat{\eta}_{\theta,N}^{(t(z_{s(k)}))})}{\frac{1}{S} \sum_{s=1}^S K(t(y_n) | \hat{\eta}_{\theta,N}^{(t(z_{s(k)}))})}, \]  

(3.5a)
Based on the MH acceptance ratio.

To versions (resp.) which adaptively find the optimal instrumental or proposal sampling weights, \( \{ \theta_s \}_{s=1}^S \), and \( \{ \theta_s \}_{s=1}^S \) iid \( \pi(\theta) \).

The general IS algorithm is given by:

### ABC Importance Sampling Algorithm (ABC-IS)

1. Sample from prior, \( \theta_s \sim \pi(\theta) \);
2. Find estimate \( \hat{\eta}_{\theta_s|N}^{t(z_{n(k)})} \) from \( N \) sampled data sets of size \( n(k) \), \( \{ z_{n(k)} = (z_{i(s)})_{i=1}^n \}_{s=1}^N \) iid \( f(y_n | \theta_s) \) (if ABC method uses \( N \geq 1 \));
3. Set the IS weight for \( \theta_s \) to \( \omega_s = K(t(y_n) | \hat{\eta}_{\theta_s|N}^{t(z_{n(k)})}) \);

end for.

The ABC-IS algorithm yields output of \( S \) samples of the model parameters and normalized sampling weights, \( (\theta_s, \omega_s = \omega_s / \sum_{j=1}^S \omega_j)^{S}_{s=1} \), which can be used to construct estimates of the posterior \( \pi_L(\theta | y) \) for parameter functions of interest. The convergence of the output can be evaluated by the Effective Sample Size statistic, \( \text{ESS} = 1 / \sum_{s=1}^S (\omega_s / \sum_{s=1}^S \omega_s)^2 \), which ranges from 1 to \( S \) (perfect outcome where \( \omega_s \) are iid) [166].

The ABC-IS algorithm is conceptually simple, and can be easily parallelized because Step (a) draws independent samples from the prior \( \pi(\theta) \) over iterations. Also, this algorithm can be applied to any one of the six types of ABC methods, with respect to specific choices of \( N \) (for Step (b)) and the kernel function \( K \) defining the importance sampling weight (for Step (c)), as summarized in second and third columns of Table 1. More details in Section 4. We want to stress that some users of the 6 different ABC methods may not at first immediately recognize the ABC-IS algorithm, but the importance sampling feature is indeed an integral part of these methods. For example, the popular, rejection ABC (R-ABC) method employs the same algorithmic Step (a) to generate a prior sample \( \theta_s \); and then samples \( N = 1 \) synthetic data set \( z_{n(k)}^{(s)} \) in Step (b) from the model likelihood \( f(y_n | \theta_s) \); and then in Step (c) employs an IS weight defined by a binary (0 or 1) valued function indicating whether the summarized data \( t(y_n) \) is close in distance to the summary \( t(z_{n(k)}^{(s)}) \) of the sampled synthetic data set.

Alternatively, an MH algorithm can be used (with weights \( \omega_s \equiv 1 \), by changing the ABC-IS algorithm so that step (a) draws \( \theta^* \sim q(\theta_s | \theta_{s-1}) \) from a proposal density (distribution) \( q \), and step (c) accepts \( \theta_s \equiv \theta^* \) with probability:

\[
\min \left\{ 1, \frac{K(t(y_n) | \hat{\eta}_{\theta^*|N}^{t(z_{n(k)})}) \pi(\theta^*) q(\theta_{s-1} | \theta_s)}{K(t(y_n) | \hat{\eta}_{\theta_{s-1}|N}^{t(z_{n(k)})}) \pi(\theta_{s-1}) q(\theta^* | \theta_{s-1})} \right\},
\]

(3.6)

based on the MH acceptance ratio.

Either the ABC-IS algorithm or the Metropolis algorithm can be extended to versions (resp.) which adaptively find the optimal instrumental or proposal
density (resp.) over iterations, with the aim of yielding Monte Carlo samples of $\theta$ that more quickly converge to samples from the posterior distribution $\pi_L(\theta \mid y_n)$. This includes Population Monte Carlo (PMC) [51], adaptive multiple importance sampling [55], and adaptive Metropolis algorithms [e.g., 231], among others.

The following review of ABC methods is cast within the ABC-IS algorithm, for simplicity and without loss of generality, unless otherwise indicated.

4. ABC Methods

Sections 4.1-4.6 review the six types of ABC methods (Table 1). They each can be combined with other MC, VI, or simulated annealing algorithms, as mentioned in Section 5.

4.1. Rejection ABC (R-ABC)

The R-ABC method is the oldest [98, 277, 216, 23]. R-ABC draws $N = 1$ synthetic data set $z_n \sim f(\cdot \mid \theta)$ in ABC-IS step (b), and then in step (c), it accepts the sample $\theta_s$ when the distance $\rho_t(y_n,t(z_n))$ between $t(y_n)$ and $t(z_n)$ is within a chosen tolerance $\epsilon \geq 0$, thereby using the IS weight $\omega_s \equiv 1(\rho_t(y_n),t(z_n) \leq \epsilon)$ with indicator (kernel) function $1(\cdot)$. The sampling algorithm is run until the desired number of acceptances is obtained. Actually, the first R-ABC approach [253] did not employ a sampling step, but instead based rejection decisions on a maximum likelihood estimate $\hat{\theta} = \arg \max_{\theta \in \Theta} f_t(t(y_n) \mid \theta)$ using a sufficient summary statistic $t(y_n)$ of the data. However, this early method is limited to relatively simple Bayesian modeling scenarios in which $f_t(t(y_n) \mid \theta)$ can readily be computed and maximized over $\theta$, whereas this limitation can be avoided by employing the sampling step [23, pp.2025-6].

R-ABC approximates the exact model likelihood $f(y \mid \theta)$ by the proportion of synthetic data sets that are similar to the observed data [69]. For discrete data $y_n$ it may be natural to use no tolerance ($\epsilon = 0$) and summary statistics $(t(y_n) \equiv y_n, t(z_n) \equiv z_n)$ [253]. For continuous data, some tolerance and summary statistics are more useful [98]. When $t$ is sufficient, the R-ABC posterior density function

$$
\pi_L(\theta \mid y_n) \propto \int 1(\rho_t(y_n),t(z_n) \leq \epsilon) f(z_n \mid \theta) dz_n \pi(\theta)
$$ (4.1)

converges to the true posterior $\pi(\theta \mid y_n) \propto f(y_n \mid \theta)\pi(\theta)$ as $\epsilon \downarrow 0$ [29]. Then, $\pi(\theta \mid y_n) = \pi(\theta \mid t(y_n))$ for all $\theta$ [144, 154]. Hence the tolerance $\epsilon$ represents model error [280].

Sampling only one ($N = 1$) synthetic data set per IS iteration provides a good trade-off between computational and posterior estimation efficiency. This is also true for kernel ABC (Section 4.2) and R-ABC-MCMC (Section 5) [38].

The output of R-ABC can greatly depend on the choice of the tuning parameters ($\rho, t, \epsilon$). This has motivated developments of other ABC methods that
Table 1

The six types of ABC methods, by kernel (K), and number (N) of synthetic data sets sampled per IS iteration.

| ABC Method          | Kernel, K, of approximate likelihood:                                                                 | N      | Indirect Inference |
|---------------------|---------------------------------------------------------------------------------------------------------|--------|--------------------|
| Rejection           | \( \mathbb{1}(\rho_k(y_n), t(z_n)) \leq \epsilon \)                                                        | 1      | \( \eta \equiv \rho \) |
| Kernel              | \( K(\rho_k(y_n), t(z_n)) \); smooth                                                                  | 1      | \( \eta \equiv \rho \) |
| Coupled             | \( \int \mathbb{1}(\rho_k(y_n), t(z_n(u, \theta)))\pi(u)du \)                                        | 0      | \( \eta \equiv \rho \) |
| Synthetic Likelihood| \( n(t(y_n) | \hat{\mu}_{\theta, N}, \sum_{\theta, N} (t(z_n(k))) \) or \( K(t(y_n) | \hat{\eta}_{\theta, N}) \) | \( \geq 1 \) large | \( \eta \equiv (\mu, \Sigma) \) or \( \eta \equiv K \) |
| Empirical Likelihood| \( \hat{\pi}_n(y_n | \theta) = \max_{p(\theta) \in [0, 1]^n} \prod_{i=1}^n p_i(\theta) \) \( p_i \in [0, 1], \sum_{i=1}^n p_i = 1 \) | 0      | \( \eta \equiv p(\theta) \) |
| Bootstrap Likelihood| \( \hat{f}_n(y_n | \theta) (\text{or } \{ \hat{f}_{n,s}(y_n | \theta) \}_{s=1}^S) \) estimated from nested, single, \((n)_m \), or \(n/m\) bootstrap of data \( y_n \) (per MC iteration) | 0      | No                 |

\( y_n \): data set, size \( n \); \( f(\cdot | \theta) \): original/exact model likelihood;
\( \{ z_{n(k)} \}_{k=1}^N \) are \( N \) samples of synthetic data sets \( z_{n(k)} \) of size \( n(k) \);
\( t(\cdot) \): data summary statistic (vector); \( \mathbb{1}(\cdot) \): indicator function;
\( \rho_k(y_n), t(z_n) \) (e.g. Euclidean) distance of \( t(z_n) \) to \( t(y_n) \); \( \epsilon > 0 \) tolerance;
\( K(t(y_n) | \hat{\eta}_{\theta, N}, \{ t(z_{n(k)}) \}) \): density of \( t(y_n) \); given estimate \( \hat{\eta} \) from \( \{ t(z_{n(k)}) \}_{k=1}^N \);
\( n(t(y_n) | \hat{\mu}, \hat{\Sigma}) \): multivar. normal p.d.f., given estimate \( \hat{\eta} = (\hat{\mu}, \hat{\Sigma}) \);
\( \mathbb{E}_f[h(Y, \theta)] \): function \( h(Y, \theta) \) expectation over \( f(y | \theta) \);
\( \hat{f}_n \): estimate of \( f(\cdot | \theta) \);
decrease or eliminate tuning parameter dependence, as described next in Sections 4.2-4.6.

### 4.2. Kernel ABC (K-ABC)

K-ABC employs a smooth kernel function $K(\rho)$ without a tolerance $\epsilon$, resulting in the approximate posterior density:

$$
\pi_L(\theta \mid y_n) \propto \int K(\rho_{t(y_n), t(z_n)}) f(z_n \mid \theta) dz_n \pi(\theta).
$$

(4.2)

After running the ABC-IS algorithm, the posterior mean of $\theta$ is estimated by:

$$
\frac{\sum_{s=1}^{S} K_{\delta}(||t(y_n) - t(z_n(s))||) \theta_s}{\sum_{s=1}^{S} K_{\delta}(||t(y_n) - t(z_n(s))||)}.
$$

(4.3)

K-ABC may employ the Epanechnikov kernel $K_{\rho}(\rho_{t(y_n), t(z_n)}) \equiv K_{\delta}(||t(y_n) - t(z_n)||)$ with bandwidth $\delta > 0$ and Euclidean norm $||\cdot||$ [23], and need not employ summary statistics [280, 261, 264].

For K-ABC and R-ABC, if the summary statistic(s) obeys a central limit theorem, then the posterior mean estimator of any parameter function can be asymptotically normal (as $n \to \infty$), with mean square error equal to that of the maximum likelihood estimator based on the summary statistic(s). Further, for kernel ABC, this estimator is efficient in the sense that the MC error of ABC increases its mean square error only by a factor of $1 + O(1/S)$ for a fixed MC sample size $S$ [159, 65].

### 4.3. Coupled ABC (C-ABC)

C-ABC [190] treats ABC as an inverse problem. A c.d.f. $F(y) = \Pr(Y \leq y)$ has a (generalized) inverse $F^{-1}(u) = \inf_y \{y : F(y) \geq u\}$, and $F^{-1}(U) \sim Y$ if $U \sim U(0,1)$. This means that it is possible to use a deterministic (coupling) function $Z = f(\theta, u)$ to map every realization $y$ of the model likelihood $f(\cdot \mid \theta)$ to a realization $u \in [0,1]^d$ of the random vector $U$ having p.d.f. $\pi(u)$. Further, multiple coupled synthetic data sets can be simulated as $z_n(u, \theta_1), z_n(u, \theta_2), \ldots, z_n(u, \theta_k)$, using the same $u$ over $k$ parameter values, $\theta_1, \theta_2, \ldots, \theta_k$, according to the solution of the inverse problem based on identifying the set $\Theta_z = \{\theta : z = z_n(u, \theta)\}$, given $u$. Table 1 shows that C-ABC assumes an approximate likelihood defined by the kernel $K(\rho_{t(y_n), t(z_n(u, \theta))})$ that is marginalized over the p.d.f. $\pi(u)$.

### 4.4. Synthetic Likelihood (SL) Methods

A SL method generates multiple ($N \geq 1$) samples of synthetic data sets per sampling iteration. The classical SL method assumes the approximate likelihood
to be the multivariate normal p.d.f. \(n(\cdot | \mu, \Sigma)\), with \(\hat{\eta}_{s (n(k))} = (\hat{\mu}_{s (n(k))}, \hat{\Sigma}_{s (n(k))})\) the maximum likelihood estimate (MLE) obtained from \(\{t(z_{n(k)})\}_{k=1}^{N}\), assuming that the summary statistics \(t\) are asymptotically normal [283, 121]. In terms of the ABC-IS algorithm, iterative step (a) generates a prior sample \(\theta_s \sim \pi(\theta)\); step (b) estimates \(\hat{\eta}_{s (n(k))} = (\hat{\mu}_{s (n(k))}, \hat{\Sigma}_{s (n(k))})\) from \(N\) sampled synthetic data sets, and step (c) weights \(\theta_s\) by \(\omega_s \equiv n(t(y_n) | \hat{\mu}_{s (n(k))}, \hat{\Sigma}_{s (n(k))})\).

Several other SL methods relax the normality assumption, including those that replace the normal SL by: a GARCH model with time-dependent normal heteroscedastic variances [99]; a finite mixture of normal experts model with covariate-dependent kernel densities and mixture weights [88]; a Gaussian process (GP) for each individual (marginal) summary statistic, assuming independent summary statistics [184, 126]; a GP for the log SL [281], estimated by sequential history matching [58]; a GP for the discrepancy between observed and simulated synthetic data [111], estimated by Bayesian optimization [136]; and other general SLs [99, 74, 77, 111].

Other SL methods relax normality by instead employing: nonparametric kernel density estimation [31, 152, 262, 188, 111]; minimum distance estimation [96]; estimation via Hamiltonian dynamics [183]; an unbiased estimator of the normal density function [100] assuming asymptotically normal summary statistics \(t\); and MC posterior estimation of the normal parameters \((\mu, \Sigma)\) [215].

### 4.5. Empirical Likelihood Method (EL-ABC)

EL-ABC specifies the kernel function by the empirical likelihood (EL),

\[
L_{\eta}(y_n | \theta) \equiv \hat{L}_{n}^{el}(y_n | \theta) = \max_{\{p(\theta): p \in [0,1]^n; \sum p_i(\theta) = 1\}} \prod_{i=1}^{n} p_i(\theta),
\]

subject to chosen constraints of the form \(E_F[h(Y, \theta)] = 0\) [185]. For example, if the model parameter represents the mean, \(\theta = \theta = E_F[Y]\), and \(h(y, \theta) = y - \theta\), then the constraint is \(\theta = \sum_{i=1}^{n} p_i y_i\). The EL (4.4) assumes \(n\) i.i.d. observations, but it can handle dependent observations by reformulating it as a dynamic regression model that captures underlying iid structure. In terms of the ABC-IS algorithm, EL-ABC in iterative step (a) draws a prior sample \(\theta_s \sim \pi(\theta)\); in step (b) finds the EL \(\hat{L}_{n}^{el}(y_n | \theta_s)\); and in step (c) assigns the IS weight \(\omega_s \equiv \hat{L}_{n}^{el}(y_n | \theta_s)\).

### 4.6. Bootstrap Likelihood Method (BL-ABC)

BL-ABC [285] first estimates the exact model likelihood by a kernel density estimate \(L_{\eta}(y_n | \theta) \equiv \hat{L}_{n}^{bl}(y_n | \theta)\) of nested bootstrap samples of a point-estimator \(\tilde{\theta}\) of \(\theta\), from the original data \(y_n\) [64]. The nested bootstrap has two stages. At the first stage, \(J\) bootstrap samples of data sets \(\{y_{n,j}^{(j)}\}_{j=1}^{J}\) are generated, then point
estimates \( \{ \hat{\theta}^*_j = \hat{\theta}(y_n^{(j)}) \}_{j=1}^J \) are computed from them (resp.), where each bootstrap sample \( y_n^{(j)} \) is formed by drawing \( n \) samples with replacement from the original data \( y_n \), for \( j = 1, \ldots, J \). At the second stage, for each of \( j = 1, \ldots, J \), a total \( K \) bootstrap samples of data sets \( \{ y_n^{(j,k)} \}_{k=1}^K \) from \( y_n^{(j)} \) are generated (\( K = 1000 \) recommended) to yield point estimates \( \{ \hat{\theta}_{j,k} = \hat{\theta}(y_n^{(j,k)}) \}_{k=1}^K \), and the kernel density estimate:

\[
\hat{L}^b_n(y_n | \theta) = \hat{f}(\theta | \hat{\theta}_j) = \frac{1}{K} \sum_{k=1}^K \ker\left( \frac{\theta - \hat{\theta}_{j,k}}{h} \right),
\]

where \( \ker(\cdot) \) is a smooth (e.g., Epanechnikov) kernel with bandwidth \( h > 0 \). Then the bootstrap likelihood (BL) is constructed by fitting a scatterplot smoother to the \( J \) pairs \( \{ (\hat{\theta}^*_j, \log \hat{f}(\theta | \hat{\theta}_j)) \}_{j=1}^J \). Here, \( \hat{\theta}_n = \hat{\theta}(y_n) \), and \( \hat{f}(\theta | \hat{\theta}_j) \) provides an estimate of the likelihood of \( \hat{\theta}_n \) given \( \theta \equiv \hat{\theta}_j \) [64].

For BL-ABC, the ABC-IS algorithm is run with step (a) drawing a prior sample \( \theta_n \sim \pi(\theta) \); step (b) is skipped; and step (c) calculates the importance sampling weight by \( \hat{\pi}_n = \hat{L}_n(y_n | \theta_n) \). The empirical and bootstrap likelihoods asymptotically agree to order \( n^{-1/2} \), and converge to the true model likelihood \( f(y | \theta) \) as \( n \to \infty \) [64].

BL-ABC can be extended in a few ways, owing to the general nature of the bootstrap method. First, if \( \theta - \hat{\theta} \) is a pivotal quantity such that \( \theta - \hat{\theta} \sim H \), with \( H \) not involving \( \theta \), then the bootstrap likelihood estimate \( \hat{L}^b_n(y_n | \theta) \) can be more simply constructed by the ordinary single bootstrap [37]. Second, BL-ABC can be easily extended to handle non-iid dependent data through the use of the regression residual, parametric, or the pairs bootstrap [285]. Third, BL-ABC can incorporate R-ABC, but at a higher computational cost [285]. Fourth, if the model parameter is scalar-valued (\( \theta \equiv \theta \)), BL-ABC can be used to construct an empirical likelihood using a single bootstrap, without kernel density estimation [198]. Finally, BL-ABC can be extended to \( "n \) choose \( m \)" or \( m/n \) bootstrap (\( m \leq n \)) sampling per iteration [161].

5. Combining ABC with Other Algorithms

ABC methods each have been combined with MCMC (usually MH), SMC, PMC, VI, and simulated annealing (SA) algorithms, usually in order to speed up posterior computations.

R-ABC-MCMC [179, 39, 275, 152, 101, 170], R-ABC-SMC [241, 229, 258, 200, 203, 67, 237, 94, 103], R-ABC-PMC [24, 11, 189, 123] typically provide automatic tolerance (\( \epsilon \)) selection. The variance bounds and geometric ergodicity of R-ABC-MCMC were studied in relation to that of the MH algorithm for models with intractable likelihood [153]. Also, VI including expected-propogation (EP) methods were proposed to define K-ABC-EP, R-ABC-VI and K-ABC-VI methods [15, 16, 259], and simulated annealing (SA) was proposed to define a K-ABC-SA method [5].
K-ABC-MCMC [264] and C-ABC-MCMC [191, 245] can mix better than R-ABC-MCMC, especially in the tails of the target posterior distribution [241]. This may also be true for SL-MCMC [99, 74, 205, 19], SL-VI [196], EL-ABC-MCMC, EL-ABC-PMC, EL-ABC-SMC [185], and BL-ABC-MCMC with MH [161].

Random forests [42] was proposed to estimate the MH acceptance ratio as a function of simulated summary statistics [205], based on bootstrap aggregation [41] of the optimal classification predictions of many Classification and Regression Trees [CARTs; 43] fitted over resamples of the data $y_n$. Classical SL’s [283] normal synthetic likelihood amounts to assuming the quadratic discriminant analysis classifier.

6. ABC for Model Choice

Model choice aims to find the model from a set of $D$ considered models $\{M_d\}_{d=1}^D$ that has the best predictive utility for the underlying process that generated the given data set, $y_n$. There are several ABC methods for model choice [216].

One method for R-ABC or K-ABC estimates the posterior model probabilities from a multinomial logit regression of model indices on summary statistics $t(z_n)$ sampled from an R-ABC algorithm, locally-weighted and conditionally on $t(x_n)$ [86, 20, 33, 84, 212]. A method for R-ABC [97] approximates each model’s deviance information criterion [246] by using kernel density estimation (tolerance $\epsilon$ bandwidth) of the deviance statistic, obtained from summary statistics of posterior predictive samples generated per sampling iteration. Another R-ABC method [143] employs an MH algorithm that proposes jumps between models, based on the pseudo-marginal approach that handles intractable likelihoods [9].

A general ABC model choice method employs random forests [217], as follows. First, a prior probability $\pi(M_d)$ is assigned to each model $M_d$ with intractable likelihood $f_d(z_n | \theta_d)$ and prior $\pi_d(\theta_d)$, for a given set $\{M_d\}_{d=1}^D$ of compared models. Then a table is constructed by taking $N_{ref}$ samples of $(d, t(z_n))$ from $\pi(M_d) \pi_d(\theta_d) f_d(z_n | \theta_d)$. Next, the method fits a CART $T_b$ that classifies model indices with $t(z_n)$, to each of $B$ bootstrap samples (with replacement) of size $N_{\text{boot}} < N_{ref}$ from the table. Finally, the single best predictive model from $\{M_d\}_{d=1}^D$ is identified as the one with the model index that receives the most votes (optimal classifications) from the $B$ fitted CARTs.

Finally, R-ABC, R-ABC-MCMC (MH), and R-ABC-SMC algorithms can be extended for assessing the fit of a single model to data [221, 219, 228, 220].

7. Software Packages for ABC

There are at least 28 statistical software packages that support many of the ABC methods that were mentioned earlier [in part, from 195, 145]. Table 2 provides a summary of these packages. Nearly all packages are based on R-ABC, while a few recent packages handle K-ABC or SL-ABC. Also, 9 of these packages can be
| ABC Package       | Author(s) | ABC method(s)                        | Models/Field            |
|-------------------|-----------|--------------------------------------|-------------------------|
| abc*              | [61]      | R-ABC                                | General                 |
| abc_distrb        | [23]      | R-ABC                                | General                 |
| abc_mnet          | [32]      | R-ABC                                | General                 |
| ABCreg            | [256]     | R-ABC                                | General                 |
| ABCtoolbox*       | [276]     | R-ABC, R-ABC-MCMC, R-ABC-PMC         | General                 |
| abctools          | [195]     | R-ABC                                |                         |
| ABrox*            | [186]     | R-ABC, R-ABC-MCMC, R-ABC-PMC         | Model selection focus   |
| DREAM*            | [271]     | K-ABC-MCMC                           | General                 |
| EasyABC           | [125]     | R-ABC, R-ABC-SMC, SL-ABC, K-ABC-SA   | General                 |
| synlik            | [90]      | SL-ABC                               | General                 |
| ABC-EP            | [16]      | R-ABC-EP                             | State space (& related) |
| abc-sde           | [206]     | R-ABC-MCMC                           | SDE                     |
| gk                | [211]     | R-ABC                                | g-and-k (or h) models   |
| 2BAD*             | [40]      | R-ABC                                | Population genetics     |
| ABC4F             | [95]      | R-ABC                                | Population genetics     |
| Bayes-SSC         | [7]       | R-ABC                                | Population genetics     |
| DIY-ABC*          | [54]      | R-ABC                                | Population genetics     |
| msABC             | [197]     | R-ABC                                | Population genetics     |
| onensaem          | [250]     | R-ABC                                | Population genetics     |
| PopABC            | [168]     | R-ABC                                | Population genetics     |
| REJECTOR*         | [134]     | R-ABC                                | Population genetics     |
| msBayes           | [117]     | R-ABC                                | Phylogeography          |
| MTML-msBayes*     | [120]     | R-ABC                                | Phylogeography          |
| ABC-SysBio*       | [163]     | R-ABC, R-ABC-SMC                     | Systems biology         |
| WARK              | [200]     | R-ABC                                | Archaeology             |
| abcpmc            | [4]       | R-ABC-PMC                            | Cosmology               |
| astroABC          | [131]     | R-ABC-SMC                            | Cosmology               |
| CosmoPMC*         | [141]     | R-ABC-PMC                            | Cosmology               |

Table 2

General and specific-purpose ABC software packages, including their methodological capabilities. An asterisk (*) indicates an ABC package that provides model selection. (SDE = Stochastic Differential Equation.

applied to general models, while all the other packages address specific models, scientific fields, or focus on model selection tasks.

According to Table 2 and the review of applications given in Section 1, R-ABC seems to be most widely applied in the population genetics, phylogeography, systems biology, archaeology, and cosmology fields. However, in the future it is expected that fields will more frequently apply the more recent ABC methods since they have some advantages over R-ABC.

8. Open Problems in ABC

The six types of ABC methods have proven useful for many applications of data analysis. However, they are not fully satisfactory for reasons that are summarized in Table 3. Table 3 defines the current open problems with ABC, described in the following subsections.
Inferences depend on tuning? Provides computational issues? Provides
ABC Method or estimator? Curse of dimension? big n? model choice?

| Method | Tuning Parameters | In tuning | applications | Due to | Big n? | Model choice? |
|--------|------------------|-----------|--------------|--------|--------|---------------|
| Rejection | $\rho, t, \epsilon, N$ | In tuning | Slow sampling & synthetic data sets | Posterior model probabilities from regression of model indices on $t$ | No | No |
| Kernel | $\rho, N, maybe t$ | $\rho$ parameter | $\rho, t, \epsilon, N$ | Selection | No |
| Coupled | $\rho, t, N$ | $\rho, t, N$ | $\rho, t, \epsilon, N$ | Selection | No |
| SL | $t, N$ | $t$ parameter | $\rho, t, \epsilon, N$ | Selection | No |
| EL | Needs estimator of function of $\theta$ | Parameter estimation | Slow estimation & resampling | No | No |
| BL | | | | | |

Table 3

The open problems in ABC, including the computational complexity of each ABC method.

The table conveys that several aspects can together contribute to the computational complexity of each ABC method, such as the sample size or the number of model parameters or variables. However, these issues may potentially be less important as increasing computing power continues to become more available [248].

8.1. Tuning Parameter ($\rho, t, \epsilon, N$) and Point-Estimator Dependence

Posterior inferences from R-ABC, K-ABC, C-ABC, and SL-ABC can be very sensitive to the choice of tuning parameters ($\rho, t, \epsilon, N$) [e.g., 174].

A typical choice of $\rho$ is the squared distance. But posterior inferences differ across other reasonable choices of distance measures, and there does not seem to be one "best" distance measure for general ABC practice. K-ABC employs a smooth kernel function $K_\delta(\rho)$. The kernel bandwidth needs to be carefully chosen, perhaps by matching the resulting posterior credible intervals with the correct coverage levels [213].

When employed, summary statistics $t$ should be sufficient. But sufficient statistics are not available from many Bayesian models and data sets. Insufficient summary statistics when used should be carefully selected to ensure accurate posterior inferences [e.g., 68, 175, 230]. Many statistics selection methods have been developed [137, 275, 194, 93, 3, 35, 102, 133, 236, 59, 187].

In R-ABC, the tolerance $\epsilon$ represents model approximation error [280] and controls the trade-off between computational speed and estimation accuracy. Running a R-ABC algorithm with overly-small $\epsilon$ requires many model evaluations due to the large rejection probability, making it time-consuming to get a large number of acceptances. When $\epsilon$ is too large, the algorithm poorly approximates and overstates uncertainty in the posterior distribution. Several proposed solutions include selecting the tolerance from the MC sampling run [241, 24, 258, 67, 240, 156, 52] or from posterior asymptotics [13]; and running a R-ABC algorithm for each of the $n$ components of a factorized exact model likelihood via the Markov property (if factorizable), possibly with lower tolerance and computational cost and without ($\rho, t$) [279, 15, 18].

In SL-ABC, $N$ controls the trade-off between computational speed and estimation accuracy [e.g., 77], and inferences may be highly-sensitive to $N$ when the
SL is not smooth [111, Section 4]. Recent extensions of SL-ABC can decrease this sensitivity [215].

Some issues are avoided by employing ABC methods that do not rely on all tuning parameters \((\rho, t, \epsilon)\). K-ABC and C-ABC do not use \(\epsilon\) and may not require \(t\), and SL-ABC does not use \((\rho, \epsilon)\), but they depend on other tuning parameters. C-ABC requires solving the inverse problem, which is not possible for all model likelihoods. For R-ABC, a method can select \((\rho, t, \epsilon)\) [223]. The factorization method does not require \((\rho, t)\).

In summary, there are many proposed solutions to address tuning parameter dependence in ABC, but none appear to be neat and fully satisfactory.

EL-ABC and BL-ABC do not employ any tuning parameters. But they still require a point estimator for \(p(\theta)\) and \(\theta\) (resp.), which may not be available for the given Bayesian model at hand. In EL-ABC it can be difficult to specify the moment constraints needed to estimate \(p(\theta)\). See Sections 8.2-8.3 for related issues.

8.2. The Curse of Dimensionality

The curse of dimensionality [25] can pose challenges to the tuning parameters. In R-ABC, K-ABC, and C-ABC, squared distance is a typical choice for \(\rho\), but it suffers from the curse beyond three dimensions [e.g., 119], perhaps also true for general distance measures of summary statistics [35]. Even when sufficient statistics are available, they often have the same dimensionality as the sample size. For instance, while \(\dim(t) \geq \dim(\theta)\) is required for parameter identifiability, this implies that high-dimensional summary statistics \(t\) are required to adequately describe the information of a high-dimensional \(\theta\). It is not uncommon in ABC practice that \(\dim(t) \gg \dim(\theta)\) [6, 39]. Otherwise, low-dimensional sufficient statistics may be computationally intractable.

Proposed solutions include: performing a (linear, local, or nonlinear) regression of accepted proposed parameter values onto the distance between the simulated and observed summary statistics, and then estimating the posterior distribution by sampling the regression error distribution conditionally on zero distance [23, 256, 31, 32, 193, 111]; performing regression adjustments on low-dimensional marginal posterior distributions and summary statistics [193, 160], since low-dimensional posteriors can often be estimated well; methods to reduce the dimensionality of the summary statistics [35]; and the factorized likelihood method using no tuning parameters \((\rho, t)\) [279].

A high-dimensional model parameter \(\theta\) also affects EL-ABC and BL-ABC by making point estimation of \(p(\theta)\) and \(\theta\) (resp.) more challenging and time consuming, especially when the data sample size \((n)\) is large. Then, in EL-ABC the constraints for \(p(\theta)\) are difficult to specify [285], and in BL-ABC a large number of bootstrap samples are needed for reliable kernel estimation of the approximate likelihood. Low-dimensional summary statistics may help.

The ABC-PaSS algorithm [146] (i.e., ABC for Parameter Specific Statistics ABC) was designed to tackle the problem of high-dimensionality that arises
frequently in inference for complex models, which are typical in biology and population genetics. This approach is based on Gibbs sampling, where each parameter in the model is updated independently, and this update is accepted or rejected based on the Euclidean distance of parameter-specific statistics to the observed data.

8.3. Large Sample Size \((n)\) Issues

For R-ABC, K-ABC, and SL-ABC, simulating \(N \geq 1\) synthetic data sets of size \(n\) per sampling iteration can be computationally costly, especially when the data sample size \(n\) is large. For certain parameter space regions, a small number of simulations \(N\) may suffice to conclude that the approximate likelihood cannot take on a significant value. Proposed solutions to such issues include an extension of SL-ABC that uses Bayesian optimization for estimating SL parameters instead of simulating synthetic data \([111]\); and an R-ABC IS algorithm that saves time by sometimes abandoning the simulation of synthetic data sets that likely poorly match the observed data \([210]\).

Approximate ABC (AABC) can provide a faster R-ABC method to simulate synthetic data sets in settings where it is too computationally costly to directly simulate from the exact model likelihood \([46]\). AABC initializes the ABC-IS algorithm by drawing a small number \(N^*\) of prior samples \(\{\theta^*_k\}_{k=1}^{N^*} \sim \pi(\theta)\) and synthetic data sets \(Z^* = (z^*_n(k))_{k=1}^{N^*} \sim f(\cdot | \theta)\). Then after drawing \(\theta_s\) in iterative step \((a)\), AABC in iterative step \((b)\) draws \(\phi\) from a Dirichlet distribution with precision parameters given by the Epanechnikov kernel weights of \(\{\theta^*_k\}_{k=1}^{N^*}\) centered at \(\theta_s\), and samples a synthetic data set \(z_n = (z_i)_{i=1}^n\) with probability \(\phi_j\) for \(i = 1, \ldots, n\).

Large sample size \((n)\) also slows point-estimation. This seems to be true for SL-ABC extensions that estimate a GP per sampling iteration because this can involve multiple inversions of \(n \times n\) matrices, and true for EL-ABC and BL-ABC which estimate \(p(\theta)\) and \(\theta\) (resp.) in each iteration.

8.4. ABC Model Choice Issues

All current ABC model choice methods employ summary statistics \(t\), and also a tolerance \(\epsilon > 0\) in some cases. Coherent R-ABC model choice requires sufficient summary statistics \([109, 68, 230, 45, 175, 48]\). The results of ABC model choice can be inconsistent when insufficient summary statistics are employed \([230]\), and can depend heavily on the information amount in the given data set \([247]\). But as mentioned, sufficiency is not provided by many models and data sets, and tolerance selection is not trivial.

Nearly all of the ABC model choice methods assign a prior distribution \(\pi(M_d)\) on the model space. This implicitly assumes the \(\mathcal{M}\)-closed view of model choice, namely that the true model that generated the data \(y_n\) is in the set of models \(\{M_d\}_{d=1}^D\) under consideration \([27]\). This view is not uncontroversial because the true model is often unavailable in practice, which anyway may not
accurately predict future data given the available evidence $y_n$ \cite{266}. Alternatively, an $\mathcal{M}$-open view may be adopted, avoiding the explicit construction of an actual true belief model. In this case, model choice can proceed by comparing models by posterior predictive performance of future data. This can be done under minimal modeling assumptions by employing sample re-use cross-validation methods to approximate the future data distribution.

9. Conclusions

ABC provides useful inferential methods for Bayesian models with intractable likelihoods. On the basis of approximate likelihood theory, this article provided a unifying review of ABC methods in the huge related literature. This allowed for the methods to be concisely described, classified, and directly compared, with the aim of promoting future use of ABC methods among scientists. The review also informed a summary of some of the current open problems with ABC methods. The review as a whole suggests some future research directions in ABC, possibly by combining some of the virtues of K-ABC, SL-ABC, and BL-ABC, while avoiding some of their issues.

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References

[1] Aandahl, R. Z., Reyes, J. F., Sisson, S. A. and Tanaka, M. M. (2012). A model-based Bayesian estimation of the rate of evolution of VNTR loci in Mycobacterium tuberculosis. PLoS Computational Biology 8 e1002573.
[2] Ardessalem, A. B., Dervilis, N., Wagg, D. and Worden, K. (2018). Model selection and parameter estimation in structural dynamics using Approximate Bayesian Computation. Mechanical Systems and Signal Processing 99 306-325.
[3] Aeschbacher, S., Beaumont, M. A. and Futschik, A. (2012). A novel approach for choosing summary statistics in Approximate Bayesian Computation. Genetics 192 1027-1047.
[4] Akeret, J., Refregier, A., Amara, A., Seehars, S. and Hasner, C. (2015). Approximate Bayesian comptutation for forward modeling in cosmology. Journal of Cosmology and Astroparticle Physics 2015 043.
[5] Albert, C., Künsch, H. R. and Scheidegger, A. (2015). A simulated annealing approach to approximate Bayes computations. *Statistics and Computing* **25** 1217-1232.

[6] Allingham, D., King, R. A. R. and Mengersen, K. L. (2009). Bayesian estimation of quantile distributions. *Statistics and Computing* **19** 189-201.

[7] Anderson, C. N. K., Ramakrishnan, U., Chan, Y. L. and Hadly, E. A. (2005). Serial SimCoal: A population genetics model for data from multiple populations and points in time. *Bioinformatics* **21** 1733-1734.

[8] Andrade, P. and Rifo, L. (2017). Long-range dependence and Approximate Bayesian Computation. *Communications in Statistics: Simulation and Computation* **46** 1219-1237.

[9] Andrieu, C. and Roberts, G. O. (2009). The pseudo-marginal approach for efficient Monte Carlo computations. *Annals of Statistics* **37** 697-725.

[10] Ascunce, M. S., Yang, C. C., Oakey, J., Calcotttiera, L., Wu, W. J., Shih, C. J., Goudet, J., Ross, K. G. and Shoemaker, D. (2011). Global invasion history of the fire ant Solenopsis invicta. *Science* **331** 1066-1068.

[11] Baragatti, M., Grimaud, A. and Pommeret, D. (2013). Likelihood-free parallel tempering. *Statistics and Computing* **23** 535-549.

[12] Baragatti, M. and Pudlo, P. (2014). An overview on Approximate Bayesian Computation. *ESAIM: Proceedings* **44** 291-299.

[13] Barber, S., Voss, J. and Webster, M. (2015). The rate of convergence for Approximate Bayesian Computation. *Electronic Journal of Statistics* **9** 80-105.

[14] Barnes, C. P., Silk, D. and Stumpf, M. P. H. (2011). Bayesian design strategies for synthetic biology. *Interface Focus* **1** 895-908.

[15] Barthelmé, S. and Chopin, N. (2011). ABC-EP: Expectation propagation for likelihood free Bayesian computation. In *Proceedings of the 28th International Conference on Machine Learning* (L. Getoor and T. Scheffer, eds.) 289-296. Omnipress, Madison, WI.

[16] Barthelmé, S. and Chopin, N. (2014). Expectation propagation for likelihood-free inference. *Journal of the American Statistical Association* **109** 315-333.

[17] Baudet, C., Donati, B., Sinaimeri, B., Crescenzi, P., Gautier, C., Matias, C. and Sagot, M. F. (2014). Cophylogeny reconstruction via an Approximate Bayesian Computation. *Systematic Biology* **64** 416-431.

[18] Bazin, E., Dawson, K. J. and Beaumont, M. A. (2010). Likelihood-free inference of population structure and local adaptation in a Bayesian hierarchical model. *Genetics* **185** 587-602.

[19] Beaumont, M. A. (2003). Estimation of population growth or decline in genetically monitored populations. *Genetics* **164** 1139-1160.

[20] Beaumont, M. A. (2008). Joint determination of topology, divergence time, and immigration in population trees. In *Simulation, Genetics and
Human Prehistory (S. Matsumura, P. Forster and C. Renfrew, eds.) 134-154. McDonald Institute for Archaeological Research, Cambridge.

[21] Beaumont, M. A. (2010). Approximate Bayesian Computation in evolution and ecology. Annual Review of Ecology, Evolution and Systematics 41 379-406.

[22] Beaumont, M. A. and Rannala, B. (2004). The Bayesian revolution in genetics. Nature Reviews Genetics 5 251.

[23] Beaumont, M. A., Zhang, W. and Balding, D. J. (2002). Approximate Bayesian Computation in population genetics. Genetics 162 2025-2035.

[24] Beaumont, M. A., Cornuet, J. M., Marin, J. M. and Robert, C. P. (2009). Adaptive Approximate Bayesian Computation. Biometrika 96 983-990.

[25] Bellman, R. (1961). Adaptive Control Processes: A Guided Tour. Princeton University Press, Princeton.

[26] Bennett, K. L., Shija, F., Linton, Y. M., Misanzo, G., Kadumuksa, M., Djouaka, R., Anyaele, O., Harris, A., Irish, S., Hlaing, T., Prakash, A., Lutwama, J. and Walton, C. (2016). Historical environmental change in Africa drives divergence and admixture of Aedes aegypti mosquitoes: A precursor to successful worldwide colonization? Molecular Ecology 25 4337-4354.

[27] Bernardo, J. M. and Smith, A. F. M. (1994). Bayesian Theory. Wiley, Chichester, England.

[28] Bertorelle, G., Benazzo, A. and Mona, S. (2010). ABC as a flexible framework to estimate demography over space and time: Some cons, many pros. Molecular Ecology 19 2609-2625.

[29] Blau, G., Crou, F. and Guyader, A. (2015). New insights into Approximate Bayesian Computation. Annales de l’Institut Henri Poincar, Probabilits et Statistiques 51 376-403.

[30] Blei, D. M., Kucukelbir, A. and McAuliffe, J. D. (2017). Variational Inference: A Review for Statisticians. Journal of the American Statistical Association 112 859-877.

[31] Blum, M. G. B. (2010). Approximate Bayesian Computation: A non-parametric perspective. Journal of the American Statistical Association 105 1178-1187.

[32] Blum, M. G. B. and François, O. (2010). Non-linear regression models for Approximate Bayesian Computation. Statistics and Computing 20 63-73.

[33] Blum, M. G. B. and Jakobsson, M. (2010). Deep divergences of human gene trees and models of human origins. Molecular Biology and Evolution 28 889-898.

[34] Blum, M. G. B. and Tran, V. C. (2010). HIV with contact tracing: A case study in Approximate Bayesian Computation. Biostatistics 11 644-660.

[35] Blum, M. G. B., Nunes, M. A., Prangle, D. and Sisson, S. A. (2013). A comparative review of dimension reduction methods in Approx-
imate Bayesian Computation. *Statistical Science* **28** 189-208.

[36] Bonhomme, M., Blancher, A., Cuartero, S., Chikhi, L. and Crouau-Roy, B. (2008). Origin and number of founders in an introduced insular primate: Estimation from nuclear genetic data. *Molecular Ecology* **17** 1009-1019.

[37] Boos, D. D. and Monahan, J. F. (1986). Bootstrap methods using prior information. *Biometrika* **73** 77-83.

[38] Bornn, L., Pillai, N. S., Smith, A. and Woodard, D. (2017). The use of a single pseudo-sample in approximate Bayesian computation. *Statistics and Computing* **27** 583-590.

[39] Bortot, P., Coles, S. G. and Sisson, S. A. (2007). Inference for stereological extremes. *Journal of the American Statistical Association* **102** 84-92.

[40] Bray, T. C., Sousa, V. C., Parreira, B., Bruford, M. W. and Chikhi, L. (2010). 2BAD: An application to estimate the parental contributions during two independent admixture events. *Molecular Ecology Resources* **10** 538-541.

[41] Breiman, L. (1996). Bagging Predictors. *Machine Learning* **26** 123-140.

[42] Breiman, L. (2001). Random forests. *Machine Learning* **45** 5-32.

[43] Breiman, L., Friedman, J., Stone, C. J. and Olshen, R. A. (1984). *Classification and Regression Trees*. CRC press, Boca Raton, FL.

[44] Brooks, S., Gelman, A., Jones, G. and Meng, X. L. (2011). *Handbook of Markov Chain Monte Carlo*. Chapman and Hall/CRC, Boca Raton, FL.

[45] Burr, T. and Skurikhin, A. (2013). Selecting summary statistics in Approximate Bayesian Computation for calibrating stochastic models. *BioMed Research International* **2013** 1-10.

[46] Buzbas, E. O. and Rosenberg, N. A. (2015). AABC: Approximate Approximate Bayesian Computation for inference in population-genetic models. *Theoretical Population Biology* **99** 31-42.

[47] Bchaux, C., Bodin, L., Clmenon, S. and Crpet, A. (2014). PBPK and population modelling to interpret urine cadmium concentrations of the French population. *Toxicology and Applied Pharmacology* **279** 364-372.

[48] Cabras, S., Nueda, M. E. C. and Ruli, E. (2015). Approximate Bayesian Computation by modelling summary statistics in a quasi-likelihood framework. *Bayesian Analysis* **10** 411-439.

[49] Calvet, L. E. and Czellar, V. (2014). Accurate methods for approximate Bayesian computation filtering. *Journal of Financial Econometrics* **13** 798-838.

[50] Cameron, E. and Pettitt, A. N. (2012). Approximate Bayesian Computation for astronomical model analysis: A case study in galaxy demographics and morphological transformation at high redshift. *Monthly Notices of the Royal Astronomical Society* **425** 44-65.

[51] Cappé, O., Guillin, A., Marin, J. M. and Robert, C. P. (2004). Population Monte Carlo. *Journal of Computational and Graphical Statistics*
[52] Chiachio, M., Beck, J. L., Chiachio, J. and Rus, G. (2014). Approximate Bayesian Computation by subset simulation. SIAM Journal on Scientific Computing 36 1339-1358.

[53] Cornuet, J. M., Ravigné, V. and Estoup, A. (2010). Inference on population history and model checking using DNA sequence and microsatellite data with the software DIYABC (v1.0). BMC Bioinformatics 11 401.

[54] Cornuet, J. M., Santos, F., Beaumont, M. A., Robert, C. P., Marin, J. M., Balding, D. J., Guilemaud, T. and Estoup, A. (2008). Inferring population history with DIY ABC: A user-friendly approach to Approximate Bayesian Computation. Bioinformatics 24 2713-2719.

[55] Cornuet, J. M., Marin, J. M., Mira, A. and Robert, C. P. (2012). Adaptive multiple importance sampling. Scandinavian Journal of Statistics 39 798-812.

[56] Cornuet, J. M., Pudlo, P., Veyssier, J., Dehne-Garcia, A., Gautier, M., Leblois, R., Marin, J. M. and Estoup, A. (2014). DIYABC v2.0: A software to make Approximate Bayesian Computation inferences about population history using single nucleotide polymorphism, DNA sequence and microsatellite data. Bioinformatics 30 1187-1189.

[57] Crackel, R. and Flegal, J. (2017). Bayesian inference for a flexible class of bivariate beta distributions. Journal of Statistical Computation and Simulation 87 295-312.

[58] Craig, P. S., Goldstein, M., Seheult, A. H. and Smith, J. A. (1997). Pressure matching for hydrocarbon reservoirs: A case study in the use of Bayes linear strategies for large computer experiments. In Case Studies in Bayesian Statistics (C. Gatsonis, J. S. Hodges, R. E. Kass, R. McCulloch, P. Rossi and N. D. Singpurwalla, eds.) 37-93. Springer, New York.

[59] Creel, M. and Kristensen, D. (2016). On selection of statistics for Approximate Bayesian computing (or the method of simulated moments). Computational Statistics and Data Analysis 100 99-114.

[60] Crema, E. R., Edinborough, K., Kerig, T. and Shennan, S. J. (2014). An Approximate Bayesian Computation approach for inferring patterns of cultural evolutionary change. Journal of Archaeological Science 50 160-170.

[61] Csilléry, K., François, O. and Blum, M. G. B. (2012). abc: An R package for Approximate Bayesian Computation (ABC). Methods in Ecology and Evolution 3 475-479.

[62] Csilléry, K., Blum, M. G. B., Gaggiotti, O. E. and Francois, O. (2010). Approximate Bayesian Computation (ABC) in practice. Trends in Ecology and Evolution 25 410-418.

[63] Cussens, J. (2011). Approximate Bayesian Computation for the parameters of PRISM programs. In Inductive Logic Programming: 20th International Conference, ILP 2010 (P. Frasconi and F. A. Lisi, eds.) 38-46.
G. Karabatsos and F. Leisen/Approximate Likelihood for ABC

[64] Davison, A. C., Hinkley, D. V. and Worton, B. J. (1992). Bootstrap likelihoods. Biometrika 79 113-130.

[65] Dean, T. A. and Singh, S. S. (2011). Asymptotic behaviour of approximate Bayesian estimators. ArXiv e-print 1105.3655.

[66] DelMoral, P., Doucet, A. and Jasra, A. (2006). Sequential Monte Carlo samplers. Journal of the Royal Statistics Society, Series B 68 411-436.

[67] DelMoral, P., Doucet, A. and Jasra, A. (2012). An adaptive sequential Monte Carlo method for Approximate Bayesian Computation. Statistics and Computing 22 1009-1020.

[68] Didelot, X., Everitt, R. G., Johansen, A. M. and Lawson, D. J. (2011). Likelihood-free estimation of model evidence. Bayesian Analysis 6 49-76.

[69] Diggle, P. J. and Gratton, R. J. (1984). Monte Carlo methods of inference for implicit statistical models. Journal of the Royal Statistical Society, Series B 46 193-227.

[70] Dimitrakakis, C. and Tziortziotis, N. (2013). ABC Reinforcement Learning. In Proceedings of the 30th International Conference on Machine Learning (ICML 3) (S. Dasgupta and D. McAllester, eds.) 684-692.

[71] Doksum, K. A. and Lo, A. Y. (1990). Consistent and robust Bayes procedures for location based on partial information. Annals of Statistics 18 443-453.

[72] Drovandi, C. C. (2017). Approximate Bayesian Computation. In Wiley StatsRef: Statistics Reference Online (N. Balakrishnan, T. Colton, B. Everitt, W. Pieorsch, F. Ruggeri and J. L. Teugels, eds.) 1-9. Wiley, Hoboken, New Jersey.

[73] Drovandi, C. C. and Pettitt, A. N. (2011). Likelihood-free Bayesian estimation of multivariate quantile distributions. Computational Statistics and Data Analysis 55 2541-2556.

[74] Drovandi, C. C., Pettitt, A. N. and Faddy, M. J. (2011). Approximate Bayesian Computation using indirect inference. Journal of the Royal Statistical Society, Series C 60 317-337.

[75] Drovandi, C. C. and Pettitt, A. N. (2011b). Estimation of parameters for macroparasite population evolution using Approximate Bayesian Computation. Biometrics 67 225-233.

[76] Drovandi, C. C. and Pettitt, A. N. (2013). Bayesian experimental design for models with intractable likelihoods. Biometrics 69 937-948.

[77] Drovandi, C. C., Pettitt, A. N. and Lee, A. (2015). Bayesian indirect inference using a parametric auxiliary model. Statistical Science 30 72-95.

[78] Drovandi, C. C., Graziany, C., Mengersen, K. and Robert, C. (2018). Approximating the Likelihood in Approximate Bayesian Computation. In Handbook of Approximate Bayesian Computation (S. A. Sisson, Y. Fan and M. A. Beaumont, eds.) na-na. Chapman and Hall/CRC Press, Boca Raton, Florida.

[79] Efron, B. and Tibshirani, R. J. (1993). An Introduction to the Boot-
strap. Chapman and Hall/CRC, Boca Raton, FL.

[80] Erhardt, R. and Sisson, S. A. (2016). Modelling extremes using Approximate Bayesian Computation. In Extreme Value Modeling and Risk Analysis: Methods and Applications (D. K. Dey and J. Yan, eds.) 281-306. Chapman and Hall/CRC Press, Boca Raton, FL.

[81] Erhardt, R. J. and Smith, R. L. (2012). Approximate Bayesian computing for spatial extremes. Computational Statistics and Data Analysis 56:1468-1481.

[82] Estoup, A. and Guillemaud, T. (2010). Reconstructing routes of invasion using genetic data: Why, how and so what? Molecular Ecology 19:4113-4130.

[83] Estoup, A., Beaumont, M., Sennedot, F., Moritz, C. and Cornuet, J. M. (2004). Genetic analysis of complex demographic scenarios: Spatially expanding populations of the cane toad, Bufo marinus. Evolution 58:2021-2036.

[84] Estoup, A., Lombaert, E., Marin, J. M., Guillemaud, T., Pudlo, P., Robert, C. P. and Cornuet, J. M. (2012). Estimation of demo-genetic model probabilities with Approximate Bayesian Computation using linear discriminant analysis on summary statistics. Molecular Ecology Resources 12:846-855.

[85] Estoup, A., Verdu, P., Marin, J. M., Robert, C. P., Dehne-Garcia, A., Cornuet, J. M. and Pudlo, P. (2018). Application of Approximate Bayesian Computation to infer the genetic history of Pygmy hunter-gatherers populations from West Central Africa. In Handbook of Approximate Bayesian Computation (S. A. Sisson, Y. Fan and M. A. Beaumont, eds.) na-na. Chapman and Hall/CRC Press, Boca Raton, Florida.

[86] Fagundes, N. J. R., Ray, N., Beaumont, M., Neuenschwander, S., Salzano, F. M., Bonatto, S. L. and Excoffier, L. (2007). Statistical evaluation of alternative models of human evolution. Proceedings of the National Academy of Sciences 104:17614-17619.

[87] Fan, H. H. and Kubatko, L. S. (2011). Estimating species trees using Approximate Bayesian Computation. Molecular Phylogenetics and Evolution 59:354-363.

[88] Fan, Y., Nott, D. J. and Sisson, S. A. (2013). Approximate Bayesian computation via regression density estimation. Stat 2:34-48.

[89] Fan, Y., Meikle, S. R., Angelis, G. and Sitek, A. (2018). ABC in nuclear imaging. In Handbook of Approximate Bayesian Computation (S. A. Sisson, Y. Fan and M. A. Beaumont, eds.) na-na. Chapman and Hall/CRC Press, Boca Raton, Florida.

[90] Fasiolo, M. and Wood, S. (2014). An introduction to synlik (2014). R package version 0.1.0.

[91] Fasiolo, M. and Wood, S. N. (2018). ABC in ecological modelling. In Handbook of Approximate Bayesian Computation (S. A. Sisson, Y. Fan and M. A. Beaumont, eds.) na-na. Chapman and Hall/CRC Press, Boca Raton, Florida.
[92] Fay, D., Moore, A. W., Brown, K., Filosi, M. and Jurman, G. (2015). Graph metrics as summary statistics for Approximate Bayesian Computation with application to network model parameter estimation. Journal of Complex Networks 3 52-83.

[93] Fearnhead, P. and Prangle, D. (2012). Constructing summary statistics for Approximate Bayesian Computation: Semi-automatic Approximate Bayesian Computation. Journal of the Royal Statistical Society, Series B 74 419-474.

[94] Filippi, S. (2013). On optimality of kernels for Approximate Bayesian Computation using sequential Monte Carlo. Statistical Applications in Genetics and Molecular Biology 12 87-107.

[95] Foll, M., Beaumont, M. A. and Gaggiotti, O. (2008). An approximate Bayesian computation approach to overcome biases that arise when using amplified fragment length polymorphism markers to study population structure. Genetics 179 927-939.

[96] Forneron, J. J. and Ng, S. (2018). The ABC of simulation estimation with auxiliary statistics. Journal of Econometrics na na-na.

[97] François, O. and Laval, G. (2011). Deviance information criteria for model selection in Approximate Bayesian Computation. Statistical Applications in Genetics and Molecular Biology 10 1-25.

[98] Fu, Y. X. and Li, W. H. (1997). Estimating the age of the common ancestor of a sample of DNA sequences. Molecular Biology and Evolution 14 195-199.

[99] Gallant, A. R. and McCulloch, R. E. (2009). On the determination of general scientific models with application to asset pricing. Journal of the American Statistical Association 104 117-131.

[100] Ghurye, S. G. and Olkin, I. (1969). Unbiased estimation of some multivariate probability densities and related functions. The Annals of Mathematical Statistics 40 1261-1271.

[101] Girolami, M., Lyne, A. M., Strathmann, H., Simpson, D. and Atchade, Y. (2013). Playing Russian roulette with intractable likelihoods. Technical Report, University College London.

[102] Gleim, A. and Pigorsch, C. (2013). Approximate Bayesian Computation with indirect summary statistics. Technical Report, Institute of Econometrics, University of Bonn, Germany.

[103] Golchi, S. and Campbell, D. A. (2016). Sequentially Constrained Monte Carlo. Computational Statistics and Data Analysis 97 98-113.

[104] Gourioux, C., Monfort, A. and Renault, E. (1993). Indirect Inference. Journal of Applied Econometrics 8 S85-S118.

[105] Grazian, C. and Liseo, B. (2014). Approximate integrated likelihood via ABC methods. ArXiv e-print 1403.0587.

[106] Grazian, C. and Liseo, B. (2015). Approximate Bayesian Computation for copula estimation. Statistica 75 111-127.

[107] Grazian, C. and Liseo, B. (2017a). Approximate Bayesian inference in semiparametric copula models. Bayesian Analysis 12 991-1016.

[108] Grazian, C. and Liseo, B. (2017b). Approximate Bayesian Methods for
Multivariate and Conditional Copulae In Soft Methods for Data Science 261-268. Springer International Publishing, Cham.

[109] Grelaud, A., Robert, C. P., Marin, J. M., Rodolphe, F. and Taly, J. F. (2009). ABC likelihood-free methods for model choice in Gibbs random fields. *Bayesian Analysis* 4 317-335.

[110] Groendyke, C. and Welch, D. (2018). epinet: An R package to analyze epidemics spread across contact networks. *Journal of Statistical Software* 83 1-22.

[111] Gutmann, M. U. and Corander, J. (2016). Bayesian optimization for likelihood-free inference of simulator-based statistical models. *Journal of Machine Learning Research* 17 1-47.

[112] Hainy, M., Müller, W. G. and Wagner, H. (2016). Likelihood-free simulation-based optimal design with an application to spatial extremes. *Stochastic Environmental Research and Risk Assessment* 30 481-492.

[113] Hamilton, G., Currat, M., Ray, N., Heckel, G., Beaumont, M. and Excoffier, L. (2005). Bayesian estimation of recent migration rates after a spatial expansion. *Genetics* 170 409-417.

[114] Hartig, F., Calabrese, J. M., Reineking, B., Wiegand, T. and Huth, A. (2011). Statistical inference for stochastic simulation models - theory and application. *Ecology Letters* 14 816-827.

[115] Hegglund, K. and Frigessi, A. (2004). Estimating functions in indirect inference. *Journal of the Royal Statistical Society, Series B* 66 447-462.

[116] Hickerson, M. J., Stahl, E. A. and Lessios, H. A. (2006). Test for simultaneous divergence using Approximate Bayesian Computation. *Evolution* 60 2435-2453.

[117] Hickerson, M. J., Stahl, E. and Takebayashi, N. (2007). msBayes: Pipeline for testing comparative phylogeographic histories using hierarchical Approximate Bayesian Computation. *BMC Bioinformatics* 8 268.

[118] Holden, P. B., Edwards, N. R., Hensman, J. and Wilkinson, R. D. (2018). ABC for climate: Dealing with expensive simulators. In *Handbook of Approximate Bayesian Computation* (S. A. Sisson, Y. Fan and M. A. Beaumont, eds.) na-na. Chapman and Hall/CRC Press, Boca Raton, Florida.

[119] Holmes, C. C. and Mallick, B. K. (2003). Generalized nonlinear modeling with multivariate free-knot regression splines. *Journal of the American Statistical Association* 98 352-368.

[120] Huang, W., Takebayashi, N., Qi, Y. and Hickerson, M. J. (2011). MTML-msBayes: Approximate Bayesian comparative phylogeographic inference from multiple taxa and multiple loci with rate heterogeneity. *BMC Bioinformatics* 12 1-14.

[121] Hyrien, O., Mayer-Pröschel, M., Noble, M. and Yakovlev, A. (2005). A stochastic model to analyze clonal data on multi-type cell populations. *Biometrics* 61 199-207.

[122] Ilves, K. L., Huang, W., Wares, J. P. and Hickerson, M. J. Colonization and/or mitochondrial selective sweeps across the North Atlantic intertidal assemblage revealed by multi-taxon Approximate Bayesian Com-
putation. *Molecular Ecology* **19** 4505-4519.

[123] Ishida, E. E. O., Vitenti, S. D. P., Penna-Lima, M., Cisewski, J., de Souza, R. S., Trindade, A. M. M., Cameron, E. and Busti, V. C. (2015). cosmoabc: Likelihood-free inference via population Monte Carlo Approximate Bayesian Computation. *Astronomy and Computing* **13** 1-11.

[124] Jabot, F. and Chave, J. (2011). Analyzing tropical forest tree species abundance distributions using a nonneutral model and through approximate Bayesian inference. *The American Naturalist* **178** E37–E47.

[125] Jabot, F., Faure, T. and Dumoulin, N. (2013). EasyABC: Performing efficient Approximate Bayesian Computation sampling schemes using R. *Methods in Ecology and Evolution* **4** 684-687.

[126] Jabot, F., Lagarrigues, G., Courbaud, B. and Dumoulin, N. (2014). A comparison of emulation methods for Approximate Bayesian Computation. *ArXiv e-print 1412.7560*.

[127] Jakobsson, M., Hagenblad, J., Tavaré, S., Sall, T., Halldén, C., Lind-Halldén, C. and Nordborg, M. (2006). A unique recent origin of the allotetraploid species Arabidopsis suecica: Evidence from nuclear DNA markers. *Molecular Biology and Evolution* **23** 1217-1231.

[128] Jasra, A. (2015). Approximate Bayesian Computation for a class of time series models. *International Statistical Review* **83** 405–435.

[129] Jasra, A., Kantas, N. and Ehrlich, E. (2014). Approximate inference for observation-driven time series models with intractable likelihoods. *ACM Transactions on Modeling and Computer Simulation* **24** 13:1-13:25.

[130] Jennings, E. and Madigan, M. (2017). astroABC : An Approximate Bayesian Computation Sequential Monte Carlo sampler for cosmological parameter estimation. *Astronomy and Computing* **19** 16-22.

[131] Joyce, P. and Marjoram, P. (2008). Approximately sufficient statistics and Bayesian computation. *Statistical Applications in Genetics and Molecular Biology* **7** 1-16.
Kacprzak, T., Herbel, J., Amara, A. and Réfrégier, A. (2018). Accelerating Approximate Bayesian Computation with quantile regression: Application to cosmological redshift distributions. *Journal of Cosmology and Astroparticle Physics* **2018** 042.

Kangasrääsiö, A., Athukorala, K., Howes, A., Corander, J., Kaski, S. and Oulasvirta, A. (2017). Inferring cognitive models from data using Approximate Bayesian Computation. In *Proceedings of the 2017 CHI Conference on Human Factors in Computing Systems* 1295-1306.

Karabatsos, G. (2017, in press). On Bayesian testing of additive conjoint measurement axioms using synthetic likelihood. *Psychometrika* (na-nee).

Kilbinger, M., Benabed, K., Cappe, O., Cardoso, J. F., Coupon, J., Fort, G., McCracken, H. J., Prunet, S., Robert, C. P. and Wraith, D. (2011). CosmoPMC: Cosmology Population Monte Carlo. *ArXiv e-print 1101.0950*.

Kim, J. Y. (2002). Limited information likelihood and Bayesian analysis. *Journal of Econometrics* **107** 175-193.

Kobayashi, G. (2014). A transdimensional Approximate Bayesian Computation using the pseudo-marginal approach for model choice. *Computational Statistics and Data Analysis* **80** 167-183.

Kolmogorov, A. (1942). Definitions of center of dispersion and measure of accuracy from a finite number of observations. *Izvestiya Rossiskoi Akademii Nauk. Seriya Matematicheskaya* **6** 3-32.

Kousathanas, A., Duchen, P., and Wegmann, D. (2017). A guide to general-purpose ABC software Technical Report, University of Fribourg, Fribourg, Switzerland.

Kousathanas, A., Leuenberger, C., Helfer, J., Quinodoz, M., Foll, M. and Wegmann, D. (2016). Likelihood-Free Inference in High-Dimensional Models. *Genetics* **203** 893-904.

Koutroumpas, K., Ballarini, P., Votsi, I. and Cournde, P. H. (2016). Bayesian parameter estimation for the Wnt pathway: An infinite mixture models approach. *Bioinformatics* **32** i781-i789.

Krishnanathan, K., Anderson, S. R., Billings, S. A. and Kadirkamanathan, V. (2016). Computational system identification of continuous-time nonlinear systems using Approximate Bayesian Computation. *International Journal of Systems Science* **47** 3537-3544.

Kwan, Y. K. (1999). Asymptotic Bayesian analysis based on a limited information estimator. *Journal of Econometrics* **88** 99-121.

Kypriaos, T., Neal, P. and Prangle, D. (2017). A tutorial introduction to Bayesian inference for stochastic epidemic models using Approximate Bayesian Computation. *Mathematical Biosciences* **287** 42-53.

Lagarrigues, G., Jabot, F., Lafond, V. and Courbaud, B. (2015). Approximate Bayesian Computation to recalibrate individual-based models with population data: Illustration with a forest simulation model. *Ecological Modelling* **306** 278-286.
[152] Lee, A., Andrieu, C. and Doucet, A. (2012). Discussion of constructing summary statistics for Approximate Bayesian Computation: Semi-automatic approximate Bayesian computation. *Journal of the Royal Statistical Society, Series B* 74 449-450.

[153] Lee, A. and Latuszynski, K. (2014). Variance bounding and geometric ergodicity of Markov chain Monte Carlo kernels for Approximate Bayesian Computation. *Biometrika* 101 655-671.

[154] Lehmann, E. L. and Casella, G. (1998). *Theory of Point Estimation (2nd Ed.).* Springer-Verlag, New York.

[155] Lenine, O., Kirk, P. D. W. and Stumpf, M. P. H. (2016). Inferring extrinsic noise from single-cell gene expression data using Approximate Bayesian Computation. *BMC Systems Biology* 10 81.

[156] Lenormand, M., Jabot, F. and Deffuant, G. (2013). Adaptive Approximate Bayesian Computation for complex models. *Computational Statistics* 28 2777-2796.

[157] Lewis, A. and Bridle, A. (2002). Cosmological parameters from CMB and other data: A Monte Carlo approach. *Physical Review D* 66 103511.

[158] Li, W. and Fearnhead, P. (2016). Improved convergence of regression adjusted Approximate Bayesian Computation. *ArXiv preprint 1609.07135.*

[159] Li, W. and Fearnhead, P. (2018, in press). On the asymptotic efficiency of approximate Bayesian computation estimators. *Biometrika* na-na.

[160] Li, J., Nott, D. J., Fan, Y. and Sisson, S. A. (2017). Extending Approximate Bayesian Computation methods to high dimensions via a Gaussian copula model. *Computational Statistics and Data Analysis* 106 77-89.

[161] Liang, F., Kim, J. and Song, Q. (2016). A bootstrap Metropolis-Hastings Algorithm for Bayesian analysis of big data. *Technometrics* 58 304-318.

[162] Liepe, J. and Stumpf, M. P. H. (2018). ABC in systems biology. In *Handbook of Approximate Bayesian Computation* (S. A. Sisson, Y. Fan and M. A. Beaumont, eds.) na-na. Chapman and Hall/CRC Press, Boca Raton, Florida.

[163] Liepe, J., Barnes, C., Cule, E., Erguler, K., Kirk, P., Toni, T. and Stumpf, M. P. H. (2010). ABC-SysBio: Approximate Bayesian Computation in Python with GPU support. *Bioinformatics* 26 1797-1799.

[164] Liepe, J., Taylor, H., Barnes, C. P., Huvet, M., Bugeon, L., Thorne, T., Lamb, J. R., Dallman, M. J. and Stumpf, M. P. H. (2012). Calibrating spatio-temporal models of leukocyte dynamics against in vivo live-imaging data using Approximate Bayesian Computation. *Integrative Biology* 4 335-345.

[165] Lintusaari, J., Gutmann, M. U., Dutta, R., Kaski, S. and Corander, J. (2017). Fundamentals and recent developments in Approximate Bayesian Computation. *Systematic Biology* 66 e66.

[166] Liu, J. S. (2001). *Monte Carlo Strategies In Scientific Computing.* Springer, New York.
[167] Lombaert, E., Guillemaud, T., Thomas, C. E., Handley, L. J. L., Li, J., Wang, S., Pang, H., Goryacheva, I., Zakharov, I. A., Jousselin, E., Poland, R. L., Migeon, A., Lenteren, J. V., Clercq, P. D., Berkvens, N., Jones, W. and Estoup, A. (2011). Inferring the origin of populations introduced from a genetically structured native range by Approximate Bayesian Computation: Case study of the invasive ladybird Harmonia axyridis. *Molecular Ecology* **20** 4654-4670.

[168] Lopes, J. S., Balding, D. and Beaumont, M. A. (2009). PopABC: A program to infer historical demographic parameters. *Bioinformatics* **25** 2747-2749.

[169] Luciani, F., Sisson, S. A., Jiang, H., Francis, A. R. and Tanaka, M. M. (2009). The epidemiological fitness cost of drug resistance in Mycobacterium tuberculosis. *Proceedings of the National Academy of Sciences* **106** 14711-14715.

[170] Lyne, A. M., Girolami, M., Atchad, Y., Strathmann, H. and Simpson, D. (2015). On Russian roulette estimates for Bayesian inference with doubly-intractable likelihoods. *Statistical Science* **30** 443-467.

[171] MacGillivray, H. L. (1986). Skewness and asymmetry: Measures and orderings. *Annals of Statistics* **14** 994-1011.

[172] MacGillivray, H. L. (1992). Shape properties of the g-and-h and Johnson families. *Communications in Statistics, Theory and Methods* **21** 1233-1250.

[173] Mardulyn, P., Goffredo, M., Conte, A., Hendrickx, G., Meiswinkel, R., Balenghien, T., Sghaier, S., Lohr, Y. and Gilbert, M. (2013). Climate change and the spread of vector-borne diseases: Using Approximate Bayesian Computation to compare invasion scenarios for the bluetongue virus vector Culicoides imicola in Italy. *Molecular Ecology* **22** 2456-2466.

[174] Marin, J. M., Pudlo, P., Robert, C. P. and Ryder, R. J. (2012). Approximate Bayesian Computational methods. *Statistics and Computing* **22** 1167-1180.

[175] Marin, J. M., Pillai, N. S., Robert, C. P. and Rousseau, J. (2014). Relevant statistics for Bayesian model choice. *Journal of the Royal Statistical Society, Series B* **76** 833-859.

[176] Marjoram, P. (2013). Approximation Bayesian Computation. *OA Genetics* **1** 3-8.

[177] Marjoram, P. and Tavaré, S. (2006). Modern computational approaches for analysing molecular genetic variation data. *Nature Reviews Genetics* **7** 759-770.

[178] Marjoram, P., Zubair, A. and Nuzhdin, S. V. (2014). Post-GWAS: Where next? More samples, more SNPs or more biology? *Heredity* **112** 79.

[179] Marjoram, P., Molitor, J., Plagnol, V. and Tavaré, S. (2003). Markov chain Monte Carlo without likelihoods. *Proceedings of the National Academy of Sciences* **100** 15324-15328.

[180] McKinley, T., Cook, A. R. and Deardon, R. (2009). Inference in
epidemic models without likelihoods. *The International Journal of Biostatistics* 5 Article 24.

[181] McKinley, T. J., Ross, J. V., Deardon, R. and Cook, A. R. (2014). Simulation-based Bayesian inference for epidemic models. *Computational Statistics and Data Analysis* 71 434-447.

[182] 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. *Statistical Science* 33 4-18.

[183] Meeds, E., Leenders, R. and Welling, M. (2015). Hamiltonian ABC. ArXiv e-print 1503.01916.

[184] Meeds, E. and Welling, M. (2014). GPS-ABC: Gaussian process surrogate Approximate Bayesian Computation. ArXiv e-print 1401.2838.

[185] Mengersen, K. L., Pudlo, P. and Robert, C. P. (2013). Bayesian computation via empirical likelihood. *Proceedings of the National Academy of Sciences* 110 1321-1326.

[186] Mertens, U. K., Voß, A. and Radev, S. (2018). ABrox-A user-friendly Python module for approximate Bayesian computation with a focus on model comparison. *PLOS ONE* 13 1-16.

[187] Mitrovic, J., Sejdinovic, D. and Teh, Y. W. (2016). DR-ABC: Approximate Bayesian Computation with Kernel-Based Distribution Regression. In *Proceedings of the 33rd International Conference on Machine Learning* (M. F. Balcan and K. Q. Weinberger, eds.) 1482-1491. International Machine Learning Society, New York.

[188] Moores, M. T., Drovandi, C. C., Mengersen, K. and Robert, C. P. (2015). Pre-processing for Approximate Bayesian Computation in image analysis. *Statistics and Computing* 25 23-33.

[189] Murakami, Y. (2014). Bayesian parameter inference and model selection by population annealing in systems biology. *PloS One* e104057.

[190] Neal, P. (2012). Efficient likelihood-free Bayesian Computation for household epidemics. *Statistics and Computing* 22 1239-1256.

[191] Neal, P. and Huang, C. L. T. (2015). Forward simulation Markov Chain Monte Carlo with applications to stochastic epidemic models. *Scandinavian Journal of Statistics* 42 378-396.

[192] Neuenschwander, S., Largiadèr, C. R., Ray, N., Currat, M., Vonlanthen, P. and Excoffier, L. (2008). Colonization history of the Swiss Rhine basin by the bullhead (Cottus gobio): Inference under a Bayesian spatially explicit framework. *Molecular Ecology* 17 757-772.

[193] Nott, D. J., Fan, Y., Marshall, L. and Sisson, S. A. (2014). Approximate Bayesian Computation and Bayes linear analysis: Toward High-Dimensional ABC. *Journal of Computational and Graphical Statistics* 23 65-86.

[194] Nunes, M. A. and Balding, D. J. (2010). On optimal selection of summary statistics for Approximate Bayesian Computation. *Statistical Applications in Genetics and Molecular Biology* 9 1-18.

[195] Nunes, M. A. and Prangle, D. (2015). abctools: An R package for
tuning Approximate Bayesian Computation analyses. *The R Journal* 7 189-205.

[196] ONG, V. M. H., NOTT, D. J., TRAN, M. N., Sisson, S. A. and DROVANDI, C. C. (2018). Variational Bayes with synthetic likelihood. *Statistics and Computing* 28 971-988.

[197] PAVLIDIS, P., LAURENT, S. and STEPHAN, W. (2010). msABC: A modification of Hudsons ms to facilitate multi-locus ABC analysis. *Molecular Ecology Resources* 10 723-727.

[198] Pawitan, Y. (2000). Computing empirical likelihood from the bootstrap. *Statistics and Probability Letters* 47 337-345.

[199] PETERS, G. W., FAN, Y. and Sisson, S. A. (2012a). On sequential Monte Carlo, partial rejection control and Approximate Bayesian Computation. *Statistics and Computing* 22 1209-1222.

[200] PETERS, G. W., FAN, Y. and Sisson, S. A. (2012b). On sequential Monte Carlo, partial rejection control and Approximate Bayesian Computation. *Statistics and Computing* 22 1209-1222.

[201] PETERS, G. W., PANAYI, E. and SEPTIER, F. (2018). SMC-ABC methods for estimation of stochastic simulation models of the limit order book. In *Handbook of Approximate Bayesian Computation* (S. A. Sisson, Y. Fan and M. A. Beaumont, eds.) na-na. Chapman and Hall/CRC Press, Boca Raton, Florida.

[202] PETERS, G. W. and Sisson, S. A. (2006). Bayesian inference, Monte Carlo sampling and operational risk. *Journal of Operational Risk* 1 27-50.

[203] PETERS, G. W., Sisson, S. A. and FAN, Y. (2012). Likelihood-free Bayesian inference for alpha-stable models. *Computational Statistics and Data Analysis* 56 3743-3756.

[204] PETERS, G. W., NEVAT, I., Sisson, S. A., FAN, Y. and YUAN, J. (2010). Bayesian symbol detection in wireless relay networks via likelihood-free inference. *IEEE Transactions on Signal Processing* 58 5206-5218.

[205] PHAM, K. C., NOTT, D. J. and CHAUDHURI, S. (2014). A note on approximating ABC-MCMC using flexible classifiers. *Stat* 3 218-227.

[206] Picchini, U. (2013). abc-sde: A MATLAB toolbox for Approximate Bayesian Computation (ABC) in stochastic differential equation models.

[207] Picchini, U. (2014). Inference for SDE Models via Approximate Bayesian Computation. *Journal of Computational and Graphical Statistics* 23 1080-1100.

[208] Picchini, U. and ANDERSON, R. (2017). Approximate maximum likelihood estimation using data-cloning ABC. *Computational Statistics and Data Analysis* 105 166-183.

[209] Plagnol, V. and Tavaré, S. (2004). Approximate Bayesian Computation and MCMC. In *Monte Carlo and Quasi-Monte Carlo Methods 2002* (H. Niederreiter, ed.) 99-113. Springer, Berlin.

[210] Prangle, D. (2016). Lazy ABC. *Statistics and Computing* 26 171-185.

[211] Prangle, D. (2017). gk: An R package for the g-and-k and generalised g-and-h distributions. *ArXiv e-print* 1706.06889.
[212] Prangle, D., Fearnhead, P., Cox, M. P., Biggs, P. J. and French, N. P. (2014a). Semi-automatic selection of summary statistics for ABC model choice. *Statistical Applications in Genetics and Molecular Biology* **13** 67-82.

[213] Prangle, D., Blum, M. G. B., Popovic, G. and Sisson, S. A. (2014b). Diagnostic tools for Approximate Bayesian Computation using the coverage property. *Australian and New Zealand Journal of Statistics* **56** 309-329.

[214] Pratt, J. W., Raiffa, H. and Schlaifer, R. (1965). *Introduction to Statistical Decision Theory*. Wiley, New York.

[215] Price, L. F., Drovandi, C. C., Lee, A. and Nott, D. J. (2018). Bayesian Synthetic Likelihood. *Journal of Computational and Graphical Statistics* **27** 1-11.

[216] 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** 1791-1798.

[217] Pudlo, P., Marin, J. M., Estoup, A., Cornuet, J. M., Gautier, M. and Robert, C. P. (2016). Reliable ABC model choice via random forests. *Bioinformatics* **32** 859-866.

[218] Ratmann, O., Jorgensen, O., Hinkley, T., Stumpf, M., Richardson, S. and Wiuf, C. (2007). Using likelihood-free inference to compare evolutionary dynamics of the protein networks of H. pylori and P. falciparum. *PLoS Computational Biology* **3** e230.

[219] Ratmann, O., Andrieu, C., Wiuf, C. and Richardson, S. (2009). Model criticism based on likelihood-free inference, with an application to protein network evolution. *Proceedings of the National Academy of Sciences* **106** 10576-10581.

[220] Ratmann, O., Andrieu, C., Wiuf, C. and Richardson, S. (2010). Reply to Robert et al.: Model criticism informs model choice and model comparison. *Proceedings of the National Academy of Sciences* **107** E6-E7.

[221] Ratmann, O., Pudlo, P., Richardson, S. and Robert, C. (2011). Monte Carlo algorithms for model assessment via conflicting summaries. *ArXiv e-print* 1106.5919.

[222] Ratmann, O., Donker, G., Meijer, A., Fraser, C. and Koelle, K. (2012). Phylodynamic inference and model assessment with Approximate Bayesian Computation: Influenza as a case study. *PLoS Computational Biology* **8** 1-14.

[223] Ratmann, O., Camacho, A., Meijer, A. and Donker, G. (2013). Statistical modelling of summary values leads to accurate Approximate Bayesian Computations. *ArXiv e-print* 1305.4283.

[224] Rayner, G. and MacGillivray, H. (2002). Numerical maximum likelihood estimation for the g-and-k and generalized g-and-h distributions. *Statistics and Computing* **12** 57-75.

[225] Robert, C. P. (2011). Simulation in statistics. In *Proceedings of the 2011 Winter Simulation Conference* (S. Jain, R. R. Creasey, J. Him-
G. Karabatsos and F. Leisen/Approximate Likelihood for ABC

[26] ROBERT, C. P. (2016). Approximate Bayesian Computation: A Survey on Recent Results. In Monte Carlo and Quasi-Monte Carlo Methods (R. COOLS and D. NUYENS, eds.) 185-205. Springer International Publishing, Cham.

[27] ROBERT, C. P. and CASELLA, G. (2004). Monte Carlo Statistical Methods (2nd Ed.). Springer, New York.

[28] ROBERT, C. P., MENGERSEN, K. and CHEN, C. (2010). Model choice versus model criticism. Proceedings of the National Academy of Sciences 107 E5.

[29] ROBERT, C. P., BEAUMONT, M. A., MARIN, J. M. and CORNUET, J. M. (2008). Adaptivity for ABC algorithms: The ABC-PMC scheme. ArXiv e-print 0805.2256.

[30] ROBERT, C. P., CORNUET, J. M., MARIN, J. M. and PILLAI, N. S. (2011). Lack of confidence in Approximate Bayesian Computation model choice. Proceedings of the National Academy of Sciences 108 15112-15117.

[31] ROBERTS, G. O. and ROSENTHAL, J. S. (2009). Examples of Adaptive MCMC. Journal of Computational and Graphical Statistics 18 349-367.

[32] RODRIGUES, G. S., FRANCIS, A. R., SISSON, S. A. and TANAKA, M. M. (2018). Inferences on the acquisition of multidrug resistance in mycobacterium tuberculosis using molecular epidemiological data. In Handbook of Approximate Bayesian Computation (S. A. Sisson, Y. Fan and M. A. Beaumont, eds.) na-na. Chapman and Hall/CRC Press, Boca Raton, Florida.

[33] ROSENBLUM, E. B., HICKERSON, M. J. and MORITZ, C. (2007). A multilocus perspective on colonization accompanied by selection and gene flow. Evolution 61 2971-2985.

[34] RUBIN, D. B. (1984). Bayesianly justifiable and relevant frequency calculations for the applied statistician. Annals of Statistics 12 1151-1172.

[35] RUBIO, F. J. and JOHANSEN, A. M. (2013). A simple approach to maximum intractable likelihood estimation. Electronic Journal of Statistics 7 1632-1654.

[36] RULLI, E., SARTORI, N. and VENTURA, L. (2016). Approximate Bayesian Computation with composite score functions. Statistics and Computing 26 679-692.

[37] SEDKI, M., PUDLO, P., MARIN, J. M., ROBERT, C. P. and CORNUET, J. M. (2012). Efficient learning in ABC algorithms. ArXiv e-print 1210.1388.

[38] SEIGNEURIN, A., FRANÇOIS, O., LABARÈRE, J., OUDEVILLE, P., MONLONG, J. and COLOonna, M. (2011). Overdiagnosis from non-progressive cancer detected by screening mammography: Stochastic simulation study with calibration to population based registry data. BMJ 343 d7017.

[39] SHIROTA, S. and GELFAND, A. (2016). Approximate Bayesian Computation and model validation for repulsive spatial point processes. ArXiv preprint 1604.07027.
[240] Silk, D., Filippi, S. and Stumpf, M. P. H. (2013). Optimizing threshold-schedules for Approximate Bayesian Computation sequential Monte Carlo samplers: Applications to molecular systems. *Statistical Applications in Genetics and Molecular Biology* **12** 603-618.

[241] Sisson, S. A., Fan, Y. and Tanaka, M. M. (2007). Sequential Monte Carlo without likelihoods. *Proceedings of the National Academy of Sciences* **104** 1760-1765.

[242] Sisson, S. A. and Fan, Y. (2011). Likelihood-Free Markov Chain Monte Carlo. In *Handbook of Markov Chain Monte Carlo* (S. Brooks, A. Gelman, G. L. Jones and X. L. Meng, eds.) 313-338. Chapman and Hall/CRC, Boca Raton, FL.

[243] Sisson, S. A., Fan, Y. and Beaumont, M. A. (2018). Overview of Approximate Bayesian Computation. In *Handbook of Approximate Bayesian Computation* (S. A. Sisson, Y. Fan and M. A. Beaumont, eds.) 9-19. Chapman and Hall/CRC Press, Boca Raton, Florida.

[244] Slater, G. J., Harmon, L. J., Wegmann, D., Joyce, P., Revell, L. J. and Alfaro, M. E. (2018). Fitting models of continuous trait evolution to incompletely sampled comparative data using Approximate Bayesian Computation. *Evolution* **66** 752-762.

[245] Spence, M. A. and Blackwell, P. G. (2016). Coupling random inputs for parameter estimation in complex models. *Statistics and Computing* **26** 1137-1146.

[246] Spiegelhalter, D. J., Best, N. G., Carlin, B. P. and der Linde, A. V. (2002). Bayesian measures of model complexity and fit. *Journal of the Royal Statistical Society, Series B* **64** 1-34.

[247] Stocks, M., Siol, M., Lascoux, M. and De Mitra, S. (2014). Amount of information needed for model choice in Approximate Bayesian Computation. *PLoS ONE* **9** 1-13.

[248] Sunnåker, M., Busetto, A. G., Numminen, E., Corander, J., Foll, M. and Dessimoz, C. (2013). Approximate Bayesian Computation. *PLoS Computational Biology* **9** 1-10.

[249] Tallmon, D. A., Luikart, G. and Beaumont, M. A. (2004). Comparative evaluation of a new effective population size estimator based on Approximate Bayesian Computation. *Genetics* **167** 977-988.

[250] Tallmon, D. A., Koyuk, A., Luikart, G. and Beaumont, M. A. (2008). COMPUTER PROGRAMS: onesamp: A program to estimate effective population size using Approximate Bayesian Computation. *Molecular Ecology Resources* **8** 299-301.

[251] Tanaka, M. M., Francis, A. R., Luciani, F. and Sisson, S. A. (2006). Using Approximate Bayesian Computation to estimate tuberculosis transmission parameters from genotype data. *Genetics* **173** 1511-1520.

[252] Tavare, S. (2005). Ancestral inference for branching processes. In *Branching Processes in Biology: Variation, Growth, Extinction* (P. Haccou, P. Jagers and V. Vatutin, eds.) 208-217. Cambridge University Press, Cambridge, UK.

[253] Tavaré, S., Balding, D. J., Griffiths, R. C. and Donnelly, P.
(1997). Inferring coalescence times from DNA sequence data. *Genetics* **145** 505-518.

[254] Tavaré, S., Marshall, C. R., Will, O., Soligo, C. and Martin, R. D. (2002). Using the fossil record to estimate the age of the last common ancestor of extant primates. *Nature* **416** 726.

[255] Technow, F., Messina, C. D., Totir, L. R. and Cooper, M. (2015). Integrating crop growth models with whole genome prediction through Approximate Bayesian computation. *PloS One* **10** e0130855.

[256] Thornton, K. R. (2009). Automating Approximate Bayesian Computation by local linear regression. *BMC Genetics* **10** 1-5.

[257] Toni, T. and Stumpf, M. P. H. (2010). Simulation-based model selection for dynamical systems in systems and population biology. *Bioinformatics* **26** 104-110.

[258] Toni, T., Welch, D., Strelkowa, N., Ipsen, A. and Stumpf, M. P. H. (2009). Approximate Bayesian Computation scheme for parameter inference and model selection in dynamical systems. *Journal of the Royal Society Interface* **6** 187-202.

[259] Tran, M. N., Nott, D. J. and Kohn, R. (2017). Variational Bayes with intractable likelihood. *Journal of Computational and Graphical Statistics* **26** 873-882.

[260] Tsutaya, T. and Yoneda, M. (2013). Quantitative reconstruction of weaning ages in archaeological human populations using bone collagen nitrogen isotope ratios and Approximate Bayesian Computation. *PLOS ONE* **8** 1-10.

[261] Turner, B. M. and Sederberg, P. B. (2012). Approximate Bayesian Computation with differential evolution. *Journal of Mathematical Psychology* **56** 375-385.

[262] Turner, B. M. and Sederberg, P. B. (2014). A generalized, likelihood-free method for posterior estimation. *Psychonomic Bulletin & Review* **21** 227-250.

[263] Turner, B. M. and Van Zandt, T. (2012). A tutorial on Approximate Bayesian Computation. *Journal of Mathematical Psychology* **56** 69-85.

[264] Turner, B. M. and Van Zandt, T. (2014). Hierarchical Approximate Bayesian Computation. *Psychometrika* **79** 185-209.

[265] Vakilzadeh, M. K., Huang, Y., Beck, J. L. and Abrahamsson, T. (2017). Approximate Bayesian Computation by subset simulation using hierarchical state-space models. *Mechanical Systems and Signal Processing* **84** 2-20.

[266] Vehtari, A. and Ojanen, J. (2012). A survey of Bayesian predictive methods for model assessment, selection and comparison. *Statistics Surveys* **6** 142-228.

[267] Verdu, P., Austerlitz, F., Estoup, A., Vitalis, R., Georges, M., Thry, S., Froment, A., Le Bomin, S., Gessain, A., Hombert, J. M., Van der Veen, L., Quintana-Murci, L., Bahuchet, S. and Heyer, E. (2009). Origins and genetic diversity of Pygmy hunter-gatherers from Western Central Africa. *Current Biology* **19** 312-318.
[268] Vo, B. N., Drovandi, C. C., Pettitt, A. N. and Pettet, G. J. (2015a). Melanoma cell colony expansion parameters revealed by Approximate Bayesian Computation. *PLoS Computational Biology* 11 e1004635.

[269] Vo, B. N., Drovandi, C. C., Pettitt, A. N. and Simpson, M. J. (2015b). Quantifying uncertainty in parameter estimates for stochastic models of collective cell spreading using Approximate Bayesian Computation. *Mathematical Biosciences* 263 133-142.

[270] Volz, E. M., Koopman, J. S., Ward, M. J., Brown, A. L. and Frost, S. D. W. (2012). Simple epidemiological dynamics explain phylogenetic clustering of HIV from patients with recent infection. *PLoS Computational Biology* 8 e1002552.

[271] Vrugt, J. A. (2016). Markov chain Monte Carlo simulation using the DREAM software package: Theory, concepts, and MATLAB implementation. *Environmental Modelling and Software* 75 273-316.

[272] Vrugt, J. A. and Sadegh, M. (2013). Toward diagnostic model calibration and evaluation: Approximate Bayesian Computation. *Water Resources Research* 49 4335-4345.

[273] Wang, J. and Atchadé, Y. F. (2014). Approximate Bayesian Computation for exponential random graph models for large social networks. *Communications in Statistics-Simulation and Computation* 43 359-377.

[274] Wegmann, D. and Excoffier, L. (2010). Bayesian inference of the demographic history of chimpanzees. *Molecular Biology and Evolution* 27 1425-1435.

[275] Wegmann, D., Leuenberger, C. and Excoffier, L. (2009). Efficient Approximate Bayesian Computation coupled with Markov chain Monte Carlo without likelihood. *Genetics* 182 1207-1218.

[276] Wegmann, D., Leuenberger, C., Neuenschwander, S. and Excoffier, L. (2010). ABCtoolbox: A versatile toolkit for Approximate Bayesian Computations. *BMC Bioinformatics* 11 116-122.

[277] Weiss, G. and von Haeseler, A. (1998). Inference of population history using a likelihood approach. *Genetics* 149 1539-1546.

[278] Weyant, A., Schafer, C. and Wood-Vasey, W. M. (2013). Likelihood-free cosmological inference with type Ia supernovae: approximate Bayesian computation for a complete treatment of uncertainty. *The Astrophysical Journal* 764 116.

[279] White, S. R., Kypraios, T. and Preston, S. P. (2015). Piecewise Approximate Bayesian Computation: Fast inference for discretely observed Markov models using a factorised posterior distribution. *Statistics and Computing* 25 289-301.

[280] Wilkinson, R. (2013). Approximate Bayesian Computation (ABC) gives exact results under the assumption of model error. *Statistical Applications in Genetics and Molecular Biology* 12 129-141.

[281] Wilkinson, R. (2014). Accelerating ABC methods using Gaussian processes. In *Proceedings of the Seventeenth International Conference on Artificial Intelligence and Statistics, Volume 33* (S. Kaski and J. Corander, eds.) 1015-1023. Microtome Publishing, Brookline, MA.
[282] Wilkinson, R. D. and Tavaré, S. (2009). Estimating primate divergence times by using conditioned birth-and-death processes. *Theoretical Population Biology* **75** 278-285.

[283] Wood, S. N. (2010). Statistical inference for noisy nonlinear ecological dynamic systems. *Nature* **466** 1102-1104.

[284] Zellner, A. (1997). The Bayesian Method of Moments (BMOM): Theory and applications. In *Advances in Econometrics* (T. Fomby and R. Hill, eds.) **12** 85-105. Emerald Group Publishing Limited, Bingley, United Kingdom.

[285] Zhu, W., Marin, J. M. and Leisen, F. (2016). A Bootstrap likelihood approach to Bayesian computation. *Australian and New Zealand Journal of Statistics* **58** 227-244.