

Retraction

Retracted: Embedded Estimation Sequential Bayes Parameter Inference for the Ricker Dynamical System

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This article has been retracted by Hindawi following an investigation undertaken by the publisher [1]. This investigation has uncovered evidence of one or more of the following indicators of systematic manipulation of the publication process:

- (1) Discrepancies in scope
- (2) Discrepancies in the description of the research reported
- (3) Discrepancies between the availability of data and the research described
- (4) Inappropriate citations
- (5) Incoherent, meaningless and/or irrelevant content included in the article
- (6) Manipulated or compromised peer review

The presence of these indicators undermines our confidence in the integrity of the article's content and we cannot, therefore, vouch for its reliability. Please note that this notice is intended solely to alert readers that the content of this article is unreliable. We have not investigated whether authors were aware of or involved in the systematic manipulation of the publication process.

Wiley and Hindawi regrets that the usual quality checks did not identify these issues before publication and have since put additional measures in place to safeguard research integrity.

We wish to credit our own Research Integrity and Research Publishing teams and anonymous and named external researchers and research integrity experts for contributing to this investigation.

The corresponding author, as the representative of all authors, has been given the opportunity to register their agreement or disagreement to this retraction. We have kept a record of any response received.

References

- [1] M. J. U. Rehman, R. Zafar, H. Dilpazir, M. F. Sohail, M. A. Khan, and R. Jahan, "Embedded Estimation Sequential Bayes Parameter Inference for the Ricker Dynamical System," *Journal of Sensors*, vol. 2022, Article ID 4540366, 8 pages, 2022.

Research Article

Embedded Estimation Sequential Bayes Parameter Inference for the Ricker Dynamical System

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The dynamical systems are comprised of two components that change over time: the state space and the observation models. This study examines parameter inference in dynamical systems from the perspective of Bayesian inference. Inference on unknown parameters in nonlinear and non-Gaussian dynamical systems is challenging because the posterior densities corresponding to the unknown parameters do not have traceable formulations. Such a system is represented by the Ricker model, which is a traditional discrete population model in ecology and epidemiology that is used in many fields. This study, which deals with parameter inference, also known as parameter learning, is the central objective of this study. A sequential embedded estimation technique is proposed to estimate the posterior density and obtain parameter inference. The resulting algorithm is called the Augmented Sequential Markov Chain Monte Carlo (ASMCMC) procedure. Experiments are performed via simulation to illustrate the performance of the ASMCMC algorithm for observations from the Ricker dynamical system.

1. Introduction

It is possible to examine the dynamical characteristics of linear and nonlinear systems using state space modelling because it provides a consistent framework for doing so. The state space modelling process is divided into two stages: the development of a model that describes the underlying system dynamics over time, known as the state space model; and (ii) the development of a model that relates observations to state space variables, known as the measurement state model (also known as the measurement state model). The class of issues covered in this paper is the inference of unknown parameters, denoted by the symbol Ω , that regulate the dynamical system under consideration. As an example of a discrete-time stochastic system representing (i) and (ii), the discrete-time stochastic system is

expanded to include Ω to solve the parameter inference issue and is given by

$$m_k = \Phi_{k-1, \Omega}(m_{k-1}, u_{k-1}), \quad (1)$$

$$y_k = \Psi_{k, \Omega}(m_k, v_k), \quad (2)$$

for $k = 1, 2, 3, \dots, T$ with $m_0 \sim p_0$ represents the known prior distribution on the initial state space variable m_0 ; in (1) and (2), k represents a generic time step and T denotes the final time, $\Phi_{k-1, \Omega}(\cdot)$ represents the transfer function in the state space model with noise u_k , and $\Psi_{k, \Omega}(\cdot)$ represents the nonlinear and non-Gaussian measurement model. Both $\Phi_{k-1, \Omega}(\cdot)$ and $\Psi_{k, \Omega}(\cdot)$ are further known only up to the unknown parameter $\Omega \in R^p$ which is the object of inference. Additionally, in (1), u_{k-1} is assumed to be distributed

according to $F_{\Omega}(\cdot)$ which is again parameterized by the components of Ω . In other words, Ω represents the collection of all unknown parameters in the dynamical system of (1) and (2), which are to be inferred based on the observed data. The development of Bayesian parameter inference methodology for the above dynamical system is the key objective of this article.

Physical, biological, neuroscience, and object tracking systems are all examples of multidisciplinary fields in which the inference problems that govern the characteristics of nonlinear dynamical systems are applied [1–10]. The most commonly used statistical frameworks for finding solutions to parameter inference problems seem to be frequentist (or non-Bayesian) approaches that use maximum likelihood estimation (ML), such as the Expectation Maximization (EM) procedure [11–16]. It is computationally difficult to infer parameters for nonlinear dynamical systems using frequentist approaches. Furthermore, these procedures return just point estimates rather than the whole distribution, indicating parameter uncertainty. It is necessary to run the estimation method a large number of times, using uncertainty estimation techniques such as bootstrapping, to get estimates of uncertainty. This entails an increase in both the computational load and the intensity.

The posterior distribution of unknown parameters, on the other hand, is used to offer both a point estimate and a corresponding estimate of uncertainty when estimating unknown parameters using Bayesian approaches. The aim of Bayesian procedures in a dynamical system setup is to obtain the posterior of Ω , $p(\Omega|y_{1:T})$, given all observations up to the final time T , $y_{1:T}$. The posterior $p(\Omega|y_{1:T})$ is generally difficult to obtain in closed form, so Bayesian computational algorithms are utilized to approximate it in the Monte Carlo sense. Markov chain Monte Carlo (MCMC) methods are the most frequently used approaches for estimating the posterior distribution when closed forms are not accessible, and they are the most accurate. Although Bayesian computational methods may be used to derive the posterior distribution of an unknown parameter, they are only justified in the limiting sense and can require a significant number of burn-ins before the MCMC algorithm converges [17–19]. In spite of this, certain computational methods are trivial to conceive and execute on computers, and standard packages are already available for many uncomplicated implementations of these procedures [20–22]. Some of the MCMC procedures are the Metropolis-Hastings (MH) algorithm, Gibbs sampler, and particle Markov Chain Monte Carlo (PMCMC) [23–25].

Several sequential Monte Carlo (SMC) approaches have been developed to address the constraints of the Markov Chain Monte Carlo (MCMC) algorithm for parameter estimation in dynamical systems. It is the core concept of SMC to utilise important samples to estimate the posterior of Ω at each k point in time and to propagate the samples sequentially via a suitable kernel. There exists an extensive literature on SMC methods (see, for example, [26–29]). The SMC-based parameter inference in nonlinear dynamical systems was first addressed in [30] where the Liu and West filter was developed. An artificial evolution of parameters

for parameter Ω is used in the Liu and West filter and assumes a mixture of normal distribution for the posterior distributions, $p(\Omega|y_{1:k})$, for $k = 1, 2, \dots, T$ within the mixture distribution. The tuning parameters govern the extent of the control of overdispersion of the mixture components [30, 31]. To minimize the weight degeneracy or particle decay, the main idea is to generate new samples from the posterior by fitting the mixture to the posterior. The Liu and West filter can generally be applied to any dynamical system, which is the main attraction of this procedure. However, due to the artificial evolution of the unknown parameter, the artificial variability is incorporated, which is the main drawback of this algorithm.

The aim of Bayesian procedures is to obtain the posterior of Ω , $p(\Omega|y_{1:T})$, given all observations up to time T , $y_{1:T}$. The posterior $p(\Omega|y_{1:T})$ is again difficult to obtain in close form, so Bayesian computational algorithms are utilized to approximate it in a Monte Carlo sense.

Another major class of SMC methods for parameter inference that does not introduce overdispersion in the posterior of Ω is particle learning algorithms [32, 33]. The original method is attributed to Storvik [34, 35] resulting in Storvik's filter (similar approaches are also proposed in [36, 37]). Storvik's filter assumes that the posterior distribution of Ω given $m_{0:k}$ and $y_{0:k}$ depends on a lower-dimensional set of sufficient statistics that can be recursively updated for each $k = 1, 2, \dots, T$. This recursion for sufficient statistics is defined by $s_{k+1} = S(s_k, m_{k+1}, y_{k+1})$, leading to the generation of Ω samples according to $\Omega \sim p(\Omega|m_{0:k}, y_{1:k}) = p(\Omega|s_k)$ for each $k = 1, 2, \dots, T$. Unlike the Liu and West filter, in Storvik's filter, there is no artificial evolution process for Ω and thus it does not suffer from overdispersion [38]. However, the crucial assumption in Storvik's filter is the availability of sufficient statistics s_k as well as the ability of sampling from the posterior $p(\Omega|s_k)$ given the sufficient statistics s_k .

Subsequent developments in SMC methods for parameter inference have extended the applicability of Storvik's filter to a variety of more general settings (see, for example, [39, 40]). The extended Liu and West (ELW) filter to estimate parameters and states [40] divides the parameter set to be inferred Ω , into two sets, Ω_0 and γ representing parameters without and with sufficient statistics, respectively. For the Ω_0 set, the ELW filter uses the Liu and West filter, where an artificial random error is introduced to the static parameter Ω_0 . The set of parameters γ updated based on Storvik's filter $\gamma \sim p(\gamma|s_k(\Omega_0))$. The sufficient statistics $s_k(\Omega_0)$ are based on the static parameters. The rest of the parameters have the artificial evolution in which overdispersion is used. The overall set of parameters is represented as $\Omega = (\Omega_0, \gamma)$. The ELW filter applies to a wider class of state space models compared to Storvik's original procedure but suffers from two drawbacks, namely, (i) artificial overdispersion of the final posterior and (ii) the requirement of the existence of the sufficient statistic $s_k(\Omega_0)$ for γ and the ability of sampling from the posterior $p(\gamma|s_k(\Omega_0))$.

Development of statistical methods in specific ecological combines the nonlinear and near chaotic behavior of the

system response for various applications [41–44]. A detailed comparison of the inference problem for nonlinear ecology and epidemiology is given in [45]. Nonlinearity is an observer in the experimental research [46]. Although the objectives of epidemiologists and ecologists are different, both are concerned about the persistence of specific species. The mathematical explanations of the population dynamics are similar in both studies [45].

The aim and scope of this paper are to use the chaotic epidemiological or ecological model and perform parameter inference. There are two objectives. First is to perform the inference for the proposed application even if sufficient statistics are not available. Second is to use an online method to perform the parameter inference. Many researchers [47, 48] have discussed the relationship between statistics and chaos. The primary inference methodology used in this manuscript is developed in [49], which is a sequential MCMC (SMCMC) procedure to obtain the unknown parameter posterior inference in dynamical systems. However, then in [49], the proposed methodology was only applicable when the considered measurement model is linear and additive Gaussian noise. In this work, the measurement model of the Ricker dynamical system incorporates a non-Gaussian distribution, and the associated dynamical system (a special case of (1) and (2)) incorporates nonlinearities via the transfer function $\Phi_{k-1,\Omega}(\cdot)$. The appropriate SMCMC algorithm for inferring Ω is developed for the Ricker dynamical system subsequently.

The remainder of this paper is organized into the following sections: In Section 2, Ricker's model is discussed. In Section 3, details of the SMCMC procedure are given. The simulation experiments are given in Section 4. In the last section, Section 5, we state our conclusions, and potential future work is discussed.

2. Ricker's Model

Theoretical ecology relies heavily on mathematical models of competition. Several mathematical models have been suggested to date to characterize the growth of contending populations; some of them are detailed in [50–52], including discrete-time models [53, 54]. The wide range of biological factors that influence ecosystem behavior makes it difficult for researchers to come to a consensus on how to simulate the dynamics of competing populations. Numerous instances of competing species and techniques for mathematical modelling are discussed in one of the pioneering publications on interspecific interaction [55]. The scramble competition has been found to fit the Ricker model [56, 57]. From order to chaos, the Ricker model illustrates dynamics [20–58]. It would be fascinating to observe what dynamic modes emerge when two Ricker maps are joined.

The Ricker's model is a classical discrete population model. It gives the expected density or numbers of individual species at each next generation.

$$\hat{m}_k = r m_{k-1} e^{-\hat{m}_{k-1} + u_{k-1}}, u_k \sim \mathcal{N}(0, \sigma^2). \quad (3)$$

Ricker's model is often used to explain the dynamics of two populations that are linked through migrations [50–58]. As a result, nothing is known about how Ricker communities evolved. In the experimental setup, a noisy model is considered in equation (3); here k represents the time evolution variable. r is a parameter to represent the intrinsic growth rate of the population. The process noise is represented by u_{k-1} , which can also be considered environmental noise. Here the process noise has a zero mean, and the covariance parameter is σ^2 . Suppose the dynamics of the population are modelled with Ricker's model, but it is not possible to know the exact population density at any time, so it is necessary to have a measurement model.

$$y_k \sim \text{Poisson}(\phi m_k). \quad (4)$$

Here y_k is the measurement parameter of the individual sampled at any time point k , and ϕ is the scale parameter.

By transforming $m_k = \log(\hat{m}_k)$, it is seen that (3) becomes

$$m_k = \log(r) + \log(m_{k-1}) - m_{k-1} + z_k, \quad (5)$$

and the measurement model (4) becomes

$$y_k \sim \text{Poisson}(\phi e^{m_k}). \quad (6)$$

Using the transformed variables, equations (5) and (6) can be seen to be special forms of the general state space and measurement model equations given by (1) and (2), respectively. We have $\Phi_{k-1,\Omega}(\cdot) = \log(r) + \log(m_{k-1}) - m_{k-1}$, and $\Psi_{k,\Omega}(\cdot)$ is the Poisson probability density function with mean ϕe^{m_k} . Thus, the Ricker dynamical system has three underlying parameters that govern the system, namely, σ^2 , $\log(r)$, and ϕ . In this paper, the latter two parameters are taken to be unknown, that is, $\Omega = [\log(r), \phi]$ and $\sigma^2 = 0.09$ is assumed fixed and known. True values of the parameters for our simulation studies are taken to be $\Omega = [\log(r), \phi] = [3.8, 0.7]$, which the same as given in [45].

3. An Augmented Sequential Markov Chain Monte Carlo Algorithm

Sequential Markov chain Monte Carlo algorithm working process is described in the subsequent text. Sequential updating characteristic of SMCMC is used in the proposed technique. The core notion is addressed in [59], which is focused on the Monte Carlo sum, but the cumulative filtering steps required for estimating the probability $p(y_k | y_{1:k-1}, \Omega)$ minimise. State variable m_k and unknown parameter Ω are supplemented at the time step of $k-1$ in [49]. Therefore, the likelihood function changes accordingly from $p(y_k | y_{1:k-1}, \Omega)$ to $p(y_k | m_{k-1}, \Omega)$. It is possible to achieve the analytical expression to avoid the need for cumulative filtering procedures. This is particularly useful when the amount of k is substantial.

The ASMCMC is an iterative procedure that starts from the initial time step $k=1$, increases sequentially, and finally

ends when $k = T$. Within the k -th step of the ASMC procedure, posterior samples are obtained based on an underlying Markov chain Monte Carlo procedure. This Markov chain Monte Carlo procedure will be called the k -th time step Markov chain Monte Carlo procedure. The target of the k -th step MCMC procedure is the posterior, $p(\Omega, m_T | y_{1:k})$, at time step k . Thus, when $k = T$, we will have obtained samples from the desired posterior $p(\Omega, m_T | y_{1:k})$ as well as $p(\Omega, y_{1:k})$ via marginalization. Details on the implementation of the k -th step Markov chain Monte Carlo procedure are as follows.

Assume that after the $(k-1)$ -th time step MCMC procedure, M samples (i.e., particles) $\xi_{k-1}^j \equiv (\Omega_{k-1}^j, m_{k-1}^j)$, $j = 1, 2, \dots, M$ are available from the posterior density $p(\Omega, m_{k-1} | y_{1:k-1})$. A class of Gaussian mixture model (GMM) is fitted using ξ_{k-1}^j , $j = 1, 2, \dots, M$ following the methodology outlined in [48–60]. This results in the estimated density $\hat{p}_{Mix}(\Omega, m_{k-1} | y_{1:k-1})$ based on GMMs. The methodology developed and implemented in [48–60] ensures that the fitted GMM is close to the true posterior density $p(\Omega, m_{k-1} | y_{1:k-1})$, that is,

$$\hat{p}_{Mix}(\Omega, m_{k-1} | y_{1:k-1}) \approx p(\Omega, m_{k-1} | y_{1:k-1}), \quad (7)$$

even though the exact form of the latter is unavailable.

To initialize the k -th time step MCMC procedure, the M samples ξ_{k-1}^j , $j = 1, 2, \dots, M$ are taken to form the starting points of Mk -th step MCMC procedures, that is, $\Omega_{k-1}^j \equiv \Omega_k^{j,0}$ and $m_{k-1}^j \equiv m_{k-1,k}^{j,0}$ for $j = 1, 2, \dots, M$. Some notations are developed here: denoted by $\Omega_k^{j,g}$ and $m_{k-1,k}^{j,g}$, respectively, to be the values of Ω and m_{k-1} at the g -th cycle of the k -th time step MCMC procedure initialized by $k_{k-1}^{j,0}$ for $j = 1, 2, \dots, M$. In other words, the Mk -th time step MCMC procedures initialized based on $\Omega_k^{j,0}$ form separate chains based on separate starting values; this entails that the M MCMC chains can be run in parallel for each time step $k = 1, 2, \dots, T$.

For details of the steps involved within each k -th step MCMC procedure, we suppress the j notation. For a generic k -th step MCMC procedure (note that there are M of them), initialize $\xi_k^0 \equiv (\Omega_k^0, m_{k-1,k}^0)$ as above from outputs of the $(k-1)$ -th chain. At step k of the k^{th} step MCMC procedure, assume $(\Omega_k^g, m_{k-1,k}^g)$ is already available. To transit from $g \rightarrow g+1$,

(i) Generate

$$(\Omega_k^*, m_{k-1,k}^*) \sim q(\Omega_k, m_{k-1,k} | \Omega_k^g, m_{k-1,k}^g), \quad (8)$$

where $q(\cdot | \cdot)$ in equation (8) is proposal density.

(ii) Compute the acceptance probability

$$\alpha_k((\Omega^g, m^g), (\Omega^*, m^*)) = \min \{ \mathbf{A} \cdot \mathbf{B}, 1 \} \text{ here} \quad (9)$$

$$\mathbf{A} = \frac{p(y_k | m_{k-1,k}^*, \Omega_k^*) \hat{p}_{Mix}(\Omega_k^*, m_{k-1,k}^* | y_{1:k-1})}{p(y_k | m_{k-1,k}^g, \Omega_k^g) \hat{p}_{Mix}(\Omega_k^g, m_{k-1,k}^g | y_{1:k-1})} \quad (10)$$

$$\mathbf{B} = \frac{q(\Omega_k^g, m_{k-1,k}^g | \Omega_k^*, m_{k-1,k}^*)}{q(\Omega_k^*, m_{k-1,k}^* | \Omega_k^g, m_{k-1,k}^g)} \quad (11)$$

where $p(y_k | m_{k-1,k}^*, \Omega_k^*)$ is the probability function of y_k given m_{k-1} and Ω as in ((13)).

Set $(\Omega_k^{k+1}, m_{k-1,k}^{k+1}) = (\Omega_k^*, m_{k-1,k}^*)$ with probability $\alpha_k((\Omega_k^g, m_{k-1,k}^g), (\Omega_k^*, m_{k-1,k}^*))$; otherwise, set

$$(\Omega_k^{k+1}, m_{k-1,k}^{k+1}) = (\Omega_k^g, m_{k-1,k}^g). \quad (12)$$

Continue the iteration from $k+1 \rightarrow k+2$.

The aforementioned Markov chain will converge as $k \rightarrow \infty$ to the stationary (and target) distribution determined by the numerator of the expression \mathbf{A} in (10), namely, $p(y_k | m_{k-1}, \Omega) \hat{p}_{Mix}(\Omega, m_{k-1} | y_{1:k-1})$. Since

$$\begin{aligned} p(y_k | m_{k-1}, \Omega) \hat{p}_{Mix}(\Omega, m_{k-1} | y_{1:k-1}) \\ \approx p(y_k | m_{k-1}, \Omega) p(\Omega, m_{k-1} | y_{1:k-1}) \propto p(\Omega, m_{k-1} | y_{1:k}). \end{aligned} \quad (13)$$

The target density of the k -th step MCMC procedure is the posterior density of (Ω, m_{k-1}) given $y_{1:k}$, where the first approximate equality is due to ((7)). In our previous work [49], $p(y_k | m_{k-1}, \Omega)$ was available in closed form due to a linear measurement model and additive noise variables distributed as Gaussian in both the state space and measurement models. In the present context,

$$p(y_k | m_{k-1}, \Omega) = \int_{m_k} \Psi_{k,\Omega}(y_k | m_k) p(m_k | m_{k-1}, \Omega) dm_k. \quad (14)$$

Subsequently, after the burn-in period B , samples of $\Omega_k^{g^*}$ only are collected for a large value of $g^* \geq B$, whereas the samples of $m_{k-1}^{g^*}$ are discarded. MCMC theory and the marginalization property ensure that $\Omega_k^{g^*}$ is distributed according to the posterior $p(\Omega | y_{1:k})$. Since there are M parallel MCMC chains, M such samples of Ω , namely, $\{\Omega_k^{g^*,j}\}_{j=1}^M$, are collected in this way. Subsequently, pure filtering steps as in given in ((15)) are performed to get the samples of m_k from $p(m_k | y_{1:k}, \Omega)$ for each Ω in the collection $\{\Omega_k^{g^*,j}\}_{j=1}^M$ [48]. Hence, the particle pairs $\{\Omega_k^{g^*,j}, m_k^j\}_{j=1}^M$ constitute M samples from the joint posterior density $p(\Omega, m_k | y_{1:k})$ and can serve as the input for the next $(n+1)$ -st time step of the ASMC Algorithm 1.

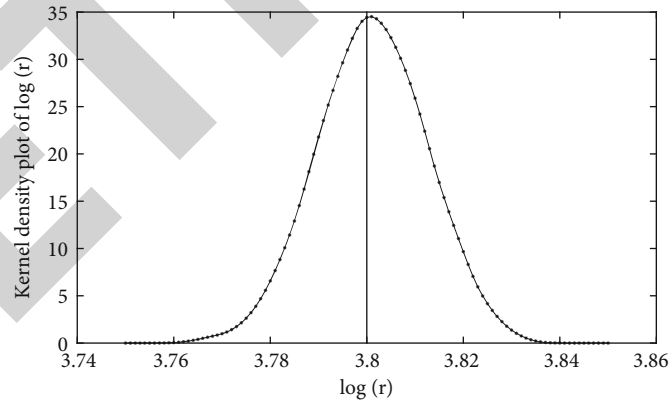
$$w_k^j \propto \frac{p(y_k | m_k^j, \Omega) p(m_k^j | m_{k-1}^j, \Omega)}{q(m_k^j | m_{k-1}^j, y_k, \Omega)} f \text{ or } j = 1, 2, \dots, M. \quad (15)$$

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[{\mathcal{m}_T^j, \Omega_T^j}_{j=1}^M] = \text{ASMC} [\{\mathcal{m}_0^j, \Omega_0^j\}_{j=1}^M]
Initialize with M initial value (\Omega_0^j, m_0^j) prior density
p_0(\Omega, m_0).
Start for k=1:T
    [{\mathcal{m}_k^j, \Omega_k^j}_{j=1}^M] = \text{AMC} [\{\mathcal{m}_{k-1}^j, \Omega_{k-1}^j\}_{j=1}^M, y_k]
    DO: M Parallel MCMC chains initialized from M pairs (\Omega_{k-1}^j, m_{k-1}^j), j = 1, 2, \dots, M.
    For the generic j-th chain:
    Start with (\Omega^0, m^0) \equiv (\Omega_{k-1}^j, m_{k-1}^j) (prior value).
    for k=1:B (burn-in chains)
        Generate samples (\Omega^*, m^*) \sim
        q(\Omega^*, m^* | \Omega^{k-1}, m^{k-1}).
        Compute the acceptance probability
        \alpha_k = \min \{A \cdot B, 1\} as in (9) and (10).
        Set (\Omega^g, m^g) = (\Omega^*, m^*) with
        probability \alpha_k
        Else (\Omega^g, m^g) = (\Omega^{k-1}, m^{(k-1)})
        with probability 1 - \alpha_k
    end for
    Obtain \Omega^B \equiv \Omega_k^j, from j = 1, 2, \dots, M
    chains.
    m_k^j \sim p(m_k^j | y_{1:k}, \Omega_k^j) Samples are based
    (12)
    Mixture fitting \hat{p}_{Mix}(\Omega, m_k | y_{1:k})
    Output: {\Omega_k^j, m_k^j}_{j=1}^M and fitted mixture model \hat{p}_{Mix, n} \equiv \hat{p}_{Mix}(\Omega, m_k | y_{1:k}).
The posterior distribution p(\Omega | y_{1:T}) is based on the collected samples of \Omega_T^j.
end for

```

ALGORITHM 1: Augmented sequential MCMC procedure.

FIGURE 1: The estimated density curves are based on final posterior samples of the parameter $\log(r)$ at the completion of the ASMC.

4. Results and Discussion

In this section, the ASMC methodology is used for parameter inference in the Ricker dynamical system. The y -observations were generated from the time-discretized Ricker's model (state space model given by (5) and the measurement model given by (6)) using the initial point mass prior at $m_0 = 7$. Starting from the initial state values generated from the prior, the state and measurement systems

are updated at every fixed time step of $k = 1, 2, \dots, T = 10$. The true value for Ω is taken as $\Omega = [\log(r), \phi] = [3.8, 0.7]$, which is the same as the choice made in [45]. The burn-in B was set at $B = 5000$. The estimated posterior density curves are obtained based on the final posterior samples of $\Omega = [\log(r), \phi]$ at the completion of the ASMC algorithm. These density curves are given in Figures 1 and 2 for the parameters $\log(r)$ and ϕ , respectively. In Figure 1, estimated density curves based on final posterior samples of

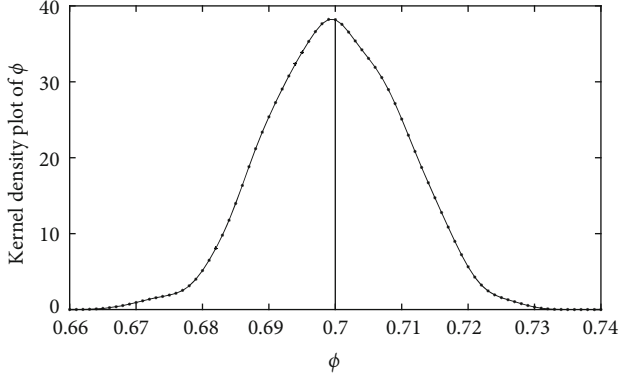


FIGURE 2: The estimated density curves are based on final posterior samples of the parameter ϕ at the completion of the ASMCMC.

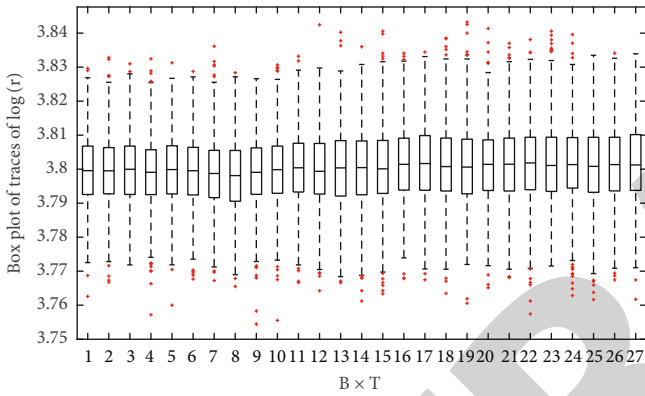


FIGURE 3: Boxplot trajectories representing the distribution of $p(\Omega|y_{1:k})$ based on the ASMCMC algorithm. The boxplots are constructed based on the M final iterates $\log(r)_k^{j,B}$.

TABLE 1: Simulation parameters.

Variable	Value	Description
$\log(r)$	3.8	True value of parameter
ϕ	0.7	True value of parameter
m_0	7	Prior of state variable
B	5000	Burn-in period

the parameter $\log(r)$ at the completion of the ASMCMC are presented. The vertical solid black line represents the true value of the parameter $\log(r) = 3.8$, whereas the estimated density curves based on the final posterior samples of the parameter ϕ at the completion of the ASMCMC are presented in Figure 3. The vertical solid black line represents the true value of the parameter $\phi = 0.7$. We note that the true values of the parameters are well within the support of their respective posterior densities, which gives credence to the parameter inference methodology using the ASMCMC procedure. The following Table 1 represents the simulation parameters considered in the experimental setup.

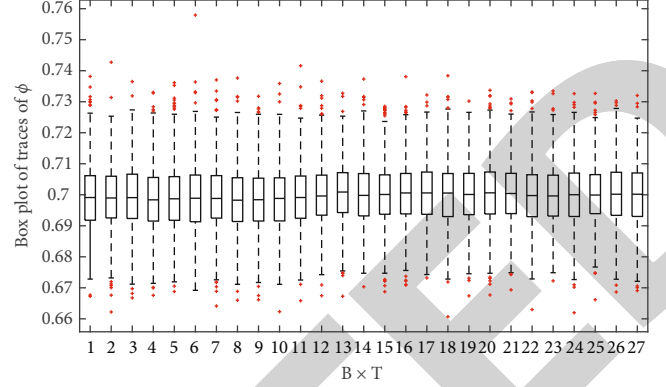


FIGURE 4: Boxplot trajectories representing the distribution of $p(\Omega|y_{1:k})$ based on the ASMCMC algorithm. The boxplots are constructed based on the M final iterates $\phi_k^{j,B}$.

To illustrate the convergence of the ASMCMC procedure, boxplot trajectories represent the distribution of $p(\Omega|y_{1:k})$ for $k = 1, 2, \dots, T$ can be plotted. These boxplots are constructed based on the M final iteration $\Omega_k^{g^*,j}$ for $j = 1, 2, \dots, M$, collected after burn-in. Figure 3 shows that the boxplot trajectories based on posterior samples of $\log(r)$. Figure 3 indicates that these boxplot trajectories have stabilized long before reaching the final time point $T = 10$. In other words, the posterior $p(\log(r)|y_{1:k})$ changes much when k approaches the final time point T , which can be taken as an indication that the estimate of $p(\log(r)|y_{1:k})$ based on the ASMCMC sampler has converged. A similar boxplot trajectory plot (shown in Figure 4) is obtained for ϕ which indicates that the convergence of its posterior distribution has been achieved.

5. Conclusion

The dynamical system based on Ricker's model is an example of a nonlinear and non-Gaussian system that has applications in ecology and epidemiology. We develop the ASMCMC algorithm for the Ricker dynamical system to perform Bayesian parameter inference. We observe that the posteriors encompass the true parameter values used to simulate observations from the Ricker dynamical system. Our future work will be to investigate the performance of the ASMCMC algorithm when σ^2 is unknown as well and for high-dimensional dynamical systems that appear in ecology and epidemiology.

Symbols

m_k :	State variable
y_k :	Observation variable
$\Phi_{k-1,\Omega}(\cdot)$:	State model
$\Psi_{k,\Omega}(\cdot)$:	Measurement model
T :	Final time point
k :	Time variable
u_{k-1} :	State noise

v_k :	Observation noise
Ω :	Unknown parameters
$p(\cdot \cdot)$:	Probability density function
$q(\cdot \cdot)$:	Proposal distribution
$y_{1:k}$:	Observation vector for time point 1 to k
s_k :	Sufficient statistics at k -th time point
w_k^j :	Weights vector at time point k
B :	Burn-in period
$\{\log(r), \phi\}$:	Unknown parameters of Ricker dynamical system
ξ_{k-1}^j :	Augmented particles of unknown state and parameters.

Data Availability

This paper does not require any dataset whereas the simulated data is used using MATLAB tool.

Conflicts of Interest

Authors of this article have no conflict of interest publishing this article in Journal of Sensors.

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