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MONTE CARLO BASED KALMAN FILTERING WITH PROPER WEIGHTING FOR BIOMEDICAL SIGNAL TRACKING APPLICATIONS

Mohammed Ashik[1]*, Ramesh Patnaik Manapuram[2], Praveen B. Choppala[3]

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Abstract

The interest of this paper is in the tracking of rhythmic biomedical signals from electronic sensor systems. The known and noisy biomedical signals and the underlying unknown clinical features like the frequency and phase can be modelled using afirst order hidden Markov state space model. It is known the Bayesian filtering is the most widely used solution for track such models. The Kalman filter is known to be a powerful Bayesian estimator. However, it is limited to linear and Gaussian systems.The particle filter, on the other hand, can be applied to a general class of nonlinear non - Gaussian systems. However, the filter involves high computational complexity due to resampling and the need to guide particles into regions that are important to the posterior probability density. This paper proposes a Monte Carlo based Kalman filter, which is a mixed implementation of the Kalman filter and the particle filter, to effectively track biomedical signals. The simulation results show that the proposed methodis superior both in terms of speed and tracking accuracy than the conventional methods.

Index Terms: Kalman filter, particle filter, resampling, Monte Carlo, biomedical signals, normalised root mean square error, computational time.

[1*,2]Dept. of Instrument Technology, Andhra University, [1]Email: ashikmd909@gmail.com,
[2]Email: ramesh patnaik@yahoo.com
[3]Dept. of E.C.E., WISTM, Andhra University, Email: praveen@wistm.edu.in

***Corresponding Author:** Mohammed Ashik
*Dept. of Instrument Technology, Andhra University, Email: ashikmd909@gmail.com,

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I. INTRODUCTION

Most clinical features of a human body, like the heartbeat and blood pressure, are rhythmic or sinusoidal in nature and hence can be characterized by parameters like the frequency, phase and amplitude. Electronic sensor systems produce a time varying rhythmic biomedical signal by which is a direct but noisy reflection of the said clinical features. A change in these clinical parameters causes a change in the biomedical signal recording over time. The extraction of these time varying clinical parameters from the rhythmic biomedical signals is critical in biomedical diagnosis and prognosis [1]–[3].

The interest of this paper is the estimation of the unknown underlying clinical quantities, generally called the target state, using known noisy rhythmic biomedical signals. Most scientific systems such as the biomedical signal estimation system can be described using a state space model that includes (a) a state transition model that governs how the state unknown target state evolves over time and (b) a measurement model that governs how a noisy measurement is observed from the state. The Bayes' filter is known to be the solution for scientific applications that require recursive estimation (or tracking) of a hidden time varying target state using noisy sensor measurements [4]. This is because sequential Bayesian estimation provides a rigorous platform to construct a probability (belief) density function (pdf) of the target state using the noisy observations from which the target state can be estimated.

A prominent Bayesian tracking algorithm for linear Gaussian state space models is the Kalman filter [5]. The filter provides an optimal Bayesian solution for state space models characterised by linear dynamics and additive Gaussian noise. This is because the first and second moments (mean and covariance) of the posterior pdf can be analytically computed for linear Gaussian systems. However biomedical signal models are nonlinear (rhythmic or sinusoidal) in nature and hence the Kalman filter cannot be straightforwardly applied. A popular Bayesian solution for nonlinear and non-Gaussian systems is the particle filter (PF) [6], [7]. The PF performs Monte Carlo approximation of the posterior pdf using a set of weighted particles. These particles span and explore the target state space using the target dynamics and weighted using the measurement density. The states of the particles and their corresponding weights aids in making a probabilistic inference of the true target state.

It is known that if the particles are indeed located in regions of importance, that is in the region of the pdf with high density value, then the Monte Carlo estimate would be accurate. However, the particles drawn from the state transition model leverage only the target dynamics but not on the incoming observation. Hence it is not guaranteed that the drawn particles will lie in regions of importance. This eventually results in the degeneracy problem [8]. This problem is overcome by resampling the particles and their weights in a way that eliminates particles having low weights, i.e., those that do not lie in regions of importance and replace them by copies of others having higher weights [8], [9].

The popularly used stochastic resampling approach operates by first evaluating the cumulative sum of the normalised particle weights and then finding a value of the sum greater than a random sample drawn from U(0,1) [6]. Sampling from the full interval (0,1) leads to large Monte Carlo error variance. This problem was overcome in the stratified [10], the residual [11] and the systematic [7] resamplers. However, resampling is a computationally intensive procedure that involves intensive communication overhead within the particles. Several methods have been proposed to alleviate the complexity with regard to hardware realization in [12]–[15]. However, these methods are algorithmically still computation intensive.

Resampling aids in guiding particles into regions of importance but comes with additional computational complexity. As an alternative, several methods have been proposed to leverage the incoming observation particle sampling process so that they draw from regions of importance. This reduces the effect of degeneracy and consequently permits the use of fewer particles. The most popular in this class is the auxiliary particle filter (APF) [16] and the improved APF (IAPF) [17], [18]. The filters draw a set of particles that lookahead to the next time step and computes their weights, then resamples the resultant and uses those resampling indices to propagate the particles at the current time step to the next time step. This causes only those particles that could probably lie in regions of importance to be propagated. Other lookahead strategies include adapted placement and others [19]–[22]. These methods however work well when the state transition noise and the measurement noise are low. Moreover, they still employ the computationally intensive resampling process.

An alternate to resampling are the class of Gaussian filters. The Gaussian particle filter (GPF) [23] and

the approximate Kalman filter (AKF) [24]. These filters approximate the posterior with a Gaussian pdf and propagates the samples using the mean and covariance estimates. Hence, they are free from resampling and are extremely fast. The recently proposed resampling free PF [25], [26] accelerated the PF operation substantially by virtue of deterministically selecting particles beyond a certain weight to replace the small weight ones. Similar methods, called the partial deterministic resampling PFs can be found in [27], [28]. However, these methods do not scale well with increasing noise and some also suffer from estimation bias.

This paper proposes Monte Carlo approximated Kalman filtering approach for tracking rhythmic nonlinear biomedical signals. The state space model for this application involves a linear Gaussian state transition model and a highly nonlinear observation model. Hence the Kalman filter cannot be directly employed. The PFs have been successfully employed in the literature but all of them suffer from the aforementioned problems. Our proposal is as follows: we use the Kalman filter-based moment generation scheme to determine the prediction. We then draw Monte Carlo samples from the state transition density and weigh them according to the measurement density and then compute those samples that contribute to the posterior using the "proper weighting" condition [8]. This condition mitigates any bias caused due to inaccurate sampling. The samples that contribute to the posterior and their corresponding weights are then used to compute the final first and second moments. These moments are recursively used in the next state. The first rationale for this proposition is that since we do not employ PF in its traditional form, we do not require resampling and consequently we do not suffer from computational complexity. The second rationale is that since we use the proper weighting condition to determine those particles that are critical for estimation, we overcome estimation bias, if any, and also track accurately in high noise conditions.

The rest of the paper is organized as follows. In section II we set the notation and introduce the state space model suitable for tracking rhythmic biomedical signals. Section III briefly describes Bayesian filtering and proposes the Monte Carlo based Kalman filter for a biomedical signal state space model. This is followed by evaluation results in section IV. We then conclude in section V.

II. THE RHYTHMIC BIOMEDICAL SIGNAL STATE SPACE MODEL

In this section, we present the rhythmic biomedical signal state space model that is of specific interest to this paper. The state space model is challenging problem of tracking multiple harmonics in periodic rhythmical signals [29]. These signals are a model of the biomedical signals including the ECG and pulse variation signals. The measurement model of (15) for this example is formulated as

$$\mathbf{y}(t) = h(\mathbf{x}_t) + \mathbf{e}_t \tag{1}$$

$$= \underbrace{\bar{y}_t \sum_{k=1}^{N_h} \left(a_{k,t}\cos(k\theta_t) + a_{k,t}\cos(k\theta_t) \right)}_{h(\mathbf{x}_t)} + \mathbf{e}_t \tag{2}$$

where N_h is the known number of harmonics (N_h = 5 in this paper), θ_t is the instantaneous phase of the fundamental frequency, $\bar{y}_t$ is the signal mean, $a_{k,t}$ and $b_{k,t}$ are the sinusoidal coefficients and $e_t \sim$ N(0,σ^2 = 5) is the additive white measurement noise variable. The state variables that transit over time are defined as

$$\theta_t = \theta_{t-1} + 2\pi t_s f_t + u_{\theta,t} \tag{3}$$

$$\bar{f}_t = g[\bar{f}_{t-1} + u_{\bar{f},t}] \tag{4}$$

$$f_t = \bar{f}_{t-1} + \alpha(f_{t-1} - \bar{f}_{t-1}) + u_{f,t} \tag{5}$$

$$a_{k,t} = a_{k,t-1} + u_{a_k,t}, k = 1, \cdots, N_h \tag{6}$$

$$b_{k,t} = b_{k,t-1} + u_{b_k,t}, k = 1, \cdots, N_h \tag{7}$$

$$\bar{y}_t = \bar{y}_{t-1} + u_{\bar{y},t} \tag{8}$$

for t = 1,$\cdots$,T where f_t is the fundamental frequency, $\bar{f}_t$ is the mean fundamental frequency, t_s = 1/f_s is the sampling interval, α = 0.99 is the auto-regressive coefficient assumed to be known and the Markov state transition noise variables are $u_{\theta,t} \sim$ N(0,10^{-4}), $u_{f,t} \sim$ N(0,10^{-4}), $u_{\bar{f},t} \sim$ N(0,10^{-6}), u_{ak},$t \sim$ N(0,10^{-6}), u_{bk},$t \sim$ N(0,10^{-6}) and $u_{y,t} \sim$ N(0,10^{-4}). The mean frequency is assumed to follow a nonlinear reflecting function

$$g[f] = \begin{cases} f_{\max} - (f - f_{\max}), & \text{if } f_{\max} \le f, \\ f, & \text{if } f_{\min} \le f \le f_{\max}, \\ f_{\min} + (f_{\min} - f), & \text{if } f \le f_{\min} \end{cases} \tag{9}$$

The state space is now $4 + 2N_h = 14$ dimensional and the state vector is

$$\mathbf{x}_t = (\theta_t, f_t, \bar{f}_t, \bar{y}_t, a_{1,t}, a_{2,t}, \cdots, a_{N_h,t}, b_{1,t}, b_{2,t}, \cdots, b_{N_h,t})^\top \quad (10)$$

The reader is referred to [29], [30] for more detailed description of the model. The state transition model of (14) can be formulated as

$$\mathbf{x}_t = \mathbf{F}\mathbf{x}_{t-1} + \mathbf{a}_t \quad (11)$$

$$\begin{pmatrix} \theta_t \\ f_t \\ \bar{f}_t \\ \bar{y}_t \\ a_{1,t} \\ a_{2,t} \\ a_{3,t} \\ a_{4,t} \\ a_{5,t} \\ b_{1,t} \\ b_{2,t} \\ b_{3,t} \\ b_{4,t} \\ b_{5,t} \end{pmatrix} = \begin{pmatrix} 1 & 2\pi t_s & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \alpha & 1-\alpha & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix} \begin{pmatrix} \theta_{t-1} \\ f_{t-1} \\ \bar{f}_{t-1} \\ \bar{y}_{t-1} \\ a_{1,t-1} \\ a_{2,t-1} \\ a_{3,t-1} \\ a_{4,t-1} \\ a_{5,t-1} \\ b_{1,t-1} \\ b_{2,t-1} \\ b_{3,t-1} \\ b_{4,t-1} \\ b_{5,t-1} \end{pmatrix} + \mathbf{a}_t \quad (12)$$

where the state transition noise variable $\mathbf{a}_t \sim \mathrm{N}(0, \mathbf{Q})$ with

$$\mathbf{Q} = \mathrm{diag}\left[10^{-4}, 10^{-4}, 10^{-6}, 10^{-4}, \underbrace{10^{-6}, \cdots, 10^{-6}}_{2N_h \text{ times}}\right] \quad (13)$$

The aim of the filter, in the context of this rhythmic biomedical signal model, is to track the clinical features like the frequency and the phase and the harmonics of the signal contained in $\mathbf{x}_t$ using the recorded measurement $\mathbf{y}_t$ for $t = 1, \cdots, T$.

III. BAYESIAN FILTERING FOR TRACKING BIOMEDICAL SIGNALS

In this section, we briefly describe Bayesian filtering and then present our proposal for fast and accurate tracking of biomedical signals.

A. Bayesian filtering

Consider a state space model defined by a Markov state transition and observation models as defined in (11) and (1) as

$$\mathbf{x}_t = \mathbf{F}\mathbf{x}_{t-1}, \mathbf{a}_t \quad (14)$$

$$\mathbf{y}_t = h(\mathbf{x}_t) + \mathbf{e}_t \quad (15)$$

for $t = 1, \cdots, T$, where $\mathbf{x}_t$ is the real-valued hidden target state at time instant $t \in \mathrm{N}$ and $\mathbf{F}$ is the state transition matrix that translates the state from time $t-1$ to t. The target dynamics are modelled as a first order hidden Markov process governed by the state transition pdf $p(\mathbf{x}_t|\mathbf{x}_{t-1})$. The sensor observation $\mathbf{y}_t$ is conditionally independent of previous observations given the state at time t and follows the observation density is $p(\mathbf{y}_t|\mathbf{x}_t)$. The function $h(.)$ is a nonlinear function that translates the target from the state space to the observation space. The random variables $\mathbf{a}_t \sim \mathrm{N}(0,\mathbf{Q})$ and $\mathbf{e}_t \sim \mathrm{N}(0,\sigma^2 I)$ are noise variables where the former corresponds to the disturbance in the state heading and the latter to the measurement noise.

Target filtering is achieved by estimating the state of a target $\mathbf{x}_t$ using the noisy sensor data $\mathbf{y}_{1:t} = \{\mathbf{y}_1, \cdots, \mathbf{y}_t\}$. The recursive Bayes' filter accomplishes by

constructing the posterior pdf $p(\mathbf{x}_t|\mathbf{y}_{1:t})$ for $t = 1,\cdots,T$. If the posterior at time $t-1$ is known to be $p(\mathbf{x}_{t-1}|\mathbf{y}_{1:t-1})$, then the filter first computes a prediction pdf according to

$$p(\mathbf{x}_t|\mathbf{y}_{1:t-1}) = \int p(\mathbf{x}_t|\mathbf{x}_{t-1})p(\mathbf{x}_{t-1}|\mathbf{y}_{1:t-1})\mathbf{x}_{t-1} \quad (16)$$

and then updates the posterior to time t using the incoming observation $\mathbf{y}_t$ according to

$$p(\mathbf{x}_t|\mathbf{y}_{1:t}) \propto p(\mathbf{y}_t|\mathbf{x}_t)p(\mathbf{x}_t|\mathbf{y}_{1:t-1}) \quad (17)$$

This recursion, described as

$$\cdots \longrightarrow p(\mathbf{x}_{t-1}|\mathbf{y}_{1:t-1}) \longrightarrow p(\mathbf{x}_t|\mathbf{y}_{1:t-1}) \longrightarrow p(\mathbf{x}_t|\mathbf{y}_{1:t}) \longrightarrow \cdots \quad (18)$$

forms the basis for the Bayes' filter.

The Kalman filter assumes the densities governing the state space model are Gaussian. Hence it propagates the first and second moments (mean and covariance) of the pdf. The Bayes' recursion in (18) will be

$$\cdots \longrightarrow \mathcal{N}(\mathrm{E}(\mathbf{x}_{t-1}|\mathbf{y}_{1:t-1}), \mathrm{Var}(\mathbf{x}_{t-1}|\mathbf{y}_{1:t-1})) \longrightarrow \mathcal{N}(\mathrm{E}(\mathbf{x}_t|\mathbf{y}_{1:t-1}), \mathrm{Var}(\mathbf{x}_t|\mathbf{y}_{1:t-1})) \longrightarrow \mathcal{N}(\mathrm{E}(\mathbf{x}_t|\mathbf{y}_{1:t}), \mathrm{Var}(\mathbf{x}_t|\mathbf{y}_{1:t})) \longrightarrow \cdots \quad (19)$$

where E(.) denotes the expectation operator and Var(.) denotes the covariance operator and the filter provides analytic expressions for the computation of these moments.

B. Our proposed method

We now propose the resampling-free Monte Carlo based Kalman filter. Let the state space model be defined by (14) and (15). If the posterior at time $t-1$ approximated by a Gaussian pdf using the first and second moment as

$$p(\mathbf{x}_{t-1}|\mathbf{y}_{1:t-1}) \approx \mathcal{N}(\mathrm{E}(\mathbf{x}_{t-1}|\mathbf{y}_{1:t-1}), \mathrm{Var}(\mathbf{x}_{t-1}|\mathbf{y}_{1:t-1})) \quad (20)$$

is known, then the predicted pdf is

$$p(\mathbf{x}_t|\mathbf{y}_{1:t-1}) \approx \mathcal{N}(\mathrm{E}(\mathbf{x}_t|\mathbf{y}_{1:t-1}), \mathrm{Var}(\mathbf{x}_t|\mathbf{y}_{1:t-1})) \quad (21)$$

where for the given state space model, the predicted mean is

$$\mathrm{E}(\mathbf{x}_t|\mathbf{y}_{1:t-1}) = \mathbf{F}\mathbf{x}_t \quad (22)$$

and the predicted covariance is

$$\mathrm{Var}(\mathbf{x}_t|\mathbf{y}_{1:t-1}) = \mathbf{F}\mathrm{Var}(\mathbf{x}_{t-1}|\mathbf{y}_{1:t-1})\mathbf{F}^\top + \mathbf{Q} \quad (23)$$

To move from $t-1$ to t, if $\mathrm{E}(\mathbf{x}_{t-1}|\mathbf{y}_{1:t-1})$ and $\mathrm{Var}(\mathbf{x}_{t-1}|\mathbf{y}_{1:t-1})$ are known, we predict the first and second moments according to (22) and (23). This is the same as the Kalman filter prediction step. However, the Kalman filter cannot be implemented further as the observation model is highly nonlinear. Hence, we resort to a Monte Carlo approximation by drawing particles from the predicted density according to

$$\{\bar{\mathbf{x}}_t^i\}_{i=1}^N \sim \mathcal{N}(\mathrm{E}(\mathbf{x}_t|\mathbf{y}_{1:t-1}), \mathrm{Var}(\mathbf{x}_t|\mathbf{y}_{1:t-1})) \quad (24)$$

These particles are then weighted using the observation density as

$$\bar{w}_t^i = \left(p(\mathbf{y}_t|\mathbf{x}_t^i)\right)^\lambda, i = 1,\cdots,N \quad (25)$$

The particles and the corresponding weights are then sorted in the descending order of weights and scaled according to

$$\bar{w}_t^i = \exp(-\lambda(i))\bar{w}_t^i, i = 1,\cdots,N \quad (26)$$

and normalised. The parameter λ controls the importance on the weights determines. $\lambda \in (0,1)$ and a high value gives very high weighting to the high weight particles and a low value do not change the weights. In this paper we chose $\lambda = 0.03$ so a minor proportion of the high weight particles are give very large weighting. This aids in tracking the mode of the posterior more accurately.

At this stage, the particles and their corresponding weights are representative of the posterior at time t as shown in (21). The GPF and the AKF uses this set to compute the weighted mean and covariance. However, this is not valid as the prediction did not

take into account the incoming measurement $\mathbf{y}_t$. Not accounting $\mathbf{y}_t$ could lead to the particles drawn from the prediction density to be located in regions of unimportance. This could lead to estimation bias. A straightforward solution to this is to resample the particles $\{\bar{\mathbf{x}}_t^i, \bar{w}_t^i\}_{i=1}^N \longrightarrow \{\mathbf{x}_t^i, w_t^i\}_{i=1}^N$ as described in the earlier section. However, this step adds to the computational complexity. This paper proposes to bypass this problem by using the "proper weighting" condition used as a measure for unbiased estimation by resampling [8].

The proper weighting condition can be explained as follows. Resampling aims to replace the low weight particles by those with high weights in such a way that every resampled particle is equally probable in representing the posterior pdf. This condition causes each resampling particle to have equal weight, meaning $w_t^i = 1/N, i = 1, \cdots, N$. This condition can be achieved when the number of times each particle is replicated follows a condition described as

$$n_t^i = N\bar{w}_t^i, i = 1, \cdots, N \tag{27}$$

and called the proper weighting condition, where n^i_t is the number of replications of the ith particle.
In this paper, we compute n^i_t using (27) rounded to the lower integer and obtain a new set of particles

$$\{\bar{\mathbf{x}}_t^i, \bar{w}_t^i\}_{i=1}^N \longrightarrow \{\mathbf{x}_t^i, w_t^i\}_{i=1}^{M \leq N}, \ \forall i : n_t^i > 0 \tag{28}$$

The new set contains only those particles for which $n^i_t > 0$ meaning that all the particles that are guaranteed to contribute to the posterior by the proper weighting condition are gathered into the new set. Hence the new set could contain fewer than N weighted particles. Then the first and second moments of the posterior can be approximated as

$$p(\mathbf{x}_t|\mathbf{y}_{1:t}) \approx \mathcal{N}(\mathrm{E}(\mathbf{x}_t|\mathbf{y}_{1:t}), \mathrm{Var}(\mathbf{x}_t|\mathbf{y}_{1:t})) \tag{29}$$

$$\mathrm{E}(\mathbf{x}_t|\mathbf{y}_{1:t}) = \sum_{i=1}^{M} w_t^i \mathbf{x}_t^i \tag{30}$$

$$\mathrm{Var}(\mathbf{x}_t|\mathbf{y}_{1:t}) = \sum_{i=1}^{M} w_t^i (\mathbf{x}_t^i - \mathrm{E}(\mathbf{x}_t|\mathbf{y}_{1:t}))(\mathbf{x}_t^i - \mathrm{E}(\mathbf{x}_t|\mathbf{y}_{1:t}))^\top \tag{31}$$

These moments form the basis for the next time step. The filter estimate is the mean of the posterior $\hat{\mathbf{x}}_t = \mathrm{E}(p(\mathbf{x}_t|\mathbf{y}_{1:t})) \approx \mathrm{E}(\mathbf{x}t|\mathbf{y}1{:}t)$.

The key merits of this proposed method are that it does not involve the computationally demanding resampling procedure. Moreover, it ensures particles are guided into regions that contribute to the posterior pdf and hence can show high tracking accuracy with fewer particles.

IV. EVALUATION

In this section, we present the evaluation of the proposed Monte Carlo approximated Kalman filter for tracking rhythmic biomedical signals. We compare the proposal with the standard PF (SPF) [7] that employs systematic resampling to push particles into regions of importance, the APF [16], the GPF [23] which uses an altogether different approach that does not necessarily account for drawing particles from importance regions and the OLPF [25], [26] that samples particles from regions of importance.

In the program preliminaries, we set the number of harmonics to $N_h = 5$, the sampling frequency and the frequency limits to $f_s = 360$, $f_{\max} = 1$, $f_{\min} = 5$ Hertz, and the noise variance to $\sigma^2 = 5$. The initial state values of the ground truth are set

to $\theta_{t=0}^{true} = 0$ and $f_{t=0}^{true} = 2, \bar{f}_{t=0}^{true} = 1.5$ Hertz, $\bar{y}_{t=0}^{true} = 10$, $a_{k,t=0}^{true} \sim \mathcal{U}(2,5)$ and $b_{k,t=0}^{true} \sim \mathcal{U}(3,7)$. The filters are initialised with $\theta^i_{t=0} \sim$ N(0,1) and $f^i_{t=0} \sim \mathcal{U}(f_{min}, f_{max}), \bar{f}^i_{t=0} \sim \mathcal{U}(0,2), \bar{y}^i_{t=0} \sim \mathcal{N}(0,1), a^i_{k,t=0} \sim \mathcal{U}(2,5)$ and $b^i_{k,t=0}$ PU(3,7) for

$i = 1, \cdots, N$. For the chosen $f_s = 360$ Hertz, we record a signal with $t = 1200$-time samples meaning that the duration of

N	OLPF	PF	APF	GPF	Proposed
25	0.93823	0.95500	0.92823	0.00000	0.91987
100	0.978618	0.937231	0.890965	0.010302	0.947978
500	0.9766519	0.9456768	0.9093298	0.0020869	0.9447219
1000	0.97902848	0.94670209	0.87678726	0.00031074	0.94335478

Table I: The table shows the normalised expectation $E(ESS)/N$ for the five methods for N = 25,100,500,1000 particles.

the signal is close to 3.33 seconds.

The two performance measures used to evaluate the efficacy of the methods are the root mean squared error (RMSE) and the normalised mean squared error (NMSE) defined by

$$XRMSE = \sqrt{\frac{\sum_{t=1}^{T} X_t^{true} - \hat{X}_t}{T}},\ X = (f_t, \bar{f}_t, \theta_t, \bar{y}_y) \tag{32}$$

$$XRMSE = 1/N_h \sum_{k=1}^{Nh} \sqrt{\frac{\sum_{t=1}^{T} X_{k,t}^{true} - \hat{X}_{k,t}}{T}},\ X = (a_{k,t}, b_{k,t}) \tag{33}$$

$$NMSE = \frac{\sum_{t=1}^{T} (y_t - \hat{y}_t).^2}{(y_t - \hat{\bar{y}}_t).^2} \tag{34}$$

where$\hat{}$. is the estimated value. The RMSE corresponding to the latent variables is a well-known measure. The NMSE, on the other hand, lies in (0, ∞) and a value of less than one indicates good harmonic tracking [29] implying that the latent target state containing the harmonic frequencies, the sinusoidal coefficients and the signal mean Are tracked accurately to such an extent that the estimate of the measurement agrees with the received.

Firstly, we evaluate the degeneracy effect in the proposed filter for small to large values of *N*. Table I shows the normalised mean value of *ESS/N* which is a measure to evaluate the effect of degeneracy within the filter. Since the expected ESS is normalised by the number of particles *N*, *E*(*ESS*)*/N* lies in (0,1) and a value of one indicates no degeneracy while a zero indicates high degeneracy. The computation-friendly GPF considers only the weighted sum of the particles regardless of their contribution to the posterior and hence does not ensure that the ESS is maintained. Therefore, it can be observed in the table that the GPF maintains low ESS throughout. This also causes the filter to be biased and also perform poorly in high noise conditions. The SPF and the APF naturally do not suffer from degeneracy as they resample the particles all the time. It can be observed that for all cases of *N*, the proposed resampling-free method exhibits high value indicating it does not suffer from degeneracy because it estimates the state using the proper weighting condition, i.e., by way of using only those particles that contribute to the posterior pdf.

Secondly, we focus on the tracking accuracy and the computational time. The state vector for the biomedical signal model is 14-dimensional as described in (10). We compute the RMSE for each of these states according to (32) and (33) and these values

Measure	*N*	OLPF	SPF	APF	GPF	Proposed
θRMSE	25	6.95351	2.37419	3.23042	-	3.49137
	100	4.95351	4.84749	4.22747	3.27195	0.00244
	500	0.01429	0.00190	0.00190	37.93506	0.00099
	1000	0.00213	0.00111	0.00109	3.50038	0.00094
*f*RMSE	25	0.36659	0.04805	0.04575	-	0.19244
	100	0.05031	0.12741	0.11225	0.16395	0.04612
	500	0.05770	0.01369	0.01370	0.23903	0.01292
	1000	0.01315	0.00810	0.00803	0.05420	0.01148
$\bar{f}$RMSE	25	0.11038	0.02108	0.02746	-	0.18698
	100	0.05220	0.13371	0.12178	0.03393	0.02461
	500	0.03576	0.05242	0.05645	0.17490	0.01534
	1000	0.03849	0.01192	0.01149	0.02139	0.01519

$\bar{y}$RMSE	25	1.65594	0.03743	0.02677	-	0.47068
	100	0.12126	0.04089	0.03914	0.06075	0.07697
	500	0.06025	0.01413	0.01705	0.05245	0.01990
	1000	0.05114	0.00967	0.00959	0.01202	0.01439
*a*RMSE	25	2.47677	0.04875	0.04887	-	0.05669
	100	0.23981	0.04798	0.04901	0.04921	0.04867
	500	0.12033	0.04829	0.04782	0.04948	0.04774
	1000	0.07840	0.04666	0.04733	0.01064	0.04762
*b*RMSE	25	1.98040	0.05204	0.05384	-	0.05840
	100	0.22809	0.05325	0.05265	0.05341	0.05313
	500	0.06955	0.05349	0.05327	0.05329	0.05249
	1000	0.10234	0.05222	0.05179	0.01117	0.05173

Table II: The table shows RMSE corresponding to the latent variables for the four methods under test for N = 25,100,500,1000 particles. The reader may replace X in *XRMSE* with the latent variable, e.g., θRMSE denotes the RMSE of the instantaneous phase estimate $\hat{\theta}_{1:T}$.

are shown in Table II. At N = 25, the GPF suffers from a large estimation bias caused due to insufficient particles that may not necessarily lie in regions that contribute to the posterior pdf. Hence its values are not shown. It can be observed that the OLPF

shows moderately higher errors in the estimation of the signal mean $\bar{y}_{1:T}$ and the sinusoidal coefficients $a_{1:Nh,1:T}$ and $b_{1:Nh,1:T}$ over the conventional methods. A possible reason for this is that the low weight particles in this filter are eliminated with unit probability. This problem is overcome in the proposed filter as it ensures that only those particles that contribute to the posterior, determined by using the proper weighting condition, are leveraged into the estimation process. The table also shows that the error reduces with increasing number of particles and all methods become stable with reliable tracking accuracy from N = 500.

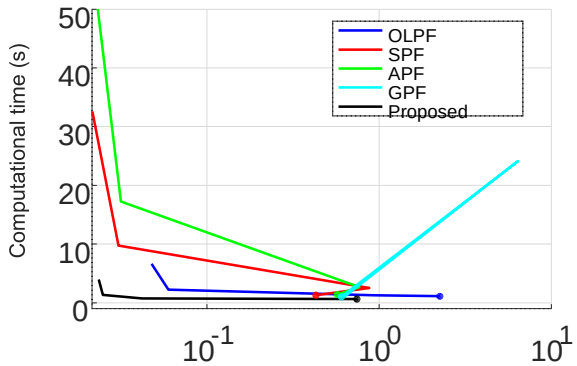
The computational time (in seconds) versus the average RMSE (ARMSE) (average of all the errors) is shown in Figure 1. It can be clearly observed that the proposed method exhibits lower ARMSE and consumes lesser computation over the conventional methods at both lower and higher values of N. This is because the Kalman based Monte Carlo prediction step inhibits particles from being drawn from regions on non-importance and the proper weighting condition applied on the drawn particles further mitigates any estimation error. Moreover, the method totally avoids the need to resample as only the first and second moments are propagated in time and hence gains tremendously in terms of computational speed.

A measure of the combined effect of tracking accuracy and the computational time is the time scaled RMSE (TRMSE) defined by

$$TRMSE = T_c \times RMSE \tag{35}$$

where T_c is the computational time in seconds. A low value of TRMSE is desired as both the computational time and the tracking error is desired to be small. Figure 1 also shows the TRMSE versus the number of particles and it can be observed that the proposed method shows an incredible improvement of 81.7%, 97.4%, 75.1% and 70.5% over the OLPF, 59.7%, 97.2%, 89.0% and 86.8% over the SPF and 57.4%, 98.0%, 99.5% and 92.5% over the APF for N = 25,100,500,1000 respectively.

The GPF totally fails due to high estimation error due to bias caused in propagating particles using the moments.



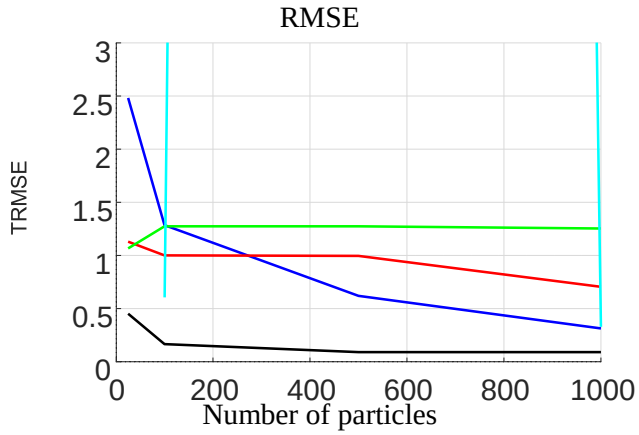


Fig. 1. The top panel shows the computational time (seconds) versus the RMSE for N =25,100,500,1000 particles. The x-axis is shown in log scale for convenience. The values at N =25 is shown using solid dot. The bottom panel shows the TRMSE versus the number of particles. The legend of the top panel applies to the bottom also.

We finally show the NMSE versus the number of particles. The NMSE is a measure of how accurately the estimated latent target states could recover the observed signal. Figure 2 shows the NMSE for varying numbers of particles. It can be observed that except for the GPF, all the other methods achieve an NMSE of less than one, indicating that the signal has been recovered well. Figure 3 shows the measured signal and the estimated signal. The estimated signal is formed by plugging in the estimated target states into (2) without the noise variable. The GPF is not shown as the earlier results have shown the filter to totally diverge until N = 500. It can be observed from the figure that the proposed method recovers the measured signal accurately even with fewer numbers of particles.

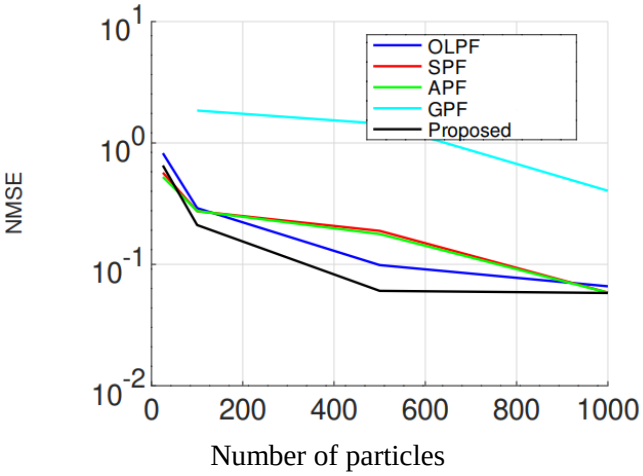
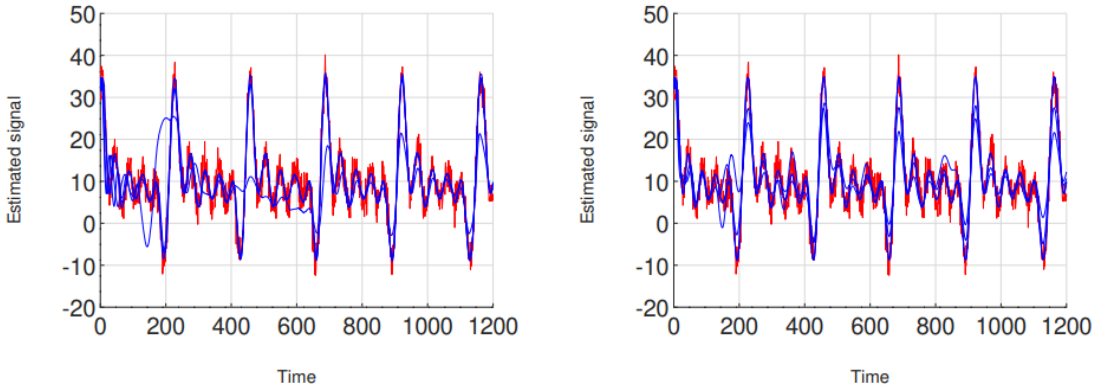


Fig. 2. The NMSE versus the number of particles.



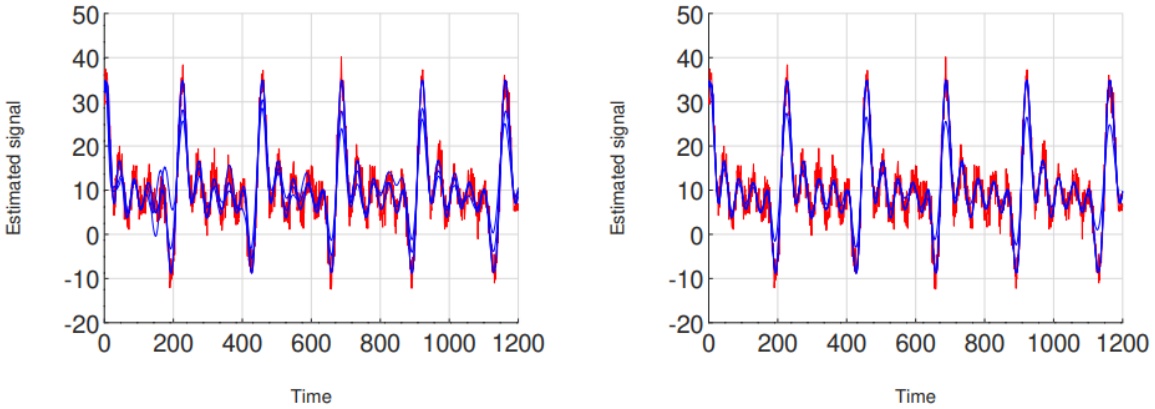


Fig. 3. The estimated and received signal versus the time step. The received signal is shown in red and the estimated (for different values of *N*) in blue. The top left panel corresponds to the OLPF, the top right to the SPF, the bottom left to the APF and the bottom right to the proposed filter.

V. CONCLUSION

This paper proposed a Kalman filtering approach using mixed Monte Carlo implementation for tracking rhythmic biomedical signals. The evaluation results have shown that the proposed filter achieves higher tracking accuracy and speed than the conventionally used PFs as it computes the filter estimate using the proper weighting condition and also totally avoids the need to resample particles. Moreover, the filter propagates the first and second moments instead of the particles hence overcomes the problem of degeneracy as do the PF.

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