

Observation Leveraged Resampling-Free Particle Filter for Tracking of Rhythmic Biomedical Signals

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Abstract: The particle filter is known to be a powerful tool to recursively estimate a hidden target state process using noisy observations from electronic sensor systems. The filter employs a set of particles that explore the state space using the Monte Carlo simulation of the target dynamics and then weighs them using the incoming observation. The congregation of the particles lead to probabilistic estimation of the true target state. However, the filter is effective only when the particles are drawn from regions of importance, i.e., the regions that contribute to the posterior probability density function. The traditional particle filter is known to suffer degeneracy as the target dynamics do not necessarily push the particles into regions of importance. This degeneracy problem can be overcome by either using a large number of particles or leveraging the incoming observation into the Monte Carlo sampling process. Since both solutions are not feasible, an additional resampling step was introduced to kill those particles that do not contribute to the posterior and replace them by copies of others that do. Furthermore, the recently proposed auxiliary particle filter and its variants improved upon the particle filter by mimicking the use of the incoming observation in the sampling process. However, the challenge of leveraging the incoming observation in the sampling process still remains a challenge. Moreover, these conventional filters still employ resampling which is a computationally expensive procedure. This paper proposes a novel particle filtering approach that takes into account the incoming observation into the sampling process without having to use resampling. This allows the particles to effectively explore the regions of importance and consequently result in fast and accurate filtering. The developed method is employed in tracking rhythmic biomedical signals and its accuracy and computational complexity are evaluated.

Index Terms: Particle filtering, resampling, biomedical signals, electrocardiogram, root mean square error, computational time

1. Introduction

Biomedical signals like the electrocardiogram (ECG) and the arterial blood pressure (BP) are rhythmic in nature. The underlying clinical parameters like the instantaneous frequency, pulse variation, etc. that cause these biomedical signals change gradually with time and extraction of these parameters is critical in biomedical diagnosis and prognosis [1], [2]. Since the biomedical signals can be characterized as a nonlinear time series function, it is appropriate to use Bayesian inference methods to track the harmonics of the signal [3], [4]. The most popular nonlinear non-Gaussian Bayesian inference filter is the particle filter (PF) [5], [6].

The PF performs Monte Carlo approximation of the posterior probability density function (pdf) using a set of weighted particles.

These particles span and explore the target state space using the target dynamics. The states of the particles and their corresponding weights aids in making a

probabilistic inference of the true target state. The critical step in the PF is the sequential importance sampling (SIS) that specifies the process of sampling new particles at each time index using target dynamics and updating their weights using the incoming observation. 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, since the particles drawn from SIS do not leverage on the incoming observation but only the target dynamics, SIS by itself, does not guarantee that the particles lie in regions of importance. This eventually results in one particle grabbing all the weight, termed degeneracy problem. This problem is overcome using two solutions. The first is to use a large number of particles. This solution is infeasible as the number of particles required increases exponentially with the target state space. The second solution is to include an additional step called resampling 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 [7], [8]. However, resampling is a computationally intensive procedure that involves intensive communication overhead within the particles.

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The stochastic resamplers are the most conventionally used ones in PFs. One of the first resampling methods, the multinomial selection [5], operates by first evaluating the cumulative sum of the normalized particle weights and then finding a value of the sum greater than a random sample drawn from $U(0, 1)$. Sampling from the full interval $(0, 1)$ leads to large MonteCarlo error variance. This problem was overcome in the stratified [9] and systematic [6] resamplers that divide the interval $(0, 1)$ into strata and draw one sample per particle from each stratum. The residual resampler [10] improved upon these by duplicating the particles stochastically using principle of proportional allocation. The stochastic resamplers are known to be theoretically accurate as they give an unbiased representation of the posterior pdf. That being said, leveraging the resampling on random samples involves sequential search and extensive communication overhead within all the particles. This leads to enormous computational complexity and hence impedes the use of more particles for accurate estimation and leads to difficulty in hardware realization [11]. Another class of resamplers developed to suit for parallel implementation include the recently proposed Metropolis resampler [12] and others [13], [14]. These aid in nearly-parallel PF implementation by reducing the communication within the particles. However, these resamplers are still algorithmically computation intensive. An alternate to resampling is the Gaussian particle filter (GPF) [15]. The GPF approximates the posterior with a Gaussian pdf and propagates the samples using the mean and covariance estimates. The filter is free from resampling and is hence very fast. However, it does not scale well with increasing noise and also suffers from estimation bias.

Resampling aids in pushing particles into regions of importance but with an additional computational complexity. As an alternative, several methods have been proposed to leverage the incoming observation in SIS so that the particles are drawn from regions of importance. This mitigates the effect of degeneracy and consequently allows the use of fewer particles. The most popular in this class to date is the auxiliary particle filter (APF) [16] and the improved APF (IAPF) [17], [18]. The filters draw a set of lookahead particles and computes their weights, then resamples the resultant and uses those resampling indices to propagate the old particles to the next time step. Other look ahead strategies include adapted placement and others [19]–[22]. These methods exhibit improved tracking accuracy as they draw particles from high importance regions. However, these methods still employ resampling.

This paper proposes a completely resampling-free method that leverages the incoming observation in the SIS step. For this we assume an additive Gaussian

observation model which the biomedical signal harmonic tracking models also follow. Our proposal is to guide the particles drawn in the SIS step to high importance regions by using the observation pdf. For additive Gaussian observation models, the observation density is 99.7% explained in the region bounded by 3 times the standard deviation of its noise covariance from the mean value, which in this context, is the incoming observation. Similarly, the density is 95% explained in the region bounded by 2 times the standard deviation. Retaining the drawn particles that lie within the region that is randomly specified within the $2\times$ and $3\times$ the standard deviation and eliminating the others and replacing them randomly by perturbed copies of those that lie within the said region facilitates in totally avoiding resampling. The key benefits of this proposal are fast filtering and total avoidance of the highly communication expensive resampling step. Hence the proposed method is named “observation leveraged resampling-free PF.”

The rest of the paper is organized as follows. Section II gives a brief description of the Bayesian PF. Section III proposes the observation leveraged resampling-free PF approach. Section IV presents the evaluation analysis for tracking harmonics of ECG signals. We finally conclude in section V.

2. Particle Filtering

In this section, we set the notation and briefly introduce the PF. Consider a state space model defined by a Markovian state transition and observation models as

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

$$\mathbf{y}_t = h(\mathbf{x}_t, \mathbf{e}_t) \quad (2)$$

for $t = 1, \dots, T$, where the real-valued hidden target state is \mathbf{x}_t at time instant $t \in \mathbb{N}$ and $f(\cdot)$ is a nonlinear function of the evolution of the target state over time. The target dynamics are modelled as a first order Markovian 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 that at time t and follows the observation density is $p(\mathbf{y}_t | \mathbf{x}_t)$. The function $h(\cdot)$ is a nonlinear function that translates the target from the state space to the observation space. \mathbf{a}_t and \mathbf{e}_t are noise variables.

Target inference is achieved by estimating the state of a target \mathbf{x}_t using the noisy sensor data $\mathbf{y}_{1:t} = \{\mathbf{y}_1, \dots, \mathbf{y}_t\}$. The recursive Bayes’ filter accomplishes this estimation by using the previous posterior pdf $p(\mathbf{x}_{t-1} | \mathbf{y}_{1:t-1})$ at time $t-1$ as

$$p(\mathbf{x}_t | \mathbf{y}_{1:t-1}) \propto \int p(\mathbf{y}_t | \mathbf{x}_t) p(\mathbf{x}_t | \mathbf{x}_{t-1}) p(\mathbf{x}_{t-1} | \mathbf{y}_{1:t-1}) d\mathbf{x}_{t-1} \quad (3)$$

In the PF Monte Carlo approximation, $p(\mathbf{x}_{t-1} | \mathbf{y}_{1:t-1})$ is approximated using a set of particles and their corresponding weights $\{\mathbf{x}_{t-1}^i, w_{t-1}^i\}_{t-1}^N$ where i is the particle index and N is the total number of particles. To obtain the approximation of $p(\mathbf{x}_t | \mathbf{y}_{1:t})$, the PF first draws new particles from the Markov transition prior

$$\bar{\mathbf{x}}_t \square p(\mathbf{x}_t | \bar{\mathbf{x}}_{t-1}^i) \quad (4)$$

and weights them according to

$$\bar{w}_t = w_{t-1}^i p(\mathbf{y}_t | \bar{\mathbf{x}}_t^i) \quad (5)$$

for $i = 1, \dots, N$. After a few iterations, the discrepancy between the weights increases causing degeneracy problems. The solution to this is resampling. Conventional systematic resampling [6] that accomplishes this obtains a new weighted set of N particles $\{\bar{\mathbf{x}}_t^i, \bar{w}_t^i\}_{t-1}^N \rightarrow \{\mathbf{x}_t^i, w_t^i\}_{t-1}^N$ as follows [7], [8]; for $i = 1, \dots, N$, we sample an index $j(i)$ distributed according to the probability $\mathbf{p}(j(i) = m) = \frac{\bar{w}_t^m}{\sum_{m=1}^N \bar{w}_t^m}$, $m = 1, \dots, N$ and assign $\mathbf{x}_t^i = \bar{\mathbf{x}}_t^{j(i)}$ and set $w_t^i = 1/N$. Then the PF approximation of the posterior becomes

$$p(\mathbf{x}_t | \mathbf{y}_{1:t}) = \sum_{i=1}^N \frac{1}{N} \delta(\mathbf{x}_t - \mathbf{x}_t^i) \quad (6)$$

where $\delta(\cdot)$ denotes the Dirac delta function. It is implicit that resampling is sequential and also exhaustive over all the particles. This renders the PF computationally expensive. One approach to mitigate the computational complexity is to resample only when the estimated effective sample size (ESS), defined as,

$$\text{ESS} = 1 / \sum_{i=1}^N (\bar{w}_t^i)^2 \quad (7)$$

falls below a certain threshold. That being said, highly nonlinear models or highly manoeuvring targets and/or low noise scenarios cause high degeneracy and require frequent resampling.

Not accounting for the incoming observation \mathbf{y}_t in the sampling process in (4) will not ensure the particles are drawn from regions of importance. The APF [16] and the IAPF variants [18] mimic the process by first propagating the means of the previous particles to the next time step and then determining which of them will survive. The relevant particles are then resampled and propagated. In the subsequent section, we propose a new filter that leverages the incoming observation in the sampling process without the need to resample.

3. Proposed Particle Filter

In this section, we propose the resampling-free approach that leverages the incoming observation in the SIS process. Let the set of N weighted particles at time $t-1$ be $\{\mathbf{x}_{t-1}^i, w_{t-1}^i\}_{t-1}^N$. To move to time t , we draw a new set of particles using the Markov transition prior and assign weights according to

$$\bar{\mathbf{x}}_t \square p(\mathbf{x}_t | \bar{\mathbf{x}}_{t-1}^i) \quad (8)$$

$$\bar{w}_t = p(\mathbf{y}_t | \bar{\mathbf{x}}_t^i) \quad (9)$$

for $i = 1, \dots, N$. Since we drew particles from the Markov transition prior and have not leveraged the incoming observation \mathbf{y}_t into the drawing process, one cannot ensure the drawn particles lie in regions of importance. To avoid this, we consider the following procedure. Assuming the observation density is assumed to be additive Gaussian as in (2), we understand that the observation density $p(\mathbf{y}_t | \mathbf{x}_t) = N(\mathbf{y}_t; h(\mathbf{x}_t), \sigma^2)$ has a mean $h(\mathbf{x}_t)$ and variance σ^2 . The drawn particle $\bar{\mathbf{x}}_t^i$ is a hypothesis of the actual target so if the hypothesis is indeed correct, then the difference $\mathbf{y}_t - h(\bar{\mathbf{x}}_t^i)$, conventionally termed the ‘‘innovation’’, would be small. Since we know that for a Gaussian pdf, a value of 3σ from the mean explains 99.79% of the pdf and a value of 2σ from the mean explains 95% of the pdf. Hence, we compute the limit

$$L = p(\mathbf{y}_t; U\sigma, \sigma^2) \quad (10)$$

where $U \sim U(2,3)$ and $U(\cdot)$ denotes a uniform pdf. We then sort the particles and weights in accordance to the ascending order of the weights as

$$\{\bar{\mathbf{x}}_t^i, \bar{w}_t^i\}_{t-1}^N : \bar{w}_t^1 \leq \bar{w}_t^2, \dots, \bar{w}_t^N \quad (11)$$

and then determine the first index \hat{i} at which the increasing weights is greater than the pdf value L corresponding to 3σ limit as

$$\bar{w}_t^{\hat{i}} \geq L \quad (12)$$

We now determine the set of dominant set of indices D that will be retained as

$$D = \{\hat{i}, \hat{i}+1, \dots, N\} \quad (13)$$

The non-dominant set of $\hat{i}-1$ particles, i.e., those having a weight less than L are eliminated and a new set of samples $\mathbf{s}_t^{i=1, \dots, \hat{i}-1}$ are drawn instead by sampling a new replacement set of $\hat{i}-1$ particles uniformly at random,

with replacement, from the set of dominant particles $\mathbf{x}_t^{-i \in D}$. The final set of particles will contain the new sampled particles $\{\mathbf{s}_t^i\}_{i=1}^{\hat{i}-1}$ appended with the particles corresponding to the dominant set $\{\mathbf{x}_t^i\}_{i=i}^{\hat{i}-1}$.

It should, however, be noted that the new set contains exact replicas of particles corresponding to the dominant set. This leads to losing particle diversity. Moreover, for very peaky weights, we may run into the problem of very few particles replicating the entire new particle set thus causing degeneracy. To avoid this, we perturb the new samples by a small regularising factor as

$$\mathbf{s}_t^i = \mathbf{x}_t^i + u, u \sim N(0, \epsilon), i = 1, \dots, \hat{i}-1 \quad (14)$$

Then the final set of particles are arranged and their weights are then computed according to

$$\mathbf{x}_t^{1:N} = \{\mathbf{s}_t^{i=1, \dots, \hat{i}-1}, \mathbf{x}_t^{\hat{i}}, \mathbf{x}_t^{\hat{i}+1}, \dots, \mathbf{x}_t^N\} \quad (15)$$

$$w_t^i = p(\mathbf{y}_t | \mathbf{x}_t^i), i = 1, \dots, N \quad (16)$$

The value of U determines the limit of the state space to which the samples are being pushed into. A value close to two indicates a tighter limit.

As an illustration, the left panel of Figure 1 shows the stem plot of $N = 100$ particles and their corresponding weights.

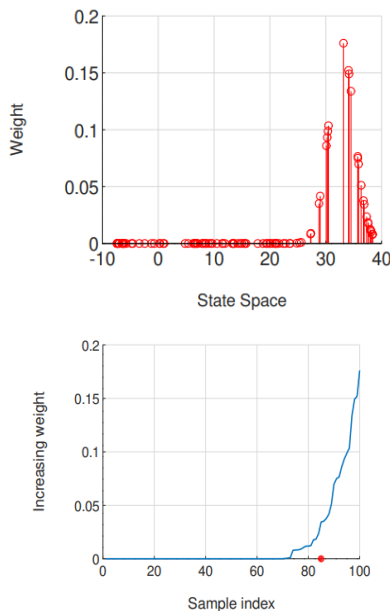


Fig. 1. The left panel shows the stem plot of the 1-D particles versus their weights. The right panel shows the increasing weight function. The first index whose weight is greater than the 3σ limit L is shown as red dot.

space that lie in region that does not contribute to the posterior. The right panel shows the sorted weights along with the maximum permissible 3σ limit L as a red dot. The indices succeeding the limit L are the dominant weights and the preceding ones are the negligible weights. From the example, it can be seen that particles from the 85th are treated dominant and the rest are non-dominant. The resampled set is shown in the left panel of Figure 2 and it can be observed that the proposed method effectively eliminates the low weight particles with perturbed copies of those with large weights. A closeup of the left panel is shown on the right and it can be observed that perturbing the dominant particles instead of replicating their exact copies will lead to particle richness among the new set (the cyan stem plot). The key merit herein is that resampling of particles is totally avoided with the proposed replacement scheme. Moreover, our proposition substantially accelerates the filtering process. In the subsequent section, we evaluate the performance of the proposed method.

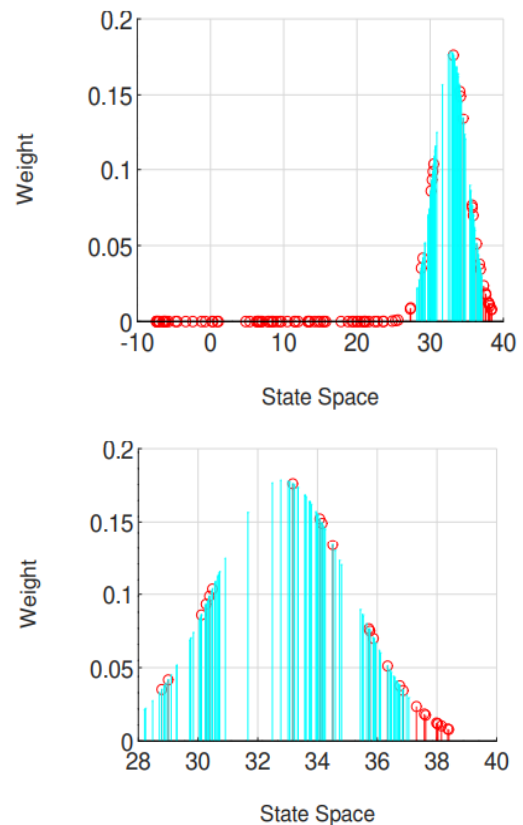


Fig. 2. Corresponding to the illustration in Figure 1, in the left panel, the red stem plot shows the 1-D particles and weights before replacement. The cyan shows the particles and weights after replacement. The right panel shows a closeup of the left to illustrate the effect of particle richness caused by perturbing the dominant particles.

It can be observed there are several particles in the state

4. Evaluation: Tracking Rhythmic Biomedical Signals

In this section, we present the evaluation of the proposed observation leveraged resampling-free PF. We compare with the standard PF [6] that employs systematic resampling to push particles into regions of importance, the APF [16], [18] that employs lookahead schemes to push particles into regions of importance, and the GPF [15] which uses an altogether different approach that does not necessarily account for drawing particles from importance regions. The standard PF resamples only when the $ESS/N \leq 0.3$.

The state space model is a challenging problem of tracking multiple harmonics in periodic rhythmical signals [3]. These signals are a model of the biomedical signals including the ECG and pulse variation signals. The measurement model for this example is

$$y(t) = \sum_{k=1}^{N_h} (a_{k,t} \cos(k\theta_t) + b_{k,t} \sin(k\theta_t)) + \bar{y}_t + e_t \quad (17)$$

where N_h is the known number of harmonics, 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 $e_t \sim N(0, \sigma^2 = 5)$ is the additive white measurement noise variable.

The state variables that transit over time are defined as

$$\theta_t = \theta_{t-1} + 2\pi t_s f_t \quad (18)$$

$$\bar{f}_t = g[\bar{f}_{t-1} + u_{\bar{f},t}] \quad (19)$$

$$f_t = \bar{f}_{t-1} + \alpha(f_{t-1} - \bar{f}_{t-1}) + u_{f,t} \quad (20)$$

$$a_{k,t} = a_{k,t-1} + u_{a_{k,t}}, k = 1, \dots, N_h \quad (21)$$

$$b_{k,t} = b_{k,t-1} + u_{b_{k,t}}, k = 1, \dots, N_h \quad (22)$$

$$\bar{y}_t = \bar{y}_{t-1} + u_{\bar{y},t} \quad (23)$$

For $t = 1, \dots, T$ where f_t is the fundamental frequency, \bar{f}_t is the mean fundamental frequency, $t_s = 1/f_s$ is the sampling interval, $\alpha = 0.99$ is the auto-regressive coefficient assumed to be known and the Markov state transition noise variables are

$$u_{f,t} \sim N(0, 10^{-4}), u_{\bar{f},t} \sim N(0, 10^{-6}),$$

$$u_{a_{k,t}} \sim N(0, 10^{-6}), u_{b_{k,t}} \sim N(0, 10^{-6}), \text{ and}$$

$$u_{\bar{y},t} \sim N(0, 10^{-4}) \text{ The mean frequency is assumed to}$$

follow a nonlinear reflecting function.

$$g[f] = \begin{cases} f_{\max} - (f - f_{\max}) & \text{if } f_{\max} \leq f, \\ f & \text{if } f_{\min} \leq f \leq f_{\max} \\ f_{\min} + (f_{\min} - f) & \text{if } f \leq f_{\min} \end{cases} \quad (24)$$

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

$$\mathbf{x}_t = (\theta_t, f_t, \bar{f}_t, \bar{y}_t, a_{1,t}, a_{2,t}, \dots, a_{N_h,t}, b_{1,t}, b_{2,t}, \dots, b_{N_h,t})^T \quad (25)$$

The reader is referred to [3] for more detailed description of the model. We set $N_h = 5, f_s = 360\text{Hz}, a_{k,t} = b_{k,t} = 1, f_{\max} = 1, f_{\min} = 5$ Hertz, $\bar{y}_{\forall t} = 0, \sigma^2 = 0.1$. The initial state values of the ground truth are set to $\theta_{t=0}^{\text{true}} = 0$ and $f_{t=0}^{\text{true}} = 2, \bar{f}_{t=0}^{\text{true}} = 1.5$ Hertz, $\bar{y}_{t=0}^{\text{true}} = 10, a_{k,t=0}^{\text{true}} \sim u(2, 5)$ and $b_{k,t=0}^{\text{true}} \sim u(3, 7)$. The filters are initialised with $\theta_{t=0}^i \sim N(0, 1)$ and $f_{t=0}^i \sim U(f_{\min}, f_{\max}), \bar{f}_{t=0}^i \sim U(0, 2), \bar{y}_{t=0}^i \sim N(0, 1), a_{k,t=0}^i \sim U(2, 5)$ and $b_{k,t=0}^i \sim U(3, 7)$ for $i = 1, \dots, N$. For the chosen $f_s = 360$ Hz, we record a 3.3 second signal, meaning the recorded signal contains $T = 1200$ time samples.

The two performance measures used are the root mean squared error (RMSE) and the normalized mean squared error (NMSE) defined by

$$XRMSE = \sqrt{\frac{\sum_{t=1}^T X_t^{\text{true}} - \hat{X}}{T}}, X = (f_t, \bar{f}_t, \theta_t, \bar{y}_t) \quad (26)$$

$$XRMSE = 1/N_h \sum_{k=1}^{N_h} \sqrt{\frac{\sum_{t=1}^T X_{k,t}^{\text{true}} - \hat{X}_{k,t}}{T}}, X = (a_{k,t}, b_{k,t}) \quad (27)$$

$$NMSE = \frac{\sum_{t=1}^T (y_t - \bar{y}_t)^2}{(y_t - \bar{y}_t)^2} \quad (28)$$

where $\hat{\cdot}$ is the estimated value. The RMSE corresponding to the latent variables is a well-known measure. The NMSE, on the other hand, lies in $(0, \infty)$ and a value of less than one indicates good harmonic tracking

[3] 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, Figure 3 shows the degeneracy effect in the proposed filter for small and large values of N .

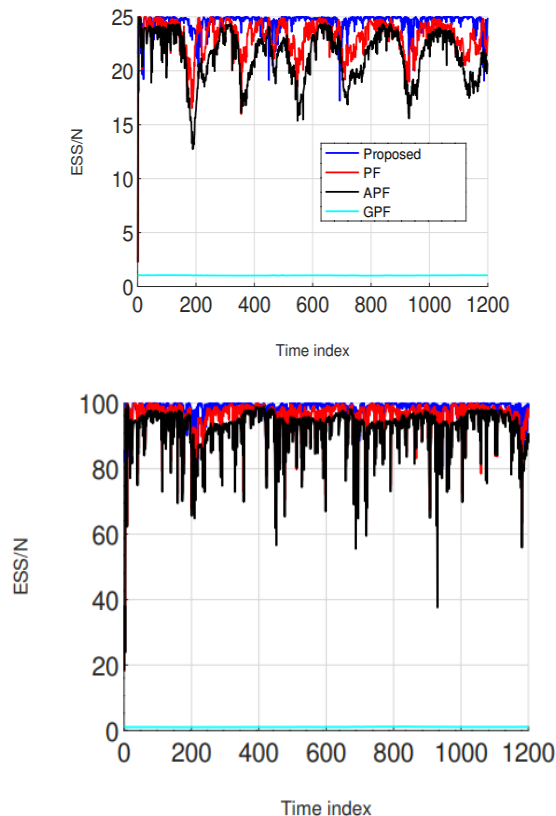


Fig. 3. The estimated ESS versus the time instant t for $N = 25$ in the top panel and $N = 100$ in the bottom panel. The legend of the top panel applies to the bottom also.

N	Method	Proposed	PF	APF	GPF
25	$E(ESS/N)/N$	0.98113	0.92640	0.85515	0.04119
25	$Std(ESS/N)$	0.82416	1.57775	2.35492	0.01161
100	$E(ESS/N)/N$	0.98057	0.94959	0.91833	0.01071
100	$Std(ESS/N)$	3.63156	6.96170	7.36638	0.04262

Table I: The table shows the normalized expectation of ESS/N and its standard deviation for the four methods for $n = 25, 100$ Corresponding to the result shown in figure 3.

Now that we have established that the proposed method does not suffer from degeneracy for the rhythmic biomedical signal model, we focus on the tracking accuracy and the computational time. The state vector for the biomedical signal model is 14-dimensional as described in (25). We compute the RMSE for each of these states according to (26) and (27) and these values are shown in Table II. It can be observed that the proposed method exhibits moderately lower errors in estimation of

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 figure that the GPF maintains low ESS throughout. This also causes the filter to perform poorly in high noise conditions. The key merit of the proposed method is that it avoids degeneracy by eliminating low weight particles and replaces them with perturbed copies of large weight particles. Accordingly, it can be observed that the normalized ESS estimate ESS/N of the proposed method stays high throughout the simulation thus overcoming degeneracy. It has been found that the standard PF and the APF require resampling at all time steps in order to maintain high ESS, and it can be seen in the figure that they indeed maintain good ESS as long as they resample. Table I shows the normalized mean value of ESS/N and its standard deviation. The normalized mean lies in $(0, 1)$ and a value of one indicates no degeneracy. It can be observed that for both cases of N , the proposed method exhibits marginally high value of nearly 7% over the standard PF and the APF for both cases of N . Additionally, the proposed method does not oscillate as much as the other methods do, as is evident in the small value of standard deviations reported in the table. The proposed method is nearly 60% and 45% less oscillative than the APF and the standard PF respectively. That is to say the proposed method is more robust to the degeneracy caused by the SIS step than the conventional methods. This shows the efficacy of the proposed method is overcoming degeneracy and ensuring the particles are indeed drawn from regions of importance.

the frequency $f_{1:T}$ and the mean frequency $\hat{f}_{1:T}$ but shows tremendous reduction of error in the estimation of the instantaneous phase $\theta_{1:T}$. It can be observed that the proposed method shows moderately higher errors in the estimation of the signal mean $\bar{y}_{1:T}$ and the sinusoidal coefficients $a_{1:N_h,1:T}$ and $b_{1:N_h,1:T}$ over the conventional

methods. A possible reason for the PFs to be more pronounced in effectively tracking the signal mean and sinusoidal coefficients could be due to the fact that resampling discards the lower weight particles with nonzero probability. The proposed method discards with unit probability. Therefore, in instances where the lower weight particles are important, e.g., when target manoeuvre is big, the proposed method is expected to show reduced tracking accuracy. The table also shows that the error reduces with increasing number of particles. The computational time (in seconds) versus the average RMSE (ARMSE) (average of all the errors) is shown in Figure 4. It can be clearly observed that the proposed method exhibits lower ARMSE and consumes lesser computation over the conventional methods at low and high values of N .

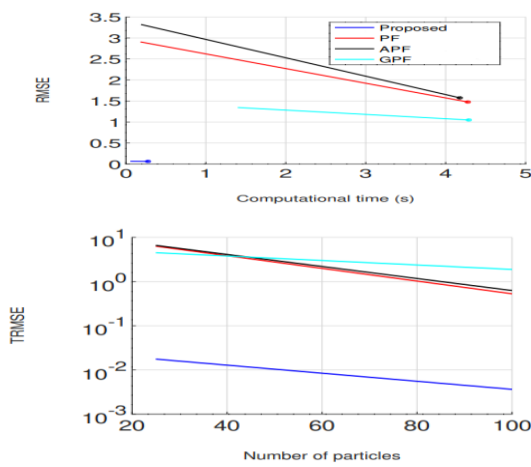


Fig. 4. The top panel shows the computational time (seconds) versus the RMSE for $N = 25, 100$. The values at $N = 25$ are shown using solid dot.

The bottom panel shows the TRMSE versus the number of particles. The legend of the top panel applies to the bottom also.

N	Method	f RMSE	\hat{f} RMSE	θ RMSE	\bar{y} RMSE	aRMSE	bRMSE
25	Prop	0.020200	0.01518	0.539472	0.27305	0.32908	0.48384
	PF	0.198390	0.21948	25.084442	0.04792	0.02123	0.09658
	APF	0.195415	0.21727	24.465122	0.06710	0.02038	0.09637
	GF	0.266362	0.11313	25.165979	0.07915	0.02021	0.09586
100	Prop	0.009401	0.02509	0.001562	0.06440	0.06477	0.16686
	PF	0.019670	0.05947	0.866295	0.03080	0.02075	0.09604
	APF	0.019457	0.05897	0.907270	0.03008	0.02119	0.09495
	GF	0.178653	0.07010	7.951485	0.07689	0.02027	0.09610

Table II: the table shows RMSE corresponding to the latent variables for the four methods under test for $N = 25, 100$. The reader may replace X in $XRMS$ with the latent variable, e.g., f RMSE denotes the RMSE of the

$$\text{frequency estimate } \hat{f}_{1:T}$$

This is because the method ensures that the particles

drawn during the SIS step are corrected in a way that they are limited to within the boundary of $y - 3\sigma$. Moreover, the method totally avoids the need to resample 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

$$TRMSE = T_c \times RMSE \quad (29)$$

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 4 also shows the TRMSE versus the number of particles and it can be observed that the proposed method shows an incredible improvement of 99.688% and 99.512% (% reduction in TRMSE) at $N = 25$ and 100 averaged over the other 3 methods.

We finally show the NMSE versus the number of particles shown in figure 5.

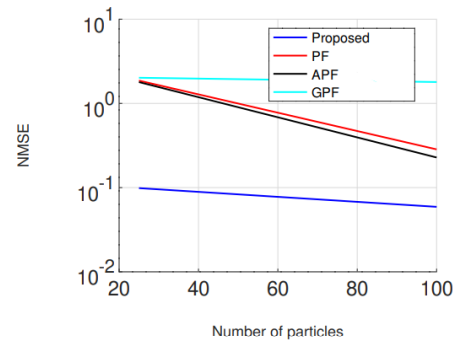


Fig. 5. The NMSE versus the number of particles.

The NMSE is a measure of how accurately the estimated latent target states could recover the observed signal. The key benefit of the proposed method can be observed clearly in that it shows a NMSE of less than one even at low $N = 25$ particles. The other methods show a NMSE of more than one at $N = 25$ but drops below one from $N = 50$. That being said, the proposed method shows NMSE that is much lesser than the conventional methods. The main reason for this is the method's ability to operate with fewer particles that are drawn from regions of importance.

This evaluation study has shown that the proposed observation leveraged resampling free PF substantially accelerates the filtering operation as it replaces the computationally intensive resampling scheme with a simple replacement strategy. The method also gains in terms of tracking accuracy by effectively exploring the regions in the state space that contribute to the posterior. This paper also notes the weakness of the proposed method, as evidenced in Table II is that it never accounts for lower weight particles. That being said, this evaluation study has shown that the method is extremely powerful when studied in conjunction with accuracy and speed.

5. Conclusion

This paper proposed a resampling-free PF approach that leverages the incoming observation in the particle sampling process. This is done by limiting the sampling to a region that is randomly specified to be within explainable limits from the incoming observation. This mitigates the effect of degeneracy within the particles. Moreover, the computationally intensive resampling step is totally avoided. The proposed method is evaluated using a biomedical signal tracking example and its tracking accuracy and computational speed are shown.

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