Fast resampling for sequential Monte Carlo with millions of particles

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Abstract

Particle filtering (PFs) and, more generally, sequential Monte Carlo (SMC) methods are essential tools for Bayesian inference. Over the years, many SMC variants have been proposed, yet their core always relies on importance sampling followed by a resampling step. While resampling is crucial to mitigate particle degeneracy and to maintain a stable approximation of the posterior distribution, it often represents a significant computational bottleneck. In this work, we present a novel, fast, resampling procedure that provides significant computational gains in demanding (often high-dimensional) scenarios where a large number of particles is required, and the effective sample size (ESS) is small. The effectiveness of the proposed approach is demonstrated through a series of numerical experiments showing remarkable performance. In addition, a theoretical analysis and related code implementation are provided.

Keywords: Bayesian inference; Sequential Monte Carlo; Particle Filtering; Resampling.

1 Introduction

Particle filtering also known as sequential Monte Carlo (SMC), has become very popular methodologies in signal processing, statistics, and machine learning [7, 9, 23, 24, 11]. These methods play a central role in Bayesian inference, particularly for nonlinear and non-Gaussian state-space models, where analytical solutions are intractable. More recently, they have also held an important place in approximate Bayesian computation (ABC) and other static inference problems. SMC methods have been adopted in various fields, including finance, geophysical systems, wireless communications, control, navigation and tracking, and robotics, to name a few

[13, 15, 18].

Many types of particle filters (PFs) or SMC methods have been introduced in the literature. However, the core of all of them is formed by and *importance sampling (IS) plus resampling* (IS+R) technique (i.e., IS followed by a resampling step), which consists of three main operations [36, 25]. The importance sampling (IS) part includes the first two operations: 1) particle propagation/generation and 2) weight computation. The last operation is 3) the resampling step.

The resampling procedure replaces the weighted particles at one iteration with another cloud of (equally weighted) particles, according to the normalized importance weights associated to the first set of particles. The resampling is essential for PFs and/or SMC methods: without this step, a PF quickly produces a degenerate set of particles, i.e., a set in which a few particles (often a unique one) dominate the rest of the particles with their weights [7, 9, 23]. This means that the obtained estimates will be inaccurate and/or have extremely large variances. With the application of the resampling, such deteriorations are prevented, which is why it is highly important to SMC methods. Hence, resampling has been extensively researched and, as a consequence, various resampling schemes have been proposed. Some examples are multinomial resampling, hereafter denoted as standard resampling (SR), stratified resampling, systematic resampling, and residual resampling [8, 21, 20]. However, all these resampling schemes differ essentially for *the variance* introduced in the overall SMC algorithm [2, 17].

Therefore, the resampling step is essential to mitigate particle degeneracy and ensure a stable approximation of the posterior distribution. More generally, resampling is employed to reduce the variance of the particle filter estimates. However, resampling often represents a significant computational bottleneck for PFs and SMC schemes. The first reason is that resampling needs normalized weights and for this scope we need a weight summation that cannot be completely parallelized (without approximations) [1, 3, 33]. The second reason is the need of cumulative sums and random sampling, which can become costly as the number of particles increases. As a consequence, resampling frequently dominates the overall computational time, especially in large-scale or real-time applications, thereby motivating the development of more efficient and adaptive resampling strategies [6]. For instance, the resampling step is often applied only at certain iterations, when effective sample size (ESS) is small [31, 12, 29]. More recent contributions can be found in [4, 14, 28, 37].

In this work, we introduce a novel resampling procedure that is substantially faster when a large number of particles is used and when the ESS is small. Both circumstances are commonly encountered in practical real-world (high-dimensional) scenarios. The idea is inspired by the

information theory concept of minimal codeword length in source coding [5]. Two groups of particles are created: one groups includes $M < N$ samples with the biggest weights, and a second group contains the remaining $N - M$ samples. Then, according to a suitable probability, the resampling is applied much more times within the first (smaller) group. The proposed procedure is particularly efficient when the first group contains an high probability mass, which is often the case in challenging scenarios. The novel scheme can be applied in combination with any resampling approach, such as multinomial, stratified, systematic, or residual, to name a few [21, 20].
We prove the unbiasedness condition of the method. Furthermore, we describe the feasible working zones where the method is useful. We also discuss the optimal choice of M providing a suitable approximation. Several numerical experiments demonstrate the computational benefits of the proposed resampling scheme, especially for large numbers of particles. Remarkable results have been obtained reducing more than 60% the computational time within a particle filter, in which resampling is applied in approximately half of the iterations. For reproducibility, related Matlab code is available at `http://www.lucamartino.altervista.org/FAST_RESAMPLING_public_code.zip`.
The rest of work is structured as follows. Section 2 contains some background material and preliminaries. Section 3 describes the proposed scheme. Section 4 is devoted to the theoretical analysis of the proposed method. The numerical experiments are given in Section 5. Some final conclusions are provided in Section 6.

2 Preliminaries

2.1 Bayesian inference

In many real world applications, the goal is to infer a variable of interest given a set of data [23, 35]. Let us denote the parameter of interest (static or dynamic) by $\boldsymbol{\theta} = [\theta_1, ..., \theta_{d_\theta}]^\top \in \mathcal{X} \subseteq \mathbb{R}^{d_\theta}$, and let $\mathbf{y} \in \mathbb{R}^{d_y}$ be the observed data. In a Bayesian analysis, all the statistical information is contained in the posterior distribution, which is given by

$$\bar{\pi}(\boldsymbol{\theta}) = p(\boldsymbol{\theta}|\mathbf{y}) = \frac{\ell(\mathbf{y}|\boldsymbol{\theta})g(\boldsymbol{\theta})}{Z(\mathbf{y})}, \tag{1}$$

where $\ell(\mathbf{y}|\boldsymbol{\theta})$ is the likelihood function, $g(\boldsymbol{\theta})$ is the prior pdf, and $Z(\mathbf{y})$ is the Bayesian model evidence (a.k.a. marginal likelihood). The marginal likelihood $Z(\mathbf{y})$ is important for model selection purposes [27]. Generally, $Z(\mathbf{y})$ is unknown, so we are able to evaluate the unnormalized target function, $\pi(\boldsymbol{\theta}) = \ell(\mathbf{y}|\boldsymbol{\theta})g(\boldsymbol{\theta})$. The analytical computation of integrals involving the posterior density $\bar{\pi}(\boldsymbol{\theta}) \propto \pi(\boldsymbol{\theta})$ is often unfeasible, hence numerical approximations are needed. Thus, the

goal is often to approximate integrals of the form

$$I = \int_{\mathcal{X}} h(\boldsymbol{\theta})\bar{\pi}(\boldsymbol{\theta})d\boldsymbol{\theta} = \frac{1}{Z}\int_{\mathcal{X}} h(\boldsymbol{\theta})\pi(\boldsymbol{\theta})d\boldsymbol{\theta}, \tag{2}$$

where $h(\boldsymbol{\theta})$ is some integrable function, and

$$Z = \int_{\mathcal{X}} \pi(\boldsymbol{\theta})d\boldsymbol{\theta}. \tag{3}$$

In the literature, random sampling or deterministic quadratures are often used [35, 32, 34]. In this work, we focus on the so-called importance sampling (IS) approach.

2.2 Importance sampling 'plus' resampling (IS+R)

Let us consider a normalized proposal density $q(\boldsymbol{\theta})$.[1] The importance sampling (IS) method consists of drawing N samples, $\boldsymbol{\theta}_1, \ldots, \boldsymbol{\theta}_N$, from $q(\boldsymbol{\theta})$ (also called particles), and then assign to each sample the following unnormalized weights

$$w_n = \frac{\pi(\boldsymbol{\theta}_n)}{q(\boldsymbol{\theta}_n)}, \quad n = 1, \ldots, N. \tag{4}$$

An unbiased estimator of the marginal likelihood Z is given by the arithmetic mean of these unnormalized weights [23, 35], i.e.,

$$\widehat{Z} = \frac{1}{N}\sum_{n=1}^{N} w_n, \quad \text{and } \bar{w}_n = \frac{w_n}{\sum_{i=1}^{N} w_i} = \frac{w_n}{N\widehat{Z}},$$

are the normalized weights, with $n = 1, \ldots, N$. The self-normalized IS estimator of I in Eq. (2) is given by

$$\widehat{I} = \sum_{n=1}^{N} \bar{w}_n f(\boldsymbol{\theta}_n).$$

More generally, regardless of the specific function $f(\boldsymbol{\theta})$, with IS, we obtain a particle approximation of the measure $\bar{\pi}$, i.e.,

$$\widehat{\pi}(\boldsymbol{\theta}) = \sum_{n=1}^{N} \bar{w}_n \delta(\boldsymbol{\theta} - \boldsymbol{\theta}_n), \tag{5}$$

[1] We assume that $q(\boldsymbol{\theta}) > 0$ for all $\boldsymbol{\theta}$ where $\bar{\pi}(\boldsymbol{\theta}) > 0$, and $q(\boldsymbol{\theta})$ has heavier tails than $\bar{\pi}(\boldsymbol{\theta})$.

where $\delta(\boldsymbol{\theta})$ is a delta function. It is important to remark that with this particle approximation, we can approximate several quantities related to the posterior $\bar{\pi}(\boldsymbol{\theta})$, such as any moments and/or credible intervals (not just a specific integral). The quality of this particle approximation is related to the discrepancy between the proposal $q(\boldsymbol{\theta})$ and the posterior $\bar{\pi}(\boldsymbol{\theta})$ [26].

Remark 1. Drawing $\bar{\boldsymbol{\theta}} \sim \widehat{\pi}(\boldsymbol{\theta})$ is usually called *resampling*. Namely, $\bar{\boldsymbol{\theta}}$ is selected within the set of samples $\{\boldsymbol{\theta}_1, ..., \boldsymbol{\theta}_N\}$ according to the probabilities $\bar{w}_n$, for $n = 1, ..., N$.

The relevance of IS+R is underscored by the fact that it constitutes the core of the well-known particle filtering techniques, also known as sequential Monte Carlo algorithms.

2.3 Standard resampling (SR) schemes

All classical resampling schemes are distinct procedures sharing the same goal: drawing N samples *with replacement* within the set $\{\boldsymbol{\theta}_1, ..., \boldsymbol{\theta}_N\}$ according to probability mass $\bar{w}_n$, $n = 1, ..., N$, i.e.,

$$\bar{\boldsymbol{\theta}}_n \sim \widehat{\pi}(\boldsymbol{\theta}) = \sum_{i=1}^{N} \bar{w}_i \delta(\boldsymbol{\theta} - \boldsymbol{\theta}_i). \tag{6}$$

The output of a resampling scheme is a new set of N particles, $\{\bar{\boldsymbol{\theta}}_1, ..., \bar{\boldsymbol{\theta}}_N\}$, where $\bar{\boldsymbol{\theta}}_n \in \{\boldsymbol{\theta}_1, ..., \boldsymbol{\theta}_N\}$, for all n. In practice, particles with higher importance weights are often replicated several times, while those with lower importance weights are often discarded. Namely, we modify the weighted particle approximation $\widehat{\pi}$ to a particle approximation $\widehat{\pi}_{\texttt{res}}$ by eliminating particles having lower importance weights and by multiplying particles having higher importance weights, i.e.,

$$\widehat{\pi}_{\texttt{res}}(\boldsymbol{\theta}) = \frac{1}{N} \sum_{n=1}^{N} \delta(\boldsymbol{\theta} - \bar{\boldsymbol{\theta}}_n) = \sum_{r=1}^{N} \frac{N_r}{N} \delta(\boldsymbol{\theta} - \boldsymbol{\theta}_r), \tag{7}$$

where $N_r \geq 0$ is a non-negative integer number, that is the number of copies of the particle $\boldsymbol{\theta}_r$ in the new set of resampled particles $\{\bar{\boldsymbol{\theta}}_1, ..., \bar{\boldsymbol{\theta}}_N\}$. Hereafter, we denote with $R \leq N$ the total count of distinct particles contained in the set $\{\bar{\boldsymbol{\theta}}_1, ..., \bar{\boldsymbol{\theta}}_N\}$.

Remark 2. There are different standard resampling schemes [20, 21], which essentially differ for the variability introduced by their procedures [17]. Generally, there is no substantial difference in the overall computational time among them. Moreover, the time required for performing the resampling procedure generally is an increasing function of N. All the results presented here regarding computational time are valid for all these different strategies.

Properness. All the resampling schemes, to be unbiased, must satisfy the proper-weighting

condition [17, 22, 30]. Namely, the expected number of times, N_m, that the m-th particle is resampled, must be proportional to $\bar{w}_m$, i.e.,

$$\mathbb{E}\left(N_m \mid \bar{w}_m\right) = N\bar{w}_m = N\frac{w_m}{N\widehat{Z}} = \frac{w_m}{\widehat{Z}}. \tag{8}$$

The main notation of the work is summarized in Table 1.

Table 1: Main notation of the work.

Notation	Description
$\bar{\pi}(\boldsymbol{\theta}) = p(\boldsymbol{\theta}\|\mathbf{y}) = \frac{\ell(\mathbf{y}\|\boldsymbol{\theta})g(\boldsymbol{\theta})}{Z(\mathbf{y})}$	Normalized posterior distribution
$\pi(\boldsymbol{\theta}) = \ell(\mathbf{y}\|\boldsymbol{\theta})g(\boldsymbol{\theta})$	Unnormalized posterior function
$w_n = \frac{\pi(\boldsymbol{\theta}_n)}{q(\boldsymbol{\theta}_n)}$	Unnormalized IS weights
$\bar{w}_n = \frac{w_n}{\sum_{i=1}^N w_i}$	Normalized IS weights
$\widehat{\pi}(\boldsymbol{\theta}) = \sum_{n=1}^N \bar{w}_n \delta(\boldsymbol{\theta} - \boldsymbol{\theta}_n)$	IS measure approximation
$\bar{\boldsymbol{\theta}}_n \sim \widehat{\pi}(\boldsymbol{\theta})$	Resampled particle
$\bar{w}_{j_n}$	Ordered (normalized) weight, i.e., $\bar{w}_{j_1} \geq \bar{w}_{j_2} \geq ... \geq \bar{w}_{j_N}$
$\widetilde{\boldsymbol{\theta}}_n = \boldsymbol{\theta}_{j_n}$	Ordered sample according to the ordered weights above, i.e., $\widetilde{\boldsymbol{\theta}}_1 = \boldsymbol{\theta}_{j_1},\ \widetilde{\boldsymbol{\theta}}_2 = \boldsymbol{\theta}_{j_2}, \ldots,\ \widetilde{\boldsymbol{\theta}}_N = \boldsymbol{\theta}_{j_N}$

3 Proposed scheme

Let us assume the normalized weights $\bar{w}_n$, $n = 1, ..., N$. We define the normalized weights sorted in decreasing order, i.e.,

$$\bar{w}_{j_1} \geq \bar{w}_{j_2} \geq ... \geq \bar{w}_{j_N}, \tag{9}$$

where $j_i \in \{1, ..., N\}$ with $i = 1, ..., N$. Namely, we have by definition $\bar{w}_{j_1} = \max \bar{w}_n$, and $\bar{w}_{j_N} = \min \bar{w}_n$. Clearly, the order is valid also for the unnormalized weights, $w_{j_1} \geq w_{j_2} \geq .. \geq w_{j_N}$. Hence, we can also order the samples

$$\widetilde{\boldsymbol{\theta}}_1 = \boldsymbol{\theta}_{j_1},\ \widetilde{\boldsymbol{\theta}}_2 = \boldsymbol{\theta}_{j_2}, \ldots,\ \widetilde{\boldsymbol{\theta}}_N = \boldsymbol{\theta}_{j_N}.$$

Then, the user chooses a integer value $M < N$, such that the particles are divided into two groups: from $\widetilde{\boldsymbol{\theta}}_1$ to $\widetilde{\boldsymbol{\theta}}_M$ and from $\widetilde{\boldsymbol{\theta}}_{M+1}$ to $\widetilde{\boldsymbol{\theta}}_N$. Moreover, the probability of selecting the first group will be

$$\bar{s}_M = \sum_{k=1}^{M} \bar{w}_{j_k} = \frac{\sum_{k=1}^{M} w_{j_k}}{\sum_{n=1}^{N} w_n}. \tag{10}$$

Remark 3. Note that $\bar{s}_M = \sum_{k=1}^{M} \bar{w}_{j_k}$ depends on M. Moreover, $\bar{s}_M \in (0, 1]$ by definition.

We can obtain the normalized weights within the first group as

$$\bar{\rho}_m = \frac{w_{j_m}}{\sum_{k=1}^{M} w_{j_k}}, \quad m = 1, ..., M, \tag{11}$$

and in the second group as

$$\bar{\gamma}_k = \frac{w_{j_k}}{\sum_{i=M+1}^{N} w_{j_i}}, \quad k = M+1, ..., N. \tag{12}$$

The proposed resampling algorithm is then given in Table 2. This procedure is partially grounded in the group importance sampling approach in [30] and other ideas applied for parallelization purpose (see also [3, 33, 28]).
Step-1 in Table 2 is equivalent to resample N times over 2 possible artificial "particles", due to the random selection of the N binary indices $b_n \in \{0, 1\}$. The number of times that we select $b_n = 1$ is denoted by R. Note that Step-2 in Table 2 consists of performing R resampling steps over M particles. Finally, in Step-3 of Table 2, we perform $N - R$ resampling steps over $N - M$ particles. Figure 1 represents graphically the proposed fast FR scheme.

Remark 4. Note that the proposed approach is compatible with any kind of resampling technique, such as multinomial, stratified, residual, and/or systematic resampling (and any other type of resampling that is unbiased).

4 Theoretical and practical analysis

In this section, we will answer questions of type: *does it properly work?* and *in which scenario is it useful?* The first question is answered in Sections 4.1 and 4.2. The second question is addressed in Section 4.3 and 4.4. Furthermore, we discuss the choice of M for the proposed fast resampling (FR) scheme in Section 4.5, respectively.

Table 2: **The proposed fast resampling (FR) scheme.**

- Initialization: Choose an integer value $M < N$. Build the group with M particles and compute $\bar{s}_M$.

1. Draw N binary indices $b_n \in \{0, 1\}$, $n = 1, ..., N$, according to the probability mass $\text{Prob}(b_n = 1) = \bar{s}_M$ and $\text{Prob}(b_n = 0) = 1 - \bar{s}_M$ (i.e., resample N times within $\{0, 1\}$ with probabilities $\bar{s}_M$ and $1 - \bar{s}_M$). Denote as $R = \sum_{n=1}^{N} b_n$ the number of indices n for which $b_n = 1$ and, as a consequence, $N - R$ is the number of indices with $b_n = 0$.

2. Draw R samples $\bar{\boldsymbol{\theta}}_i$, with $i = 1, ..., R$, within the M possible samples $\{\widetilde{\boldsymbol{\theta}}_1, ..., \widetilde{\boldsymbol{\theta}}_M\}$ according to the probability mass

$$\bar{\rho}_m = \frac{w_{j_m}}{\sum_{k=1}^{M} w_{j_k}}, \qquad m = 1, ..., M. \tag{13}$$

3. Draw $N - R$ samples $\bar{\boldsymbol{\theta}}_k$, with $k = R + 1, ..., N$, within the $N - M$ possible samples $\{\widetilde{\boldsymbol{\theta}}_{M+1}, ..., \widetilde{\boldsymbol{\theta}}_N\}$ according to the probability mass

$$\bar{\gamma}_m = \frac{w_{j,}}{\sum_{i=M+1}^{N} \bar{w}_{j_i}}, \qquad m = M + 1, ..., N. \tag{14}$$

- Output: Return all the N resampled particles $\bar{\boldsymbol{\theta}}_i$, for $i = 1, ..., N$ (the total number of resampled particles is always N).

4.1 Proper-weighting condition

Below, we show that proper-weighting condition in Eq (8) is fulfilled by the proposed fast resampling (FR) scheme.

Theorem 1. The proposed FR scheme satisfy the theoretical requirement in Eq (8), i.e.,

$$\mathbb{E}\left(N_m \mid \bar{w}_m\right) = N\bar{w}_m, \quad \forall m. \tag{15}$$

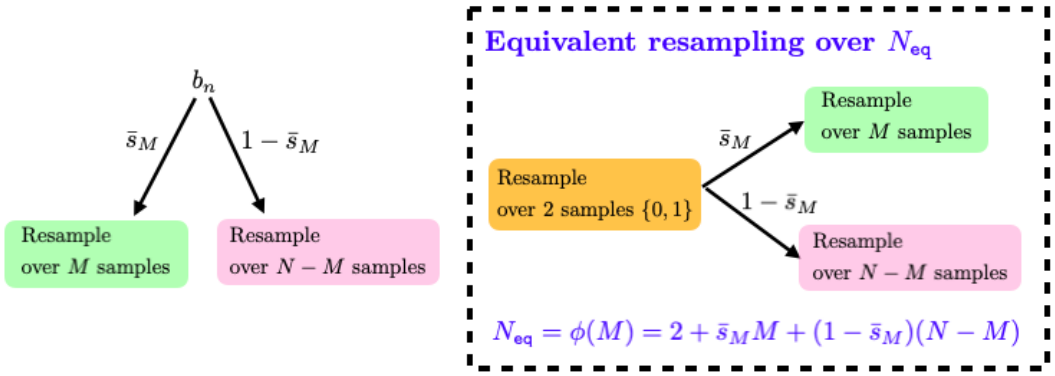


Figure 1: Graphical representation of the fast resampling (FR) scheme: the proposed method is composed of two successive resampling steps (in series). In the first block, one resampling step is performed with two possible outcomes $b_n \in \{0, 1\}$, occurring with probabilities $\bar{s}_M$ and $1 - \bar{s}_M$. This stage determines which group is resampled next. The second block in series, if $b_n = 1$, a resampling step is performed over M particles. Otherwise, if $b_n = 0$, a resampling step is performed over $N - M$ particles. The overall FR scheme can be also seen as mixture of the two resampling procedures in the second block.

Proof. First of all, note that $E[R] = N\bar{s}_M$, if $m \leq M$, we have:

$$\begin{aligned}
\mathbb{E}\left(N_{j_m} \mid \bar{w}_{j_m}\right) = E[R]\bar{\rho}_m &= N\bar{s}_M\bar{\rho}_m, \\
&= N\left(\sum_{k=1}^{M} \bar{w}_{j_k}\right)\frac{w_{j_m}}{\sum_{k=1}^{M} w_{j_k}} \\
&= N\left(\frac{\sum_{k=1}^{M} w_{j_k}}{\sum_{n=1}^{N} w_n}\right)\frac{w_{j_m}}{\sum_{k=1}^{M} w_{j_k}} \\
&= N\frac{w_{j_m}}{\sum_{n=1}^{N} w_n} = N\bar{w}_{j_m},
\end{aligned}$$

for all $m \leq M$. Otherwise, if $m > M$, we have:

$$\begin{aligned}
\mathbb{E}\left(N_{j_m} \mid \bar{w}_{j_m}\right) &= N(1-\bar{s}_M)\bar{\gamma}_m, \\
&= N\left(1-\sum_{k=1}^{M}\bar{w}_{j_k}\right)\frac{w_{j_m}}{\sum_{i=M+1}^{N} w_{j_i}}, \\
&= N\left(\frac{\sum_{n=1}^{N} w_n - \sum_{k=1}^{M} w_{j_k}}{\sum_{n=1}^{N} w_n}\right)\frac{w_{j_m}}{\sum_{i=M+1}^{N} w_{j_i}}, \\
&= N\left(\frac{\sum_{i=M+1}^{N} w_{j_i}}{\sum_{n=1}^{N} w_n}\right)\frac{w_{j_m}}{\sum_{i=M+1}^{N} w_{j_i}}, \\
&= N\frac{w_{j_m}}{\sum_{n=1}^{N} w_n} = N\bar{w}_{j_m}, \qquad (16)
\end{aligned}$$

for all $m > M$. Since $j_m \in \{1, ..., M\}$ are just re-ordered indices, we have proved Eq. (8) or Eq. (15). □

4.2 Variance of the FR scheme

the proposed approach is compatible with any kind of (unbiased) resampling technique. It is well-known that multinomial resampling exhibits the largest variance due to independent sampling, while stratified and systematic resampling reduce the variance by introducing negative dependence among offspring counts, with systematic resampling typically achieving the lowest variance. Let

$$V_N(\bar{w}_1, ..., \bar{w}_N) = V_N(\bar{w}_{1:N})$$

denote the variance of a generic resampling scheme (e.g., multinomial, stratified, or systematic) applied in the second block of Figure 1. The first block of the proposed FR scheme constructs a mixture of two resampling procedures, selected with probabilities $\bar{s}_M$ and $1-\bar{s}_M$, respectively. As a consequence, the overall variance of the FR scheme is given by

$$\text{var-FR} = \bar{s}_M V_M(\bar{w}_{j_1}, ..., \bar{w}_{j_M}) + (1-\bar{s}_M)V_{N-M}(\bar{w}_{j_{M+1}}, ..., \bar{w}_{j_N}), \qquad (17)$$

which is a convex combination of the variances associated with resampling over the two disjoint subsets of particles. As a consequence, we can write

$$\text{var-FR} \leq \max\left[V_M(\bar{w}_{j_1:j_M}), V_{N-M}(\bar{w}_{j_{M+1}:j_N})\right]. \qquad (18)$$

If the employed resampling procedure is such that the variance is super-additive with respect to the particle set, or convex in the number of particles N, we can write var-FR $\leq$ $\max\left[V_M(\bar{w}_{j_1:j_M}), V_{N-M}(\bar{w}_{j_{M+1}:j_N})\right] \leq V_N(\bar{w}_{1:N})$.

4.3 Admissible regions

Key observation. Given a probability mass function (pmf) $\{\bar{w}_n\}_{n=1}^{N}$, the computational cost of resampling according to $\bar{w}_n$ is determined mainly by the number of weights N, which corresponds to the cardinality of the support of the underlying probability mass function. As N increases, the number of resampled realizations and the associated computational burden increase accordingly.

Let us assume that the computational time required for a single resampling step over N particles is $T_{\texttt{tot}} = T_u \cdot \psi(N)$, where T_u is a unit time measure and $\psi(\cdot) : \mathbb{N} \to \mathbb{R}^+$ is a positive increasing function of the number of particles. The simplest case is $\psi(N) = N$ and, in that case, we are assuming linear scaling with respect to N of the computational time required by the chosen resampling procedure. More specifically, in a resampling context, the computational cost typically involves global operations (whose complexity depends on the total number of particles), the function $\psi(N)$ is at least additive and may exhibit super-additive behavior, i.e., $\psi(a+b) \geq \psi(a) + \psi(b)$.

The key point is to compute the averaged number of particles that are resampled in the proposed scheme of Table 2. As shown in Figure 1, the proposed FR scheme is composed of two successive resampling steps (in series). In any case, at least one resampling step is performed with two possible outcomes $b_n \in \{0, 1\}$, occurring with probabilities $\bar{s}_M$ and $1 - \bar{s}_M$, respectively, to determine which group is resampled next. If the first group is selected (i.e., $b_n = 1$), a resampling step is carried out over M particles. Conversely, if the second group is selected (i.e., $b_n = 0$), a resampling step is performed over $N - M$ particles. Hence, in the first block, a resampling step over two particles $\{0, 1\}$. In the second block (in series), a resampling step is perform is carried out over M particles (with probability $\bar{s}_M$) or over $N - M$ particles (with probability $1 - \bar{s}_M$). Consequently, the equivalent average number of particles N_{eq} is:

$$\boxed{N_{\texttt{eq}} = \phi(M) = 2 + \bar{s}_M M + (1 - \bar{s}_M)(N - M).} \tag{19}$$

Recall that $\bar{s}_M$ depends also on M hence, choosing M, we have $\bar{s}_M$. We have also denoted the equivalent number of particles N_{eq} as $\phi(M)$ to highlight that is a function of M. Moreover, we desire that the computational time required by the proposed scheme is smaller than $T_{\texttt{tot}} = T_u \cdot \psi(N)$, i.e.,

$$\begin{aligned} T_u \cdot \psi\Big(N_{\texttt{eq}}\Big) = T_u \cdot \psi\Big(2 + \bar{s}_M M + (1 - \bar{s}_M)(N - M)\Big) + \epsilon < T_u \cdot \psi(N), \\ \psi\left(2 + \bar{s}_M M + (1 - \bar{s}_M)(N - M)\right) + \epsilon < \psi(N), \end{aligned} \tag{20}$$

where $\epsilon > 0$ is the time wasted in all the tasks due to: (a) sort the weights, (b) split properly the particles in two groups and (c) the rest of required code to perform the proposed scheme.[2]

4.3.1 Feasible regions

Assuming that the wasted time ϵ in Eq. (20) is negligible, i.e., $\epsilon \approx 0$, and recalling the $\psi(\cdot)$ is monotonic increasing (and hence invertible), we have

$$\psi\left(2 + \bar{s}_M M + (1 - \bar{s}_M)(N - M)\right) < \psi(N), \tag{21}$$

$$\underbrace{2 + \bar{s}_M M + (1 - \bar{s}_M)(N - M)}_{N_{\text{eq}} = \phi(M)} < N. \tag{22}$$

Then, after some algebra, we obtain

$$\begin{aligned} &2 + \bar{s}_M M + (1 - \bar{s}_M)(N - M) < N, \\ &2 + N - \bar{s}_M N - M + 2\bar{s}_M M < N, \\ &2 - \bar{s}_M N - M + 2\bar{s}_M M < 0, \\ &\bar{s}_M(2M - N) < M - 2. \end{aligned} \tag{23}$$

Then, finally we obtain the two conditions:

$$\Rightarrow \boxed{\text{if } M < N/2 \text{ then } \bar{s}_M > \bar{u} = \frac{M-2}{2M-N},} \tag{24}$$

$$\Rightarrow \boxed{\text{if } M > N/2 \text{ then } \bar{s}_M < \bar{u} = \frac{M-2}{2M-N}.} \tag{25}$$

Recalling that $0 < \bar{s}_M < 1$ and $\bar{s}_M$ depends on M (with $M < N$), the inequalities above define the *admissible regions* of pairs $\{\bar{s}_M, M\}$ with the assumption $\epsilon \approx 0$, such that we have an improvement in terms of the computational time using the proposed FR method with respect a resampling scheme directly over the N weighted particles. The threshold $\bar{u} = \frac{M-2}{2M-N}$ is analyzed in Appendix A. Fixing N, some examples of the threshold $\bar{u} = \frac{M-2}{2M-N}$ as function of M, are shown in Figure 8 in red solid line. The main results given in Appendix A are summarized below.

Remark 5. Fixing N, the threshold $\bar{u} = \frac{M-2}{2M-N}$ is a decreasing function of M for $M < N/2$, and is an increasing function of M for $M > N/2$. See the red lines in Figure 8.

[2]One might argue that, instead of using $\psi\left(N_{\text{eq}}\right)$, a more accurate expression would be $\psi(2) + \psi\left(\bar{s}_M M + (1 - \bar{s}_M)\left(N - M\right)\right)$. However, in the context of resampling, it is reasonable to assume that the function ψ is superadditive, i.e., $\psi(a + b) \geq \psi(a) + \psi(b)$. Under this assumption, the latter expression provides a lower bound, and $\psi\left(N_{\text{eq}}\right)$ constitutes a conservative estimate of the associated computational cost.

Remark 6. At $M = N/2$, the threshold $\bar{u} = \frac{M-2}{2M-N}$ (as function of M) presents a vertical asymptote. More precisely, $\lim_{M \to N/2^-} \bar{u} = -\infty$, and $\lim_{M \to N/2^+} \bar{u} = \infty$. Since $0 \leq \bar{s}_M \leq 1$, both conditions (24)-25 are fulfilled. Hence, the pair $\{\bar{s}_M, M = N/2\}$ (and $N > 4$) is always admissible for any value of $\bar{s}_M$. Consequently, the proposed FR scheme is always beneficial in this scenario.

Remark 7. As $N \to \infty$, the threshold $\bar{u} = \frac{M-2}{2M-N}$ (versus M) falls below 0 for $M < N/2$ and exceeds 1 for $M > N/2$. Since $\bar{s}_M \in [0, 1]$, conditions (24)-(25) are asymptotically satisfied, and all pairs $\{\bar{s}_M, M\}$ become admissible as $N \to \infty$, making the proposed scheme always beneficial.

This last result ensures that the proposed FR method is always computationally advantageous as the total number of particles N increases. The previous two Remarks 5 and 6 indicate that selecting M close to $N/2$ places the method in a safe operating region, since for virtually any $\bar{s}_M$ the proposed scheme is computationally beneficial. Furthermore, there are scenarios where the FR method exhibits particularly high efficiency, beyond being simply beneficial, as we discuss below.

4.4 Extreme and best scenarios

In some scenarios, the FR method is not only beneficial but also highly efficient. Let us introduce the concept of effective sample size (ESS) using the classical definition [31, 12, 29]:

$$\text{ESS} = \frac{1}{\sum_{n=1}^{N} \bar{w}_n^2},$$

where $1 \leq \text{ESS} \leq N$. The ESS measure attains its minimum value, 1 , when a single particle carries all the mass, i.e., $\bar{w}_n = 1$ for one particle and zero for all others [31, 12, 29]. Conversely, the ESS measure reaches its maximum value, N, when the weights are uniform, i.e., $\bar{w}_n = \frac{1}{N}$ for all $n = 1, \ldots, N$. Namely, the ESS reaches its minimum when the entire probability mass is concentrated on a single particle, and reaches its maximum when all particles are equally weighted.

Remark 8. The proposed FR scheme provides particularly good performance when the ESS value is small.

Extreme favorable case. In fact, we can assert that the best (extreme) scenario for the proposed technique is when just one particle concentrates all the probability mass, i.e., minimum possible ESS value. In this case, we can create two groups one with the unique particle with normalized weight 1 (hence, we set $M = 1$ and we have $\bar{s}_1 = 1$) and, the second group with the rest of $N - 1$ particles with all the zero weights (and, hence, $1 - \bar{s}_1 = 0$). Indeed, recall that the weights are

ordered in decreasing order, so that we have:

$$\bar{w}_{j_1} = 1 > \bar{w}_{j_2} = \bar{w}_{j_3} ... = \bar{w}_{j_N} = 0, \tag{26}$$

Setting $M = 1$, the first group is formed by only one particle with weight $\bar{w}_{j_1} = 1$ and $\bar{s}_1 = 1$, as shown in Figure 2. In this case, we have $N_{\mathtt{eq}} = 2+1 = 3$ regardless the total of number of particles N (hence, N *can even diverges and* $N_{\mathtt{eq}} = 3$). Actually it is even less than 3, since the second resampling stage must not be performed because only one particle is contained in the first group (hence, we have a deterministic choice). The second group will be never chosen since $1 - s_1 = 0$.

Other related scenarios. Let us consider that $M < N$ particles over the N total particles concentrate all the probability mass. Thus, we have

$$\bar{w}_{j_1} = \bar{w}_{j_2} = ... \bar{w}_{j_M} = \frac{1}{M} > \bar{w}_{j_{M+1}} = \bar{w}_{j_{M+2}} ... = \bar{w}_{j_N} = 0. \tag{27}$$

Note that ESS $= M < N$ in this case [31, 29]. Dividing the two group considering the first M samples, so that $\bar{s}_M = 1$, and the second group considering the remaining $N - M$ samples with zero weights $(1 - \bar{s}_M = 0)$, the proposed FR scheme works over an equivalent number of particles $N_{\mathtt{eq}} = 2 + M$ instead of N. Thus, if $M + 2 < N$ we have a computational benefit.

Remark 9. Note that the resampling steps with particle filters and SMC schemes are required exactly when the ESS is small. Indeed, after a few iterations, most particles have negligible weights, while only a small fraction contributes meaningfully to the posterior approximation (a.k.a., particle degeneracy). This leads to an inefficient use of computational resources and poor representation of the target distribution. Hence, we have the coincidence/agreement between the optimal scenarios for the proposed FR algorithm and the need of resampling steps with SMC methods.

4.5 Optimal and good choices of M

In this section, we begin by defining the optimal value of M (or $\bar{s}_M$), and then examine how it can be approximated in practice.

Remark 10. We emphasize that the proposed FR scheme does not depend on an optimal tuning of M. The method remains effective over a wide range of M values, as demonstrated in the previous sections.

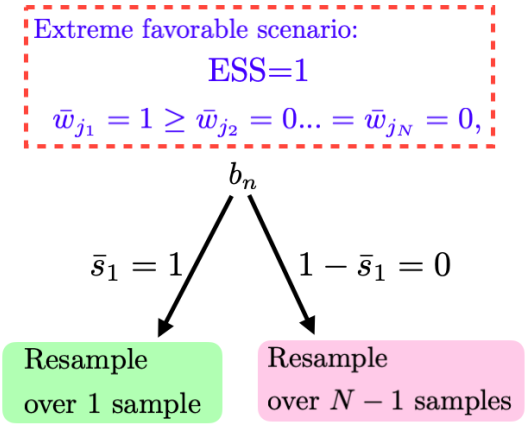


Figure 2: Graphical representation of the application of the FR scheme when the effective sample size (ESS) reaches its minimum, 1 (only one sample). Using $M = 1$, the proposed FR method is extremely fast in this case. Instead of resampling/bootstrapping over N particles, the resampling is performed over $N_{\text{eq}} = 3$. Note that The ESS is small when a particle filter suffers the so-called *particle degeneracy* (most particles have negligible weights) and that is when exactly a particle filter needs a resampling step.

4.5.1 Optimality

We should minimize the function $\phi(M) : [1, N) \to \mathbb{R}^+$,

$$\phi(M) = 2 + \bar{s}_M M + (1 - \bar{s}_M)(N - M), \tag{28}$$

$$= 2 + \left(\sum_{k=1}^{M} \bar{w}_{j_k} \right) M + \left(1 - \sum_{k=1}^{M} \bar{w}_{j_k} \right) (N - M) > 0. \tag{29}$$

The function above is positive since $1 \leq M < N$ and $0 \leq \bar{w}_{j_k} \leq 1$, $\sum_{n=1}^{N} \bar{w}_n = 1$. The optimal M^* is defined as

$$M^* = \arg\min \phi(M) = \arg\min \Big[2 + \bar{s}_M M + (1 - \bar{s}_M)(N - M) \Big], \quad \text{with } M \in [1, N). \tag{30}$$

Treating M as continuous variable and computing the first derivative $\frac{d\phi}{dM} = \phi'(M)$ and equalling to zero, we obtain

$$\begin{aligned}\frac{d\phi}{dM} = \phi'(M) &= \bar{s}_M + M\bar{s}'_M - (1-\bar{s}_M) - (N-M)\bar{s}'_M = 0,\\ &= -1 + 2\bar{s}_M + (2M-N)\bar{s}'_M = 0.\end{aligned}$$

Hence, any interior minimum within $M^* \in [1, N)$ satisfies

$$\boxed{\bar{s}'_{M^*} = \frac{2\bar{s}_{M^*} - 1}{2M^* - N}.} \tag{31}$$

As in Eqs. (24)- (25), at $M^* = N/2$, the denominator is zero.
The analytical optimization is not straightforward, but additional general considerations can be done. Observe that the function $\phi(M)$ is formed by two pieces:

$$\phi(M) = 2 + \underbrace{\bar{s}_M M}_{\texttt{strict. inc.}\uparrow} + \underbrace{(1-\bar{s}_M)(N-M)}_{\texttt{strict. dec.}\downarrow}.$$

We have a *positive, strictly increasing* part $f_i(M) = \bar{s}_M M > 0$ and a *positive, strictly decreasing* part $f_d(M) = (1-\bar{s}_M)(N-M) > 0$. Thus, we can write

$$\phi(M) = 2 + f_i(M) + f_d(M). \tag{32}$$

Both functions are positive since $\bar{s}_M \in (0, 1]$ and $0 < M < N$. The first function $f_i(M) = \bar{s}_M M$ is strictly increasing since both factors $\bar{s}_M$ and M increase as M grows. The second function $f_d(M) = (1-\bar{s}_M)(N-M)$ is strictly decreasing since both factors $1-\bar{s}_M$ and $N-M$ decrease as M grows. Moreover, $\lim_{M\to\infty} f_d(M) = 0$ and for each possible M they take finite values, $f_i(M) < \infty$, $f_d(M) < \infty$. Hence, by treating M as continuous variable, we have $f'_i(M) = \frac{df_i}{dM} > 0$ and $f'_d(M) = \frac{df_d}{dM} < 0$. Thus, we can also write

$$\phi'(M) = \underbrace{f'_i(M)}_{>0} + \underbrace{f'_d(M)}_{<0} = 0 \Longrightarrow f'_i(M^*) = -f'_d(M^*). \tag{33}$$

Additionally, the following properties hold.

Theorem 2. If $f''_i(M) \geq 0$ and $f''_d(M) \geq 0$ are convex, the function $\phi(M)$ has at most one global minimum. Namely, the function cannot $\phi(M)$ have two (or more) distinct, separated, minima.
Proof. Given the assumptions, $\phi''(M) = f''_i(M) + f''_d(M) \geq 0$, then $\phi(M)$ is convex. A convex function has at most one global minimum. □

With the previous assumptions, flat regions are possible. Adding the strictly convexity condition, we can ensure stronger statements, as shown below.

Theorem 3. if $f_i''(M) > 0$ and $f_d''(M) > 0$, i.e., they are strictly convex, if the optimal value M^* exists, it is unique. Namely, $\phi(M)$ has either no stationary point or exactly one and, in this case, it is a global minimum.
Proof. Given the assumptions, $\phi''(M) = f_i''(M) + f_d''(M) > 0$, so that $\phi(M)$ is strictly convex. Hence, if $\phi(M)$ has a stationary point, it is a unique global minimum. □

4.5.2 Adequate choices of M

It is not straightforward to compute analytically the optimal value M^*, or $\bar{s}_M^* = \bar{s}_{M^*}$. Notably, the proposed FR scheme does not require fine tuning of M and maintains good performance across a broad range of values, as confirmed in the previous sections. Some possible good choices of M are described below.

A first proxy $\widehat{M}_1$. A suitable choice of M can be obtained finding the point where the functions $f_i(M) = \bar{s}_M M$ and $f_d(M) = (1 - \bar{s}_M)(N - M)$ are equal, i.e., $f_i(M) = f_d(M)$. Hence,

$$\begin{aligned}
&\bar{s}_M M = (1 - \bar{s}_M)(N - M) \\
&\bar{s}_M M - (1 - \bar{s}_M)(N - M) = 0 \\
&\bar{s}_M M + (\bar{s}_M - 1)N + M - \bar{s}_M M = 0 \\
&(\bar{s}_M - 1)N + M = 0,
\end{aligned} \tag{34}$$

so that

$$\begin{cases}
\widehat{M}_1 = \lceil (1 - \widehat{s}_M)N \rceil, \\
\bar{s}_{M_1} = \dfrac{N - \widehat{M}_1}{N},
\end{cases} \tag{35}$$

where we have denoted as $\lceil a \rceil$ the ceiling function of a value a, i.e., the least integer greater than or equal to a. See Figure 3 for two graphical examples. The computation of $\widehat{M}_1$ is still not straightforward since both equations in (35) must be fulfilled jointly. To obtain $\widehat{M}_1$, we should increase M until reaching $\bar{s}_M = \sum_{k=1}^{M} \bar{w}_{j_k} \approx \frac{N-M}{N}$.

Remark 11. The choice $\widehat{M}_1$ in (35) provides often good performance for small N, or for linear decays of the ordered weights $\bar{w}_{j_n}$ in Eq (9). See the numerical simulations in Section 5.2.

A more useful alternative is given below.

A second proxy $\widehat{M}_2$. We have empirically found that the number of normalized weights bigger or equal to $\frac{1}{N}$, i.e.,

$$\widehat{M}_2 = \text{N-plus} = \#\left\{\bar{w}_n \geq 1/N, \quad \forall n = 1, \ldots, N\right\}, \tag{36}$$

is a good proxy for M^*. We have highlighted above that $\widehat{M}_2$ coincides with an ESS measure introduced in [31] and denoted as N-plus (or N^+). See Section 5.2, for some related numerical results.

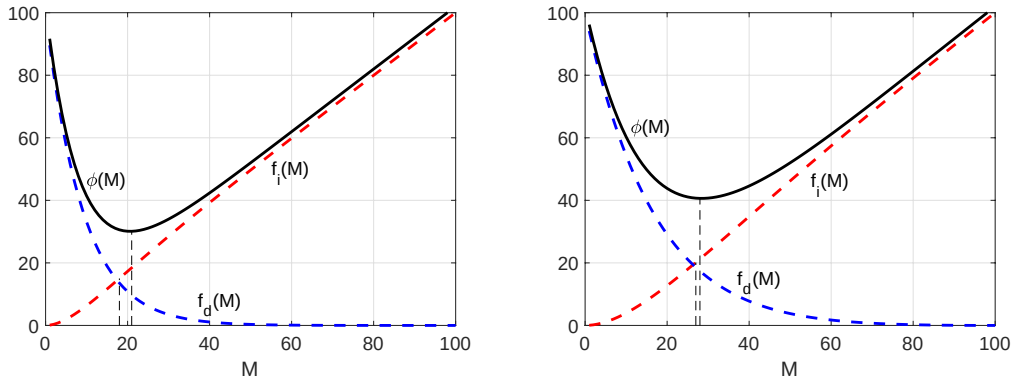


Figure 3: Graphical examples of the functions ϕ, f_i and f_d. The unnormalized weights are chosen as $w_n = \exp(-0.1n)$ in **(a)**, and $w_n = \exp(-0.05n)$ in **(b)**. The number of particle is $N = 100$. The first proxy and true optimal values are $\widehat{M}_1 = 18$, $M^* = 21$ in **(a)** and $\widehat{M}_1 = 27$, $M^* = 28$ in **(b)**.

5 Numerical simulations

In this section, we compare the proposed FR and the SR approaches in different scenarios. In Section 5.1, we consider different ESS frameworks, and test the proposed method varying the values of N and M. In a second experiment (Section 5.2). we study the behavior of the proxies

$\widehat{M}_1$ and $\widehat{M}_2$. The use within a particle filter is analyzed in Section 5.3. Related Matlab code is available at `http://www.lucamartino.altervista.org/FAST_RESAMPLING_public_code.zip`.

5.1 First experiment

In this section, the weights are constructed as

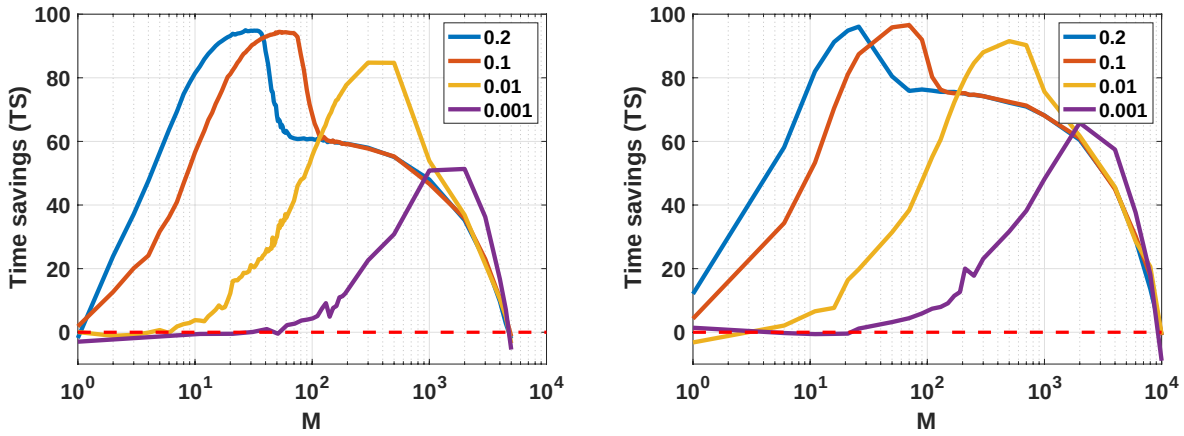
$$w_n = \exp(-\beta n), \qquad \beta > 0, \tag{37}$$

with $n = 1, ..., N$. Then, we compute $\bar{w}_n = \frac{w_n}{\sum_{i=1}^{N} w_i}$. We remark that even the weights are already sorted in decreasing order by construction, we perform the sorting procedure in the code (i.e., we apply the command '`sort`') in order to obtain a fair comparison with the standard resampling (SR) scheme. Note that as $\beta \to 0$ the ESS grows converging to its maximum value, that is N. Otherwise, if $\beta \to \infty$, the ESS decreases converging to its minimum value, that is 1 [31, 12, 29]. We test four values of $\beta\{0.001, 0.01, 0.1, 0.2\}$. We apply the proposed FR and SR and compute the percentage of time savings (TS), i.e.,

$$\mathrm{TS} = \begin{cases} \left(1 - \dfrac{\mathrm{time}(\mathtt{FR})}{\mathrm{time}(\mathtt{SR})}\right) 100. & \text{if} \quad \mathrm{time}(\mathtt{SR}) \geq \mathrm{time}(\mathtt{FR}), \\ -\left(1 - \dfrac{\mathrm{time}(\mathtt{SR})}{\mathrm{time}(\mathtt{FR})}\right) 100, & \text{if} \quad \mathrm{time}(\mathtt{SR}) < \mathrm{time}(\mathtt{FR}). \end{cases} \tag{38}$$

We have that $-100\% \leq \mathrm{TS} \leq 100\%$. Positive values of TS mean that FR is faster than SR, otherwise negative values mean that SR is faster than FR. Note that a value of $\mathrm{TS} = 100\%$ would mean that FR is extremely faster (virtually instantaneous, since $\mathrm{time}(\mathtt{FR}) = 0$). The results are averaged over 10^3 runs.

Fixing N and vary M. First of all, we fix $N \in \{5000, 10000\}$ and vary the value of M (from $M = 1$ to $M = N - 1$). The results are given in Figure 4, using a log-log-domain. The TS values are virtually always positive, thereby demonstrating the advantage of the proposed scheme. As expected, generally greater values of β provide the best results. Again as expected, Figure 4(b) corresponding to a bigger value of $N = 10^4$ depicts curves closer to 100% than Figure 4(a). Moreover, the optimal value of M, corresponding to the peaks of the curves, grows as the ESS increases (i.e., β decreases), as expected. It is important to emphasize that the values around the peaks for $\beta \in \{0.01, 0.1, 0.2\}$ are very close to the maximum possible time saving of 100%.
Fixing M and vary N. Here, we fix $M \in \{5, 20, 200\}$ (testing 3 different values) and change the number of particles N from $N = 250$ to $N = 30000$. We also consider the four different β values, i.e., $\beta \in \{0.001, 0.01, 0.1, 0.2\}$. The time savings (TS) are provided in Figure 5 (using a



(a) $N = 5000$. (b) $N = 10000$.

Figure 4: Percentage of time savings (TS) versus M in a log domain in the x-axis: **(a)** with $N = 5000$ and **(b)** with $N = 10000$. In both cases, we have a quite great value of number of particles $N \in \{5000, 10000\}$. In these scenarios, we have a positive TS almost for all values of M.

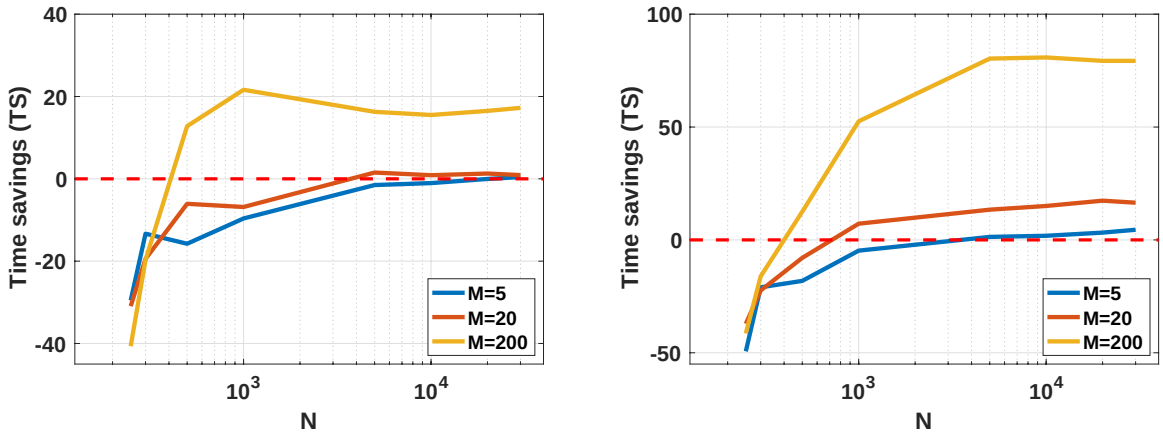
log-log-domain). As N grows, the TS values become positive for all values of M and β, confirming the benefits of the proposed scheme for great values of N. Moreover, as N grows, all the values of M seems feasible. As expected, smaller values of β (then we have bigger ESS values) requires bigger values of M. As N and β grows better results are provided, obtaining TS values close to 100%, as shown in Figure 5(d). As expected, as β grows (then we have smaller ESS values), the smaller values M work better for almost any N.

5.2 Second Experiment: behaviors of $\widehat{M}_1$ and $\widehat{M}_2$

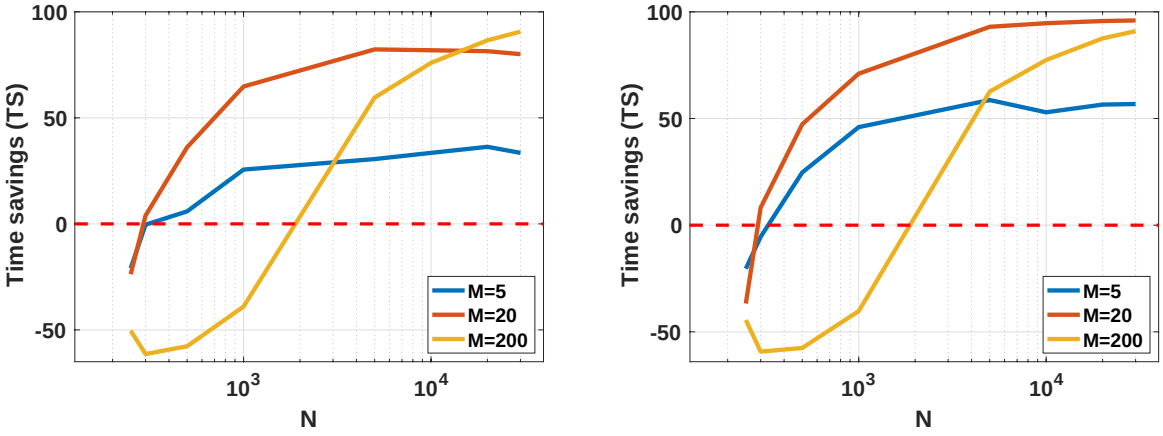
In this section, we consider different construction of the weights,

$$\begin{aligned} \textbf{first type:} \quad & w_n = \exp(-\beta n), \\ \textbf{second type:} \quad & w_n = 1 - \frac{1}{N} n, \\ \textbf{third type:} \quad & w_n = 1/n^{\alpha}, \end{aligned} \tag{39}$$

for $n = 1, ..., N$. Then, we set $\bar{w}_n = \frac{w_n}{\sum_{i=1}^{N} w_i}$ for all cases. We test different β and α, more precisely, $\beta \in \{0.001, 0.01, 0.1, 0.2\}$ and $\alpha \in \{1, 2, 3\}$. We remark again that even the weights are already sorted in decreasing order by construction, we perform the sorting procedure in the code (i.e., we apply the command '`sort`') in order to obtain a fair comparison with the standard resampling



(a) $\beta = 0.001$. (b) $\beta = 0.01$.

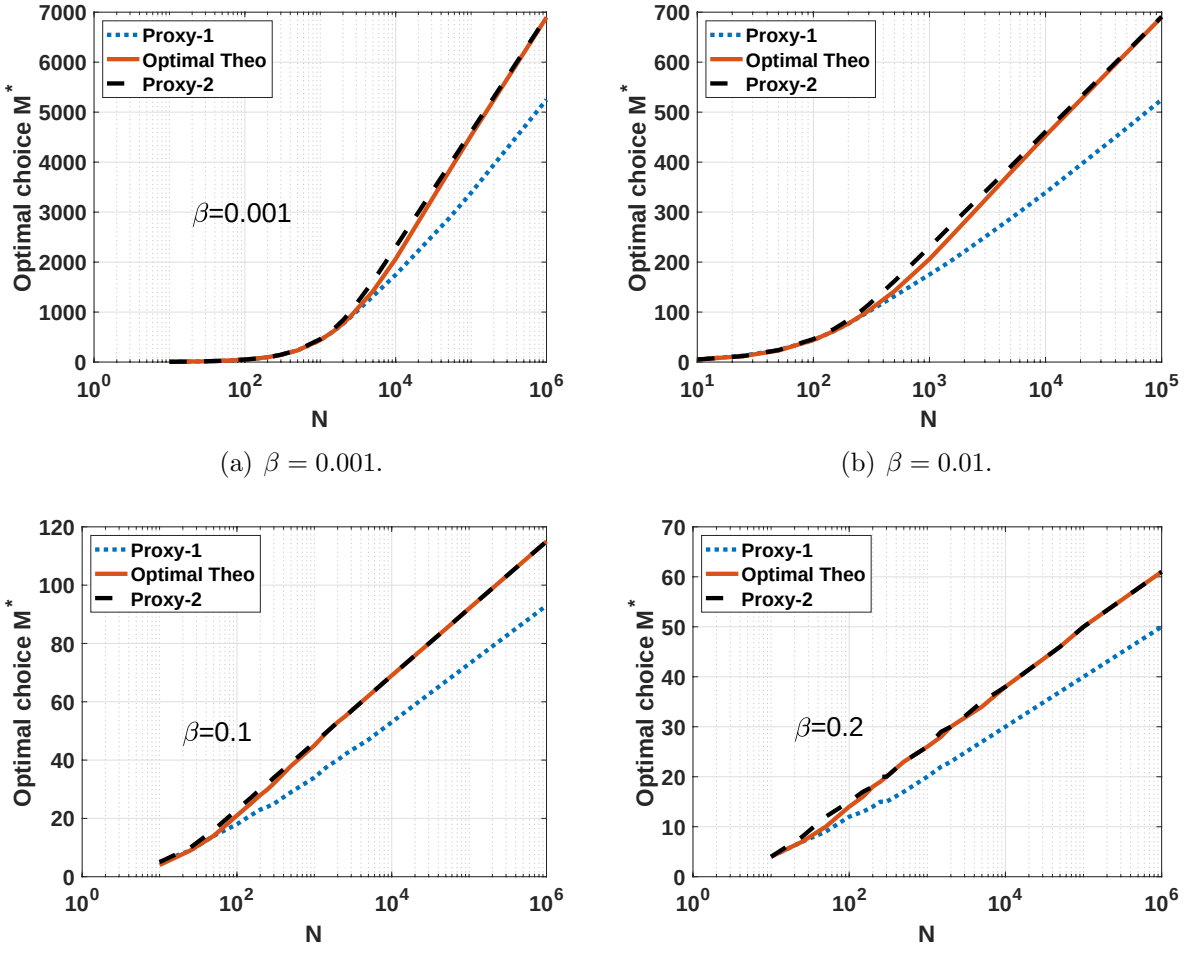


(c) $\beta = 0.1$. (d) $\beta = 0.2$.

Figure 5: Percentage of time savings (TS) versus N in a log domain in the x-axis. We test 3 different values of M, i.e., $M \in \{5, 20, 200\}$ (represented by the 3 different curves in each figure). We also consider $\beta \in \{0.001, 0.01, 0.1, 0.2\}$, each value corresponding to a figure.

(SR) scheme.

The results are provided in Figures 6 and 7. They show the curves versus N of the optimal value M^* (continuous red line), the proxy $\widehat{M}_1$ in Eq. (35) (dotted blue line), and the proxy $\widehat{M}_2$ in Eq. (36) (dashed red line), for the different the weight constructions. The proxy $\widehat{M}_2$ is an excellent



(a) $\beta = 0.001$.

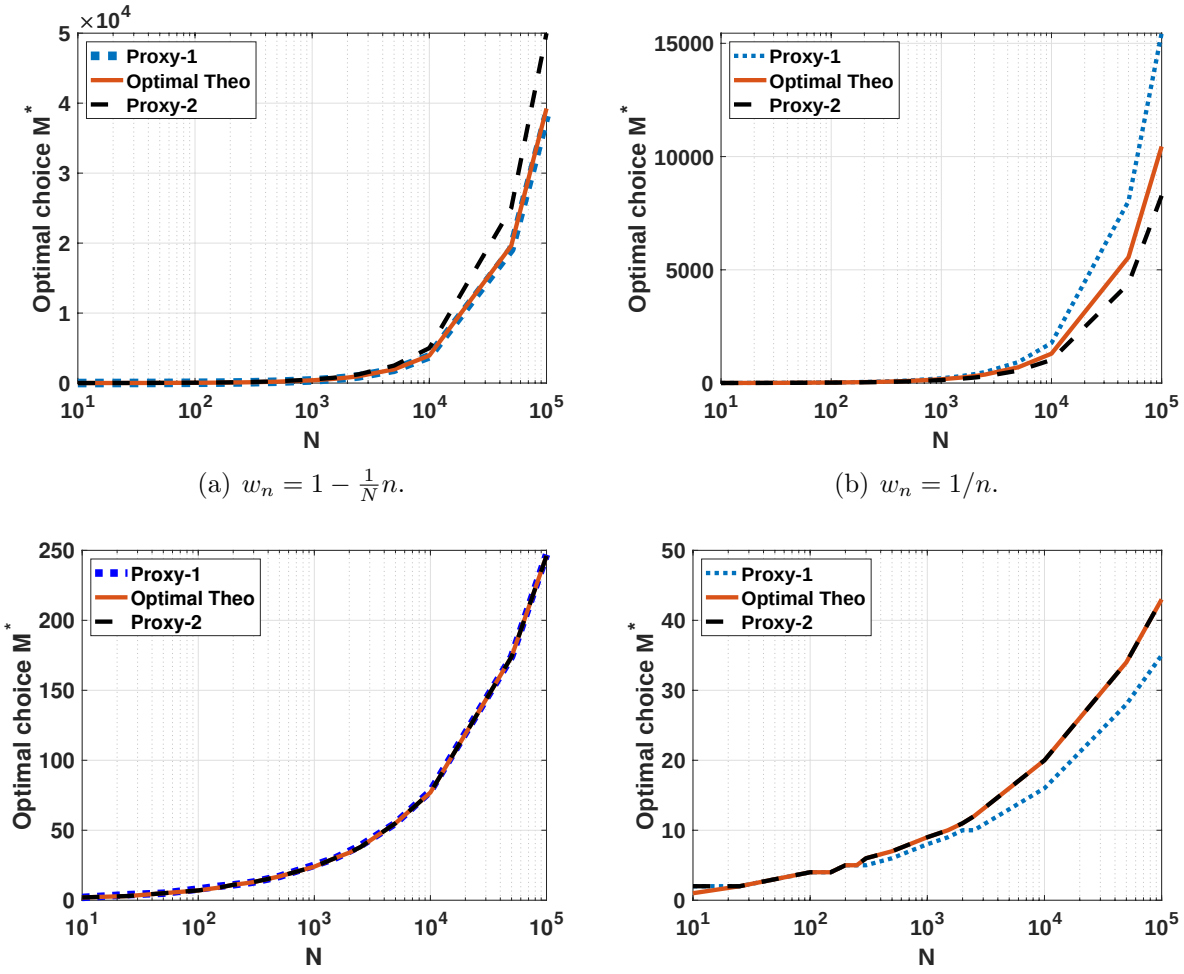
(b) $\beta = 0.01$.

(c) $\beta = 0.1$.

(d) $\beta = 0.2$.

Figure 6: The curves (versus N) of the optimal value M^* in continuous red line, the proxy $\widehat{M}_1$ in dotted blue line, and the proxy $\widehat{M}_2$ in dashed red line, for the exponential weight construction with $\beta \in \{0.001, 0.01, 0.1, 0.2\}$. We can note that $\widehat{M}_2$ is an excellent approximation of M^* in all cases.

approximation of M^*, for all values of N, in all the scenarios in Figures 6(a)-6(b)-6(c)-6(d) and Figures 7(c)-7(d). Whereas the proxy $\widehat{M}_2$ shows some difficulties in the scenarios Figures 7(a)-7(b) for great values of N, However, overall it provides a good approximation of M^*, for all values of



(a) $w_n = 1 - \frac{1}{N}n$. (b) $w_n = 1/n$.

(c) $w_n = 1/n^2$. (d) $w_n = 1/n^3$.

Figure 7: The curves (versus N) of the optimal value M^* in continuous red line, the proxy $\widehat{M}_1$ in dotted blue line, and the proxy $\widehat{M}_2$ in dashed red line, for the weight constructions $w_n = 1 - \frac{1}{N}n$ and $w_n = 1/n^\alpha$ with $\alpha \in \{1, 2, 3\}$. The proxy $\widehat{M}_2$ shows some difficulties in the scenarios (a) and (b) for great values of N, but overall it provides a good approximation of M^*, in all cases. For instance, $\widehat{M}_2$ provides virtually a perfect match in cases (c) and (d).

N. The proxy $\widehat{M}_1$ works well only for small values of N and in Figure 7(c) (corresponding to the

construction $w_n = 1/n$). For this reason, we suggest the use of $\widehat{M}_2$.

5.3 Particle filtering for a stochastic volatility model

In this example, we test the SR and the proposed FR within a particle filter (a.k.a., sequential Monte Carlo). We consider a stochastic volatility model where the hidden state θ_t follows an auto-regressive process and represents the log-volatility [19] of a time series at time $t \in \mathbb{N}$, i.e.,

$$\begin{cases} \theta_t = \alpha\theta_{t-1} + u_t, \\ y_t = \exp\left(\frac{\theta_t}{2}\right) v_t, \end{cases} \qquad t = 1, \dots, T. \tag{40}$$

where $\alpha = 0.99$, and u_t and v_t are Gaussian independent noises, with zero-mean with variances $\sigma_u^2 = 1$ and $\sigma_v^2 = 0.5$, respectively. Note that u_t is an additive noise, whereas v_t is a multiplicative noise. We implement a standard particle filter (PF) [7, 10, 16] using as propagation equation of the particles exactly the auto-regressive process of the true model, i.e., the next generation of particles $\theta_{i,t}$'s is generated as $\theta_{i,t} \sim \mathcal{N}(\theta|\alpha\theta_{i,t-1}, \sigma_u^2)$, where $i = 1, \dots, N$ is the particle index. The application of the resampling is adaptively decided according to ESS (see below). We set $T = 100$ and simulate a run of the series θ_t and y_t according to the model in Eq. (40), starting from $\theta_0 = 0$. Given, the generated data y_t, we run a particle filter with different values of numbers of particles N.

The resampling is performed adaptively, only a certain iterations. More specifically, the resampling is applied at the iteration t such that

$$\mathrm{ESS}(t) = \frac{1}{\sum_{n=1}^{N} \bar{w}_{n,t}^2} \leq \epsilon N \tag{41}$$

where $\epsilon \in [0, 1]$ is a constant threshold value (with $\epsilon = 0$, no resampling step is performed; with $\epsilon = 1$, the resampling is applied at each iteration). We set $\epsilon = 0.75$. Note that we have used the classical definition of ESS [31, 12, 29]. In one specific run, we can define the resampling rate as the number of time steps where you perform resampling divided by T, i.e.,

$$\text{res-rate} = \frac{\#\ \text{Resampling}}{T}.$$

In the proposed FR scheme we employ the proxy $\widehat{M}_2$ as choice for M. Thus, we run 100 independent particle filters using SR and FR, and calculate the averaged, required computational time. More precisely, we also compute the normalized rate of time savings (TS) in Eq. 38. We recall that $-100\% \leq \mathrm{TS} \leq 100\%$ Positive values of TS mean that FR is faster than SR,

otherwise negative values mean that SR is faster than FR. In this experiment, we also compute the percentage of time increase (TI) using SR instead of the proposed FR, i.e.,

$$\mathrm{TI} = \frac{\mathrm{time}(\texttt{SR})}{\mathrm{time}(\texttt{FR})} 100. \tag{42}$$

The results are given in Table 3. The average res-rate was ≈ 0.47, i.e., the resampling step was performed in almost half of the iterations. The reported time values naturally depend on the computational resources (here, a laptop) used to perform the experiment. However, the relevant information are the rates of time savings. We can observe that with FR, we save about 60% of the computational time when using a large number of particles N. For instance, with a million of particles ($N = 10^6$), we spend around 10 hours instead an entire day (more than 23 hours).

Table 3: Time (seconds; in the first row) required for executing the particle filters with different number of particles N. The actual time values clearly depend on the specific machine (laptop) employed for running the experiment. The relevant values are the percentages of time increase using SR in Eq. (42), and time savings (TS) obtained using FR instead SR, defined as in Eq. (38).

N	10^3	$5 \cdot 10^3$	10^4	$5 \cdot 10^4$	10^5	$2 \cdot 10^5$	10^6
time(SR)	0.08 s.	1.47 s.	4.70 s.	87.07 s. 1:27 min.	360.9 s. 06:01 min.	1573.8 s. 26:13 min	83801.2 s. 23:16:41 h.
time(FR)	0.06 s.	0.94 s.	2.44 s.	39.86 s.	149.8 s. 02:29 min.	600.7 s. 10:01 min	34133.2 s. 09:28:53 h.
$\frac{\mathrm{time}(\texttt{SR})}{\mathrm{time}(\texttt{FR})}\%$	133.3%	156.4%	192.6%	218.5%	241.0%	262.0%	245.5%
Time savings (TS)	25%	36.05%	48.09%	54.22%	58.49%	61.83%	59.26%

6 Conclusions

In this work, we propose a novel resampling scheme that outperforms existing techniques in terms of speed when a large number of particles is used. The new fast resampling (FR) method is based on the division of the particles into two groups: a first set with M most weighted particles, and a second group with the rest of $N - M$ particles. The proposed algorithm is highly efficient when the first group contains only a small number of particles M but capturing a significant probability mass. This occurs when the effective sample size (ESS) is small, which is precisely the situation

in which resampling becomes necessary in particle filtering/SMC methods. The novel scheme is compatible with all the resampling approaches, including multinomial, stratified, systematic, and residual, to name a few. We have theoretically analyzed the proposed resampling scheme (a) by verifying the validity of the proper-weighting condition, (b) obtaining bounds for the variance, (c) characterizing the feasible regions, and (d) discussing the optimal choice of M^*. We have also found a good approximation of M^*, denoted as $\widehat{M}_2$. Thus, the resulting method is fully automatic, as the choice of M is determined directly by the algorithm.
The behavior of the proposed FR scheme have been widely analyzed in different numerical scenarios. The numerical results confirm that FR is convenient for large values of N and small ESS values. Remarkable results have been obtained within a particle filter in which resampling is applied in approximately half of the iterations (10 hours instead of approximately 1 day of computation). Clearly, the more resampling steps are performed, the greater the advantages provided by the proposed FR procedure. The corresponding (non-optimized) Matlab code is also made available for reproducibility at `http://www.lucamartino.altervista.org/FAST_RESAMPLING_public_code.zip`.

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A Properties of the threshold $\bar{u}$

Interesting considerations are given below.

Property 1. Fixing N, $\bar{u} = \frac{M-2}{2M-N}$ is always a decreasing function of M, with a vertical asymptote at $M = N/2$. For $M < N/2$, it starts with the value $\bar{u} = \frac{1}{N-2}$ at $M = 1$, and tends to $-\infty$ at $M \to \frac{N}{2}^-$. Whereas, for $M > N/2$, the function $\bar{u} = \frac{M-2}{2M-N}$ decreases from $+\infty$ at $M \to \frac{N}{2}^+$ until $1/2$ for $M \to \infty$ (i.e., there is an horizontal asymptote for $M \to \infty$). More precisely,

$$\lim_{M \to \frac{N}{2}^-} \bar{u} = -\infty, \qquad \lim_{M \to \frac{N}{2}^+} \bar{u} = \infty, \quad \text{for all } N. \tag{43}$$

See Figure 8.

Property 2. Note that, for the decreasing property of $\bar{u}$, we have: for $M < N/2$, the value of $\bar{u}$ at $M = 1$ is the maximum value, $\frac{1}{N-2} > \frac{M-2}{2M-N}$. For $M > N/2$, the value of $\bar{u}$ at $M = N - 1$, i.e., $\frac{N-3}{N-2}$, is the minimum value (considering $M = N - 1$ the maximum value of M). Hence, we have $\bar{u} = \frac{M-2}{2M-N} > \frac{N-3}{N-2}$. As summary, we have

$$\bar{u} = \frac{M-2}{2M-N} < \frac{1}{N-2}, \quad \text{for } M < N/2, \tag{44}$$

$$\bar{u} = \frac{M-2}{2M-N} > \frac{N-3}{N-2}, \quad \text{for } M > N/2. \tag{45}$$

Property 3. The first threshold value $\bar{u} = \frac{1}{N-2}$ (at $M = 1$) vanishes to zero, as $N \to \infty$. The last value $\bar{u} = \frac{N-3}{N-2}$ (at $M = N-1$) tends to 1, as $N \to \infty$. Since $\bar{s}_M \in (0, 1]$ and considering Eqs. (25)-(24) and Property 2 with Eq. (44)-(45) above, this means that any pair $\{\bar{s}_M, M\}$ tend to be feasible as N grows.

Property 4. Let us consider $N > 4$. At $M = \frac{N}{2}$, the threshold value $\bar{u} = \frac{M-2}{2M-N}$ diverges to $\pm\infty$ as shown in Eq.(43), for all N. Thus we always have $\bar{s}_M > \bar{u} \to -\infty$ at $M = \frac{N}{2}^-$ and $\bar{s}_M < \bar{u} \to +\infty$ at $M = \frac{N}{2}^+$. Then, any pair $\{\bar{s}_M, M = \frac{N}{2}\}$ is always feasible.

With $N = 4$ and $M = \frac{N}{2} = 2$, we have indeterminate form $\bar{u} = \frac{0}{0}$. However, replacing $N = 4$ and $M = \frac{N}{2} = 2$ into $\phi(M)$, we obtain $2 + 2\bar{s}_M + 2(1 - \bar{s}_M) = 4$ that is not smaller than 4, then the pairs $\{\bar{s}_M, M = \frac{N}{2} = 2\}$, for a generic $\bar{s}_M$, are all unfeasible. It can be shown that this statement is also valid for $N < 4$. Finally note that, in the overall analysis, we have not considered that the samples are ordered (as in the proposed resampling scheme).

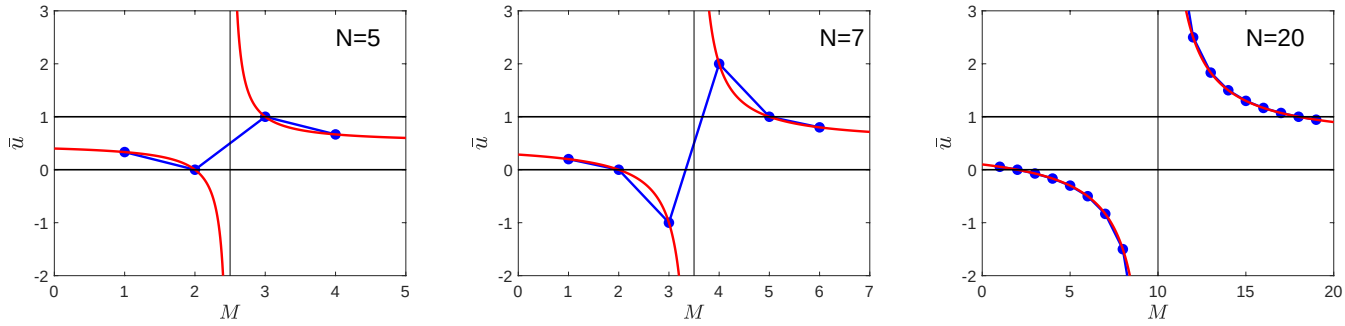

Figure 8: The threshold $\bar{u} = \frac{M-2}{2M-N}$ versus $M = 1, 2, ..., N-1$, for different values of $N \in \{5, 7, 20\}$. The function $\bar{u} = \frac{M-2}{2M-N}$, considering M as a continuous variable, is shown with a red solid line. The blue circles depict the $\bar{u}$-values at the discrete values $M = 1, 2, ..., N-1$ (note that for $N = 6$, at $M = 3$ we have $\bar{u} \to \infty$). Recall that the feasible zones are defined by $\bar{s}_M < \bar{u}$ for $M < N/2$, and $\bar{s}_M > \bar{u}$ for $M > N/2$. Recall also that $\bar{s}_M \in (0, 1]$, hence negative values of $\bar{u}$ for $2M < N$, and values greater than 1, $\bar{u} \geq 1$ for $2M > N$, mean that any value of $\bar{s}_M$ is suitable.

Clearly all these considerations have been done assuming the ideal conditions $\epsilon \approx 0$ in Eq. (20). In a non-ideal and practical scenario, the feasible zones are generally more restricted. See, for instance, Figures 5 in the numerical experiments. However even in real practical scenarios, as N

grows, all the pairs $\{\bar{s}_M, M\}$ tends to be feasible.