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MapReduce Particle Filtering with Exact Resampling and Deterministic Runtime

Jeyarajan Thiyagalingam · Lykourgos Kekempanos · Simon Maskell

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Abstract Particle filtering is a numerical Bayesian technique that has great potential for solving sequential estimation problems involving non-linear and non-Gaussian models. Since the estimation accuracy achieved by particle filters improves as the number of particles increases, it is natural to consider as many particles as possible. MapReduce is a generic programming model that makes it possible to scale a wide variety of algorithms to Big data. However, despite the application of particle filters across many domains, little attention has been devoted to implementing particle filters using MapReduce.

In this paper, we describe an implementation of a particle filter using MapReduce. We focus on a component that what would otherwise be a bottleneck to parallel execution, the resampling component. We devise a new implementation of this component, which requires no approximations, has $O(N)$ spatial complexity and deterministic $O\left((\log N)^2\right)$ time complexity. Results demonstrate the utility of this new component and culminate in consideration of a particle filter with 2^{24} particles being distributed across 512 processor cores.

Keywords MCMC Methods, Particle Filters, Big data Sampling, MapReduce, Resampling.

1 Introduction

Particle filters are a Bayesian Monte-Carlo method that provide a general framework for estimation in response to an incoming stream of data. The key idea is to represent the probability density function (pdf) of the state of a system using random samples (known as particles). These samples are propagated

Department of Electrical Engineering and Electronics,
University of Liverpool, Liverpool, L69 3GJ, UK.
E-mail: {T.Jeyarajan, L.Kekempanos, S.Maskell}@liverpool.ac.uk

across iterations in time in a way that capitalises on an application-specific non-linear, non-Gaussian state-space model. This state-space model describes both the dynamic evolution of the state and the relationship between the state and the measurements. The use of random samples to articulate uncertainty means that particle filters can be applied to a variety of real-world problems without any need to approximate the models used. This is in contrast to alternative techniques (e.g., the Extended Kalman filter, EKF) that approximate the models such that the uncertainty present can be approximated using a parametric probability density (a multivariate Gaussian in the case of an EKF). The result is that a particle filter typically outperforms such alternative techniques in scenarios involving pronounced departures from linear-Gaussian models. Such scenarios are widespread. This is arguably the reason why particle filters, since their inception [17], have been applied successfully in such a diverse range of contexts [14, 18, 37, 41].

Particle filters have the appealing property that, as the number of samples increases, the ability of the samples to represent the pdf increases and the accuracy of estimates derived from the particles improves: an upper-bound on the variance of an estimate scales as $O\left(\frac{1}{N}\right)$. It is therefore natural to seek to use as many particles as possible. However, when the number of samples becomes very large, the samples will not physically fit within the memory space of a single compute node. Big data platforms have been developed to address the generic problem of which this is a special case. These platforms work by identifying abstractions of algorithms that make the potential for parallelism apparent. The platforms (and not the programmer) are then able to exploit the available computational resources to distribute the processing. One popular abstraction is MapReduce (which is described in more detail in section 2.2). Various techniques have been developed to distribute particle filters across multiple processor-cores (see section 7 for the details), but MapReduce has not been used with particle filters extensively (that said, [9] and [10] are counter-examples we are aware of).

The resampling component is a critical component of a particle filter and non-trivial to parallelise. As will be discussed in more detail in section 7, previous approaches to distributing the resampling step have focused on modifying the resampling process with the aim of making it more amenable to distributed implementation. One notable exception exists [33][1] and ensures that the output from the distributed implementation is exactly that output from a single-processor implementation while also ensuring deterministic data transfer and runtime. Such deterministic runtime is important in real-time applications (which are widespread) where the output of the particle filter is used to feed the input of another process, which needs to receive that input within a specified latency.

In this paper, we present an improved parallel implementation strategy for the resampling component, a MapReduce representation of the particle filter (including this resampling component) and instantiate the particle filter in the

[1] Though we are not aware of any empirical analysis of this approach being published.

context of two Big data platforms. In doing so, this paper makes the following key contributions:

- We propose an improved implementation of an exact deterministic resampling algorithm that has better temporal complexity compared to the current state-of-the-art [33]. More specifically, the proposed version of the parallel algorithm has the complexity of $\mathcal{O}((\log_2 N)^2)$ compared to the original complexity of $\mathcal{O}((\log_2 N)^3)$.
- We provide two different MapReduce variants of our new algorithm that fit both with the in-memory processing and out-of-core processing models. These are the processing models used by Hadoop and Spark respectively.
- We perform detailed performance and scalability analysis of our new algorithm in comparison to both the pre-existing state-of-the-art [33] and an implementation optimised for a single processor-core. We deliberately chose an application that stresses the resampling component of the particle filter such that our analysis relates to worst-case performance.

The remainder of this paper is organised as follows: In section 2, we provide a brief overview of Big data processing, and the MapReduce programming model. This is then followed by a detailed description of particle filtering in section 3. In section 4, we describe the fundamental building blocks that are used to construct the implementations of the particle filtering algorithm, including, in section 4.8.2, the new component of the resampling algorithm. We then describe our MapReduce-based particle filtering implementation in section 5. We follow this section with an evaluation of our algorithms on key two MapReduce frameworks in Section 6. Section 7 highlights related work before section 8 concludes.

2 Big data Processing

The focus in this paper is on the problem of using large numbers of samples within a particle filter. Big data processing frameworks (e.g., Apache projects such as: Hadoop [1], Spark [4] and Storm [5][2]) are designed for handling large amounts of data and can therefore be applied in this context[3]. We therefore focus in this paper on using such frameworks in conjunction with parallel computational resources, such as clusters, to handle large volumes of data[4]. In this section, we discuss the use of such Big data frameworks in general and, in

[2] Including the associated ever-growing ecosystem of tools (e.g., Mahout [2] and GraphX for Spark [39]).

[3] Conventional High Performance Computing (HPC) approaches use parallel computations to optimise processing time. We refer the reader to [8] for a good coverage of HPC-bound approaches for parallelising applications.

[4] We anticipate that the 'heat wall' (i.e., the inability to remove enough heat from transistors that switch ever faster) will mean that for chip manufacturers to meet the expectation set by Moore's law, they will soon (if not already) be doubling the number of cores (not transistors per square inch) used in each processor each year. In ten years' time, if this trend continues, we would have desktop computers with a thousand times as many cores as today. This trend motivates the authors to design implementation strategies for particle filters

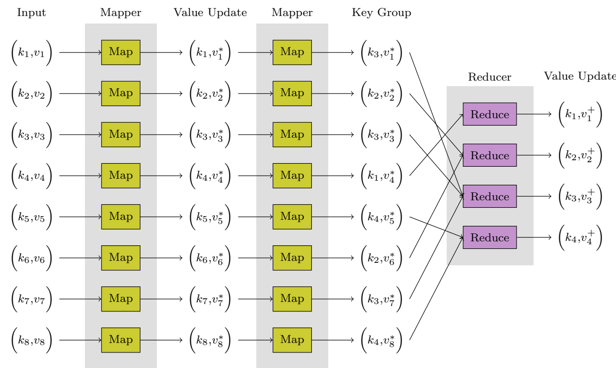


Fig. 1 General MapReduce Processing Model.

particular, one of the programming models that underpins such frameworks, the MapReduce programming model.

2.1 Big data Frameworks

An attractive approach for scaling the problem with data is to use Big data frameworks. More strictly, Big data frameworks go beyond the issue of data volume and address much wider issues covering augmented V's of data, for instance *volume, velocity, variety, value* and *veracity* [38]. Big data framework-based solutions are process-centric: the programmer describes the algorithm in a way that enables the framework itself to understand (and attempt to exploit) the potential to distribute the data and processing[5]. The result of this delegation of the optimisation for speed to the framework is that, while many of today's Big data frameworks can handle large volumes of data, none can match the runtime performance of conventional HPC systems [36].

There are a growing number of different programming models that are used to describe algorithms within Big data frameworks. These models include MapReduce [15], Stream Processing [4, 5, 22] and Query-based techniques [3, 42]. Here, we focus on one such programming model, MapReduce.

2.2 The MapReduce Programming Model

MapReduce is a popular programming model used in many Big data processing frameworks (and even some HPC frameworks). The key focus of the MapReduce model is on enabling the framework to distribute the processing

that are well suited to the multi-core processors which will, we believe, become increasingly prevalent over time.

[5] This contrasts HPC-based solutions, where the programmer aims to exploit intricate knowledge of the underlying architecture to ensure that data movement and processing are jointly optimised for the specific hardware.

of a large dataset by expressing algorithms in terms of *map* and *reduce* operations, via defining *mappers* and *reducers*. Mappers, when applied to each datum, output a list of *(key, value)* pairs. The framework then collates all the values associated with each key. Reducers are then applied to the list of values for each key to output a single value. Note that both the map and reduce operations are inherently parallel across all data and keys respectively[6]. To exemplify this, consider a dataset where each datum is a sentence in a Big document (e.g., Wikipedia). The problem of counting the total number of occurrences of each word in the document corpus can then be described as using the words as the key, a mapper that outputs a (non-zero) count of the number of times each word occurs in each sentence[7] and a reducer that calculates the sum of the counts. For each word, the reducer's output is then the sum over all sentences of the counts per sentence. Another example is shown in Figure 1 and illustrates the ability to pass (key, value) pairs into a mapper and thereby use the output of one mapper as the input into a second mapper.

Two key frameworks that support MapReduce, albeit in slightly different ways, are Hadoop and Spark. These are now considered in turn.

2.2.1 Hadoop

MapReduce is one of the two fundamental components of Hadoop. The other is the Hadoop Distributed File System (HDFS). HDFS enables multiple computers' disks to be accessed in much the same way as if it were a single (Big) disk. In Hadoop, the mapper and reducer generate files which are stored in HDFS, such that Hadoop implements data movement entirely via the file system.

2.2.2 Spark

The Spark framework operates using a different principle. First, at the Application Programming Interface (API) level, Spark provides a distributed data structure known as a Resilient Distributed Dataset (RDDs) [43]. MapReduce is then just one of a large number of *transformations* that (via a rich set of APIs) can be applied to RDDs. It is also important to realise that evaluations in Spark are *lazily* executed. This means, unlike conventional processing engines (e.g., Hadoop), executions never actually happen when transformations are defined. Instead, transformations are used to compose a data-flow graph and execution happens when forced through *actions* (i.e., when necessary). This delayed evaluation enables the Spark framework to optimise (and

[6] The exact number of mapper and reducer processes on a parallel resource (for instance, a multi-node cluster) varies depending on the configuration, but the important point is that the algorithm developer does not need to worry about how the processes are distributed when defining the algorithm. Of course, that does not mean that there is not utility in the developer describing algorithms using mappers and reducers that are well suited to the problem being tackled and to the configuration being used.

[7] Note that the output from each sentence would only be for the words that occur in that sentence, not every word that ever occurs in the corpus.

plan) the execution[8]. The result is often significant improvements in runtime performance. Another important property of RDDs is that they can reside in memory, disk or in combination. Indeed, although Spark can make use of HDFS, the data movements in Spark are primarily via memory. Again, this can result in significant improvements in runtime performance relative to Hadoop.

3 Particle Filtering

We now provide a brief description of particle filtering. The reader unfamiliar with particle filtering is referred to [7]. Here, we aim to introduce notation and contextualise the discussion in subsequent sections.

Let $\{\mathbf{x}\}_{k=1,2,..}$ be the discrete-time Markov process representing the collection of states and $\{\mathbf{z}\}_{k=1,2,..}$ be the sequence of measurements. $p(\mathbf{x}_k|\mathbf{x}_{k-1})$ is the state transition probability and $p(\mathbf{z}_k|\mathbf{x}_k)$ is the likelihood. Recursive Bayesian filtering is the solution to the problem of using these models to process incoming data to obtain the posterior probability density function, $p(\mathbf{x}_k|\mathbf{z}_{1:k})$, where $\mathbf{z}_{1:k} = \{\mathbf{z}_i, i = 1, \ldots, k\}$ is the sequence of measurements up to and including time k. $p(\mathbf{x}_k|\mathbf{z}_{1:k})$ is the sufficient statistic used to calculate, for example, estimates of the current state vector.

In a particle filter, the posterior is approximated using a set of N random samples, where the ith sample is $\mathbf{x}_k^i$ and has a weight of w_k^i.

The weights are normalised such that $\sum_{i=1}^{N} w_k^i = 1$. Estimates associated with the posterior at time k can then be approximated as:

$$\int f(\mathbf{x}_k)p(\mathbf{x}_k|\mathbf{z}_{1:k}) \approx \sum_{i=1}^{N} w_k^i f(\mathbf{x}_k^i) \tag{1}$$

where $f(.)$ is a function (e.g., $f(\mathbf{x}_k) = \mathbf{x}_k$ when calculating the mean). As the number of samples increases, the approximation becomes increasingly accurate. In fact, the variance of the estimate in (1) can be shown to be upper-bounded by a quantity that is proportional to $\frac{1}{N}$.

3.1 Sequential Importance Sampling

Importance sampling [19] is a technique for approximating one pdf using weighted samples from another pdf. A Sequential Importance Sampler (SIS) involves applying importance sampling to the path[9] through the state-space, $x_{1:k}$. The samples up to time k are also assumed to be generated by extending

[8] This can make it hard for a programmer to debug algorithmic implementations, particularly if the programmer is unfamiliar with debugging software performing lazy evaluation.

[9] While the derivation involves consideration of a path, the resulting algorithm only needs to store the most recent state.

the samples of the path up to time $k-1$. This enables the weights in SIS to be derived as [16]:

$$w_k^i \propto \frac{p(\mathbf{z}_k|\mathbf{x}_k^i)p(\mathbf{x}_k^i|\mathbf{x}_{k-1}^i)}{q(\mathbf{x}_k^i|\mathbf{x}_{k-1}^i,\mathbf{z}_k)} w_{k-1}^i \tag{2}$$

where $q(\mathbf{x}_k|\mathbf{x}_{k-1},\mathbf{z}_k)$ is the *proposal distribution* used to generate $\mathbf{x}_k$ and where

$$w_1^i \propto \frac{p(\mathbf{z}_1|\mathbf{x}_1^i)p(\mathbf{x}_1^i)}{q(\mathbf{x}_1^i)} \tag{3}$$

where $p(\mathbf{x}_1^i)$ and $q(\mathbf{x}_1^i)$ are distributions associated with the initial state and the initial distribution of samples (both at $k=1$).

Note that, when each measurement is received, SIS involves sampling particles from $q(\mathbf{x}_k|\mathbf{x}_{k-1},\mathbf{z}_k)$ and then updating their weights using (2).

3.2 Degeneracy Problem

With the SIS algorithm, the variance of the importance weights can be proved to increase over time [16][10]. Empirically, this results in *degeneracy*: all but one particle ends up having negligible normalised weights such that a single particle dominates the weighted average in (1). A way to quantify this effect is to calculate the effective sample size, N_{eff}, introduced in [31] and estimated as follows:

$$N_{eff} = \frac{1}{\sum_i^N (w_k^i)^2} \tag{4}$$

where, since $0 \leq w_k^i \leq 1$ and $\sum_{k=1}^N w_k^i = 1$, $1 \leq N_{eff} \leq N$.

3.3 Sequential Importance Resampling

N_{eff} dropping below a threshold, N_T, indicates that estimates are likely to be inaccurate. The key to addressing this is to introduce *resampling.* The basic idea of resampling is to eliminate samples with low importance weights and replicate samples with larger weights[11]. While there are a number of variants of the resampling algorithm, they all consist of two core stages: calculating how many copies of each sample to generate; generating that number of copies of each sample. The different resampling variants differ in terms of how their calculate the number of copies to generate. We focus here on *minimum variance resampling* (also known as *systematic* resampling) which minimises the errors inevitably introduced by the resampling process (and is discussed in more detail in section 4.6). The use of resampling with SIS is often known as the Sampling Importance Resampling (SIR) filter and has been at the heart of particle filters since their invention [17, 28, 30].

[10] A good choice of proposal density can delay but not stop the effect [16].
[11] This, of course, leads to a loss of diversity among the particles.

Algorithm 1 SIR Filter — Sequential (Vectorized) Version

```
1: Function sirFilter( p(x_0), p(z_κ|x_κ), p(x_κ|x_{κ-1}), q(x_κ|x_{κ-1}, z_κ) )
2: ▷ p(x_0): the initial prior
3: ▷ p(z_κ|x_κ): measurement model
4: ▷ p(x_κ|x_{κ-1}): dynamic model
5: ▷ q(x_κ|x_{κ-1}, z_κ): proposal
6: ▷ Initialize the Particles
7: x_0 ← drawSample(p(x_0))
8: w_0 ← 1/N
9: ▷ The time step loop
10: for k = 1 to T do
11:     ▷ Importance Sampling
12:     x_k ← drawSample(q(x_k|x_{k-1}, z_k))
13:     ▷ Calculate New Weights
14:     w*_k ← w_{k-1} p(z_k|x_k)p(x_k|x_{k-1}) / q(x_k|x_{k-1}, z_k)
15:     ▷ Normalise the Weights
16:     w_k ← w*_k / Σ w*_k
17:     ▷ Calculate Effective Sample Size
18:     N_eff ← 1 / Σ w_k^2
19:     ▷ Perform Conditional Resampling
20:     if N_eff ≤ N_t then
21:         ▷ The m represents the number of copies
22:         m ← minimumVarianceResampling(w_k)
23:         (m, x_k) ← quickSort(m, x_k)
24:         x_k ← redistribute(m, x_k)
25:     end if
26:     ▷ Estimate the Mean (or any other quantities of interest)
27:     μ_k ← Σ x_k / N
28: end for
29: EndFunction
```

Algorithm 1 shows pseudocode for the SIR filter. Note that the algorithm is expressed in vector notation, such that each vector operation implicitly comprises at least one *for* loop, and in terms of building blocks that operate on such vectors. The algorithm relies on a number of functions, which are covered in detail later in this paper. Briefly these functions include:

- $(a) \leftarrow$ `drawSample(`$q(.)$`)` draws samples from the supplied distribution, $q(.)$;
- $(m) \leftarrow$ `minimumVarianceResampling(`w`)` determines the number of times each particle needs to be replicated. The function takes the particles' weights, w, as input.
- $(m,x) \leftarrow$ `quickSort(`m,x`)` calculates the permutation that would sort vector m, and applies this permutation to both inputs. While this sort is not necessary with a single processor implementation, we will exploit the fact that the output has been sorted in section 4.8.2.
- $x' \leftarrow$ `redistribute(`m,x`)` returns the new population of particles, x', where m, as mentioned previously, defines the number of replications of each of the old population of particles, x.

3.4 Parallel Particle Filtering

The bulk of the operations comprising the particle filter (as described in Algorithm 1) are readily parallelised. However, it is resampling (the redistribution process in particular) that complicates parallel implementation of particle filters.

The complications primarily arise because, if each of multiple processors are considering subsets of the particles, the data transfers that the redistribution process demands are data-dependent. It is therefore non-trivial to implement a particle filter in a way that the run-time is not data-dependent. A similar problem has been encountered with sorting algorithms[12]. In the subsequent sections of this paper, we describe how to implement the components of the particle filter in a way that run-time in not data-dependent, but deterministic.

4 Parallel Instantiations of the Algorithmic Components of Particle Filtering

Prior to mapping the particle filter algorithm on to a MapReduce form, it is essential to understand how the operations used by a particle filter can be implemented in a fully distributed form. While a more detailed discussion of these operations (and others) can be found in [12], we now discuss each of the operations that constitute the algorithm described in algorithm 1. We summarise these operations and the associated complexities in table 1, both for the fundamental building blocks and some of the algorithmic components that can be built from those components. Our focus is on implementations with a time-complexity that is as fast as possible in terms of its dependence on N, the number of data.

Table 1 Complexities of Various Algorithmic Components of the Particle Filter.

Section	Algorithmic Component	Time	Space
4.1	Element-wise operations	$\mathcal{O}(1)$	$\mathcal{O}(N)$
4.2	Rotation	$\mathcal{O}(1)$	$\mathcal{O}(N)$
4.3	Sum/Max/Min	$\mathcal{O}(\log N)$	$\mathcal{O}(N)$
4.4	Cumulative Sum	$\mathcal{O}(\log N)$	$\mathcal{O}(N)$
4.5	Normalising the Weights	$\mathcal{O}(\log N)$	$\mathcal{O}(N)$
4.6	Minimum Variance Resampling	$\mathcal{O}(\log N)$	$\mathcal{O}(N)$
4.7	(Bitonic) Sort	$\mathcal{O}((\log N)^2)$	$\mathcal{O}(N)$
4.8.1	Redistribution from [33]	$\mathcal{O}((\log N)^3)$	$\mathcal{O}(N)$
4.8.2	Improved Redistribution	$\mathcal{O}((\log N)^2)$	$\mathcal{O}(N)$

[12] For instance, although Quicksort [24] can be parallelised, the load distributions across the processors is dependent on the pivots used and the run-time will therefore be data-dependent.

4.1 Element-wise Operations

Perhaps the simplest type of operation to implement in parallel involves applying an element-wise operation[13]. Given a function f and a vector $\mathbf{v}$, the element-wise operation $f \mapsto \mathbf{v}$ applies the function f on every element of the vector such that:

$$f \mapsto \mathbf{v} = [f(v_1), f(v_2), \ldots, f(v_N)]$$

In our case, normalizing the weights is an example of an element-wise operation. Another example is a vector of *if* operations, $\mathsf{Vif}(\mathbf{a}, \mathbf{b}, \mathbf{c})$ where the ith element in the output is b_i if a_i is true and c_i otherwise.

It should be evident that operations that involve two inputs and a single output (e.g., element-wise sum or difference) are similarly easy to implement in parallel.

4.2 Rotation

Another operation that we will use involves rotating (with wrapping (i.e., cyclic shift) or without) the elements of a vector by a given distance, δ, such that if the input is $\mathbf{a}$ and the output is $\mathbf{b}$, after the rotation, we have $b(\mod(i+\delta, N)) = a(i)$ where $\mod(x, y)$ is x modulus y. Once again, this algorithmic component is readily parallelised.

We will also use partial rotations such that we have a vector of distances, Δ, and not a single 'global' distance, δ. This vector, Δ, has $N' < N$ elements where N' is a power of two. The rotations are then implemented locally to each set of $M = \frac{N}{N'}$ elements. For example if the jth element of Δ is δ_j then $b\left((j-1) \times M + \mod(i + \delta_j, M)\right) = a\left((j-1) \times M + i\right)$ for $1 \leq i \leq M$.

4.3 Sum, Max and other Commutative Operations

To calculate a sum of a vector of numbers, we can use an 'adder-tree'. The numbers are associated with the leaves of the tree. By recursing up the tree, the sum of pairs of numbers can be calculated (in parallel across all pairs). The sum of all pairs of pairs of numbers can then be calculated (in parallel across all pairs of pairs). This is exemplified in figure 2(a-c). This process can repeat until we reach the root node of the tree and calculate the sum of all the numbers by summing the sum of the two halves of the data. See figure 2(d).

In fact, as has been known since the development of the infamous Array Programming Language (APL) [29], this same approach can be used for any binary operation, $\oplus$, that is commutative such that:

$$((a \oplus b) \oplus c) \oplus d = (a \oplus b) \oplus (c \oplus d) \tag{5}$$

[13] Such operations are an example of 'embarrassingly parallel' operations that are arguably trivial to parallelise.

Relevant examples of operations which can be calculated in this way include the sum but also the maximum (and minimum) and first non-zero element of a set of numbers (which we will denote $\mathsf{First}(.)$ in, for example, algorithms 2 and 3). For such operations, with N processors processing N data and a binary tree, the time-complexity is the depth of the tree, i.e., $\log_2 N$.

As should be evident, an upside-down version of the same tree can be used to implement an $\mathsf{Expand}(a)$ operation, which involves making all elements of a vector equal to the single value of a.

4.4 Cumulative Sum

While the ability to use a tree to calculate a sum efficiently is well known, the ability to use a closely related approach to calculate a cumulative sum[14] efficiently appears to be less well known by researchers working on particle filters. Of course, a naïve implementation involves computing the cumulative sum by simply adding each element of the input to the previous element of the output. Such an approach would have a run-time of N. However, a more-efficient approach has existed since the development of APL if not for longer[15].

To ensure the reader has some intuition as to how this could be possible, the key idea is to exploit the partial sums that are calculated in an adder-tree and to express each element of the cumulative sum as a sum of these (efficiently calculated) partial sums. The process that exploits this insight then involves a second tree in which the values at every level are propagated to the level below, replacing the values that were calculated in the adder-tree. More specifically, in the downward propagation, the value at each parent node is propagated to its right child and to its left child. The new value for the left child is the difference between the value at the parent node and the value at the right child node (as calculated in the adder-tree). The new value for the right child is just the same value as the parent node. See figures 2(e)-(g) for an example.

With this forward and backward pass of the tree, we can obtain the cumulative sum in $2 \log_2 N$ steps.

4.5 Normalising the Weights

Normalising the weights is an example of an operation that can be implemented using the building blocks described to this point. The sum is calculated using an adder-tree (as described in section 4.3), distributed to all the data

[14] Note that the cumulative sum is sometimes referred to as a prefix sum: there is no difference between a prefix sum and a cumulative sum.

[15] APL describes an approach to calculating a sum, maximum or minimum as *reduction* operations. The approach to calculating a cumulative sum is described as a *scan* operation and can be used to calculate, for example, cumulative maximums and minimums. Scan operations take a binary operator $\oplus$ and an N-element vector $\mathbf{a} = [a_1, a_2, \ldots, a_N]$, and return an N-element vector $\mathbf{a}_\oplus = [a_1, (a_1 \oplus a_2), \ldots, (a_1 \oplus a_2 \oplus a_3 \oplus \ldots \oplus a_N)]$. However, here we are only concerned with cumulative sums.

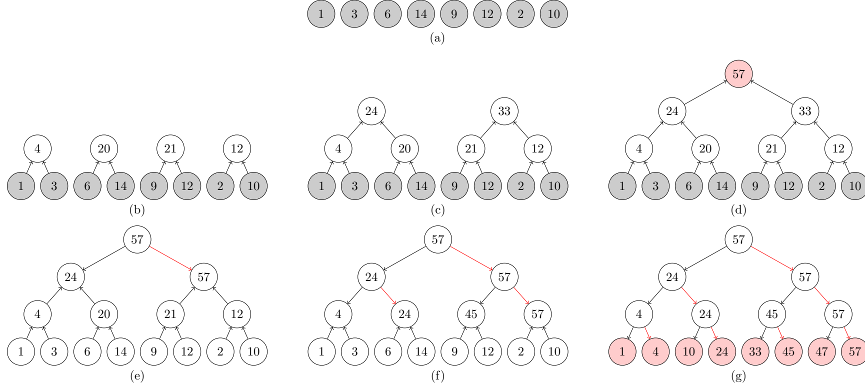


Fig. 2 Example of cumulative sum for N=8 numbers. Subfigures (a)-(d) describe the sum computation, while the remaining balanced binary trees shown in subfigures (e)-(g) describe how the backward pass culminates in calculation of the cumulative sum of the given sequence.

(as also described in section 4.3) and an element-wise divide (see section 4.1) used to calculate the normalised weights.

4.6 Minimum Variance Resampling

As explained in section 3.3, resampling involves determining the number of copies of each particle that are needed. We specifically describe minimum variance resampling, for which the number of copies of the ith particle is:

$$m_i = \lfloor C_i \times N \rfloor - \lceil C_{i-1} \times N \rceil + 1 \tag{6}$$

where $\lceil x \rceil$ and $\lfloor x \rfloor$ are respectively the ceiling[16] and the floor[17] of x, where

$$C_i = \sum_{j=1}^{i} w_i + \epsilon \tag{7}$$

is the cumulative sum and where $\epsilon \sim \left[0, \frac{1}{N}\right]$ and $C_0 = 0$.

(6) uses only element-wise operations (as described in section 4.1) and a rotation (by a single element and as described in section 4.2). (7) involves a cumulative sum (as described in section 4.4) and an addition (as described in section 4.1). Thus, the building blocks described to this point can be used to implement (6) and (7).

[16] The ceiling of x is the smallest integer larger than or equal to x.

[17] The floor of x is the largest integer smaller than or equal to x.

4.7 Sorting

Quicksort [24] is well known and has an average time complexity of $\mathcal{O}(N \log_2 N)$. However, we focus on the bitonic sort algorithm [11], which has a time complexity of $\mathcal{O}((\log_2 N)^2)$ and a spatial complexity of $\mathcal{O}(N)$. The main reason for this choice is that we want to guarantee the time taken to perform sorting. While it is possible to parallelise quicksort, the ability to do so is data dependent. In contrast, bitonic sort has deterministic time complexity (with a balanced load across (up to) N processors).

At the fundamental level, a *bitonic sequence* forms the basis for the bitonic sort. A sequence $\mathbf{a} = [a_1, a_2, \ldots, a_N]$ is a bitonic sequence if $a_1 \leq a_2 \leq \ldots \leq a_k \geq \ldots \geq a_N$ for some k, $1 \leq k \leq N$ or if this condition holds for any rotation of $\mathbf{a}$.

To try to provide some intuition as to how the algorithm works, note that at a certain point it the algorithm, we have N data in a bitonic sequence. The first 'half' of the data are sorted in ascending order and the second half are sorted in descending order[18]. Consider the ith element in the first half and the ith element in the second half. There are $\frac{N}{2} - 1$ data between these two elements. They must all be larger than the smallest of the two elements which the data are between. There must therefore be at least $\frac{N}{2}$ data that are larger than the smallest of the two elements. This smallest element must therefore be one of the lowest $\frac{N}{2}$ data (it cannot be one of the largest $\frac{N}{2}$ data if there are at least $\frac{N}{2}$ data larger than it). An upside-down version of the same argument makes clear that the largest of these two elements must be one of the largest $\frac{N}{2}$ data. Finally, it also transpires that after this operation, the first $\frac{N}{2}$ data are a bitonic sequence and the second $\frac{N}{2}$ data are a bitonic sequence. Thus, given a bitonic sequence, by comparing all pairs of data that are a distance of $\frac{N}{2}$ apart and swapping the points if needed, we can ensure all the larger elements are in the first $\frac{N}{2}$ data, which forms a bitonic sequence, and all the smaller elements are in the second $\frac{N}{2}$ data, which also forms a bitonic sequence. We can then apply the same comparison structure on each of the two bitonic (smaller) sequences. This process can be applied recursively until pairs of points are compared and the data are sorted.

This process is known as the 'bitonic merge' and requires $\mathcal{O}(\log_2 N)$ steps (with $\mathcal{O}(N)$ spatial complexity) to convert a bitonic sequence into a sorted sequence. To generate the bitonic sequence needed from arbitrary input data[19], we apply bitonic sort to put the first $\frac{N}{2}$ input data into ascending order and apply bitonic sort again to put the second $\frac{N}{2}$ input data into descending order. Analysis of this recursive use of bitonic sort gives rise to bitonic sort requiring $\frac{n^2-n}{2}$ iterations where $n = \log_2 N$ and, at every step, the algorithm performs $\frac{N}{2}$ comparisons. Each comparison involves comparing two data and swapping them according to a criterion that is defined by the position of the comparison

[18] A similar argument works if the first half are sorted in descending order and the second half are sorted in ascending order.

[19] This process is sometimes known as 'bitonic build'.

in the network (and can be implemented using the building blocks described in sections 4.1 and 4.2).

An example of bitonic sort with eight numbers is provided in figure 3.

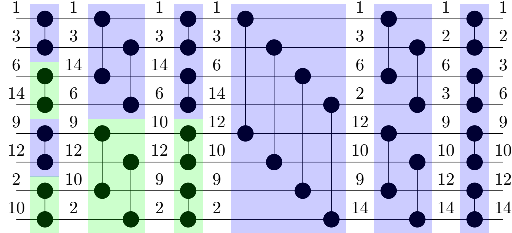


Fig. 3 Example of bitonic sort using eight numbers. Each horizontal wire corresponds to a core. The blue color denotes that the larger value will be stored at the lower wire after the comparison, while the green color the opposite.

4.8 Redistribution

4.8.1 Original Version from [33]

The redistribution algorithm takes two inputs, the old population of particles $\mathbf{x}$, and the number of copies $\mathbf{m}$, and produces the new population of particles, $\mathbf{x}^*$, as the output.

In [33], a divide-and-conquer algorithm was described for implementing the redistribute. The procedure involves sorting the particles in decreasing order of the number of copies. With N data, the sum of the elements of $\mathbf{m}$ must be N. The approach is then to divide the data into two smaller datasets, each of which has $\frac{N}{2}$ elements and is such that the corresponding elements of $\mathbf{m}$ are sorted and sum to $\frac{N}{2}$. This can be achieved by finding the *pivot*, which we define as leftmost element in $\mathbf{m}$ for which the associated value of the cumulative sum is $\frac{N}{2}$ or greater. In general, the pivot needs to be split into two constituent parts such that the two smaller datasets can both sum to $\frac{N}{2}$. We refer to these two parts as the left-pivot and right-pivot. The data to the left of the pivot and including the left-pivot can be used to produce one of the two smaller datasets. The right-pivot and the data to the right of the pivot can be used to produce the other of the two smaller datasets. Both smaller datasets are then sorted[20] such that they are in decreasing order of $\mathbf{m}$. Note that there is a special case that occurs when the value of the right-pivot is zero: the rotation needed is one less than otherwise in this case. It can be intuitive to think of this procedure as operating on a tree. Applying the procedure recursively down the tree, until the leaf nodes are encountered,

[20] The first dataset is actually already sorted, but the second dataset is, in general, not sorted.

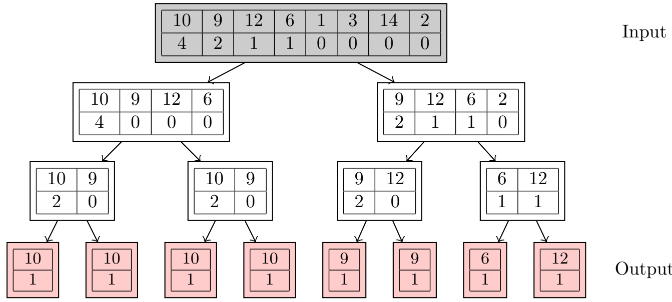


Fig. 4 An example of the redistribution for $\mathbf{x} = [10, 9, 12, 6, 1, 3, 14, 2]$ and $\mathbf{m} = [4, 2, 1, 1, 0, 0, 0, 0]$. The first and the second rows represent the old population of particles and the number of copies needed to generate the new population, $\mathbf{x}^* = [10, 10, 10, 10, 9, 9, 6, 12]$.

results in the redistribute completing. See figure 4 for an illustrative example of this procedure.

The procedure can be described using element-wise operations (see section 4.1), sum (see section 4.3), cumulative sum (see section 4.4), rotations (see section 4.2) and sort (see section 4.7). Algorithm 2 provides a description of this algorithm. Note that the description makes use of three functions ($\mathsf{LeftHalf}(.)$, $\mathsf{RightHalf}(.)$ and $\mathsf{Combine}(.)$) which are included to aid exposition (and actually have zero computational cost). Also note that the implementation is described in a way that involves recursion. It is possible to 'unwrap' the recursive implementation such that all operations (at all stages in the tree) are implemented on datasets of the same size (a size of N). Doing so is conceptually straightforward though the bookkeeping required is non-trivial.

The time complexity of this redistribution algorithm $\mathcal{O}((\log_2 N)^3)$ in parallel with N processors since a (bitonic) sort (with complexity of $\mathcal{O}((\log_2 N)^2)$) is used at each stage in the divide-and-conquer. Note that this contradicts the (erroneous) claim in [33] that the time complexity of this algorithm is $\mathcal{O}((\log_2 N)^2)$.

4.8.2 Improved Redistribution

The redistribution algorithm described in section 4.8.1 is a divide-and-conquer algorithm that ensures that, at each node in the tree, $\mathbf{m}$ sums to its length, N, and is sorted. The sorting is sufficient to ensure that rotation can be used to replace some of the (rightmost) zeros with the (rightmost) non-zero elements of $\mathbf{m}$ that sum to $\frac{N}{2}$.

Here we exploit the observation that it is possible to define an alternative divide-and-conquer strategy. More specifically, we ensure that, at each node in the tree, $\mathbf{m}$ sums to its length, N, and has all its non-zero values to the left of all values that are zero. Since such a sequence only has trailing zeros,

Algorithm 2 Redistribute: $\mathcal{O}((\log_2 N)^3)$ implementation.

1: **Function** $\mathbf{x} = \mathsf{Redistribute}(\mathbf{m}, \mathbf{x})$
2: ▷ $\mathbf{m}$: Number of copies (sorted in descending order)
3: ▷ $\mathbf{x}$: Particles
4: **if** $\mathsf{Length}(\mathbf{m}) > 1$ **then**
5: ▷ Calculate Cumulative Sum
6: $\mathbf{c} \leftarrow \mathsf{CumSum}(\mathbf{m})$
7: ▷ Identify Pivot
8: $i_p \leftarrow \mathsf{First}(\mathbf{c} \geq \frac{N}{2})$
9: $\mathbf{p} \leftarrow \mathsf{Expand}(i_p)$
10: ▷ Calculate Left-Pivot and Right-Pivot
11: ▷ $\mathbf{i}$ simply indexes the elements of $\mathbf{m}$ and $\mathbf{0}$ is a vector of zeros
12: $\mathbf{lp} \leftarrow \mathsf{Vif}(\mathbf{i} = \mathbf{p}, \mathbf{c} - \frac{N}{2}, \mathbf{0})$
13: $\mathbf{rp} \leftarrow \mathsf{Vif}(\mathbf{i} = \mathbf{p}, \frac{N}{2} - \mathsf{Rotate}(\mathbf{c}, 1), \mathbf{0})$
14: ▷ Generate Smaller Datasets
15: $\mathbf{l} \leftarrow \mathsf{LeftHalf}(\mathsf{Vif}(\mathbf{i} < \mathbf{p}, \mathbf{m}, \mathbf{lp}))$
16: $\mathbf{lx} \leftarrow \mathsf{LeftHalf}(\mathbf{x})$
17: $\mathbf{r} \leftarrow \mathsf{Vif}(\mathbf{i} > \mathbf{p}, \mathbf{m}, \mathbf{rp})$
18: ▷ Calculate Rotation of $\mathbf{r}$
19: $inc \leftarrow \mathsf{Sum}(\mathsf{Vif}(\mathbf{c} = \frac{N}{2}, \mathbf{1}, \mathbf{0}))$
20: $\mathbf{r} \leftarrow \mathsf{RightHalf}(\mathsf{Rotate}(\mathbf{r}, i_p + inc))$
21: $\mathbf{rx} \leftarrow \mathsf{RightHalf}(\mathsf{Rotate}(\mathbf{x}, i_p + inc))$
22: ▷ Sort Right Half
23: $\mathbf{r} \leftarrow \mathsf{Sort}(\mathbf{r})$
24: ▷ Divide-and-conquer
25: $\mathbf{lx} \leftarrow \mathsf{Redistribute}(\mathbf{l}, \mathbf{lx})$
26: $\mathbf{rx} \leftarrow \mathsf{Redistribute}(\mathbf{r}, \mathbf{rx})$
27: ▷ Combine Outputs
28: $\mathbf{x} \leftarrow \mathsf{Combine}(\mathbf{lx}, \mathbf{rx})$
29: **end if**
30: **EndFunction**

we call such a sequence an All-Trailing-Zeros (ATZ) sequence[21]. While a sort is sufficient to generate an ATZ sequence, it is easier, as we will demonstrate shortly, to generate an ATZ sequence than it is to generate a sorted sequence.

The new algorithm, at each node in the tree, starts with $\mathbf{m}$, which sums to its length, N, and is an ATZ sequence. To proceed, as previously, we find the pivot (as defined in section 4.8.1). As previously, the data to the left of the pivot and the left-pivot can be used to produce one of the two smaller datasets. However, in contrast to the approach described in section 4.8.1, we can simply use the right-pivot and the data to the right of the pivot to generate the second smaller dataset (without any need for sort). Both these smaller datasets then sum to $\frac{N}{2}$ and are ATZ sequences. Note that, as with the approach described in section 4.8.1, there is a special case that occurs when the value of the right-pivot is zero.

To initiate the algorithm, we need to generate an ATZ sequence. To achieve this, we propose to use (bitonic) sort (once). After this initial sort, the procedure can be described using element-wise operations (see section 4.1), sum (see

[21] We suspect such a sequence may have a name in a literature we do not currently have sight of. However, here we simply adopt an intuitive name for ease of exposition.

section 4.3), cumulative sum (see section 4.4) and rotations (see section 4.2). We emphasise that there is no need for a sort after the initial generation of an ATZ sequence. As a result, while the algorithm described in section 4.8.1 has time-complexity of $\mathcal{O}((\log_2 N)^3)$, the algorithm described in this section has time-complexity of $\mathcal{O}((\log_2 N)^2)$. To aid understanding algorithm 3 provides a description of this algorithm. Note the very strong similarity to algorithm 2 and that, once again, it is possible to 'unwrap' the recursive implementation albeit with some non-trivial bookkeeping.

Algorithm 3 Redistribute: $\mathcal{O}((\log_2 N)^2)$ implementation.

```
1: Function x = Redistribute(m, x)
2: ▷ m: Number of copies (in an ATZ sequence)
3: ▷ x: Particles
4: if Length(m) > 1 then
5:     ▷ Calculate Cumulative Sum
6:     c ← CumSum(m)
7:     ▷ Identify Pivot
8:     i_p ← First(c ≥ N/2))
9:     p ← Expand(i_p)
10:    ▷ Calculate Left-Pivot and Right-Pivot
11:    ▷ i simply indexes the elements of m and 0 is a vector of zeros
12:    lp ← Vif(i = p, c − N/2, 0)
13:    rp ← Vif(i = p, N/2 − Rotate(c, 1), 0)
14:    ▷ Generate Smaller Datasets
15:    l ← LeftHalf(Vif(i < p, m, lp))
16:    lx ← LeftHalf(x)
17:    r ← Vif(i > p, m, rp)
18:    ▷ Calculate Rotation of r
19:    inc ← Sum(Vif(c = N/2, 1, 0))
20:    r ← RightHalf(Rotate(r, i_p + inc))
21:    rx ← RightHalf(Rotate(x, i_p + inc))
22:    ▷ Divide-and-conquer
23:    lx ← Redistribute(l, lx)
24:    rx ← Redistribute(r, rx)
25:    ▷ Combine Outputs
26:    x ← Combine(lx, rx)
27: end if
28: EndFunction
```

5 Mapping Particle Filtering into MapReduce

The descriptions provided in the section 4 describe distributed operations that can manipulate vectors (albeit after some unwrapping of the recursive descriptions).

As discussed in the section 2.2, the fundamental notion of MapReduce is the processing of (key, value) pairs. In the context of particle filtering, none of the properties of the particles (weight or state) qualifies to be a key. However, we can give each particle a unique index and use this index as the key, such

Details	Single Node System	Multi-Node System
Name	Platform 1	Platform 2
Number of Nodes	1	28
Hardware Cores	16	512
Operating System	Linux	IBM Unix
Primary Memory	16GB	384GB
Spark Version	1.6.2	1.4.1
Hadoop Version	2.7.2	2.7.1

Table 2 Details of the Experimental Platform used for Evaluation.

that we think of the particles as being a set $\{i, x_i, w_i\}$ where $i \in \{1, \ldots, N\}$ and, as previously, where N is the number of particles, x_i is the state and w_i is the corresponding weight of the ith particle.

6 Evaluation

We performed extensive evaluation of our algorithm on two different systems. We provide the details of these systems in table 2. The evaluation process included the algorithms outlined in the section 4 on the two key frameworks that support MapReduce and which were mentioned in section 2: Hadoop and Spark. We used the standard estimation problem (involving a scalar state and a computationally inexpensive proposal, likelihood and dynamic model) that is widely used in the particle filtering community [7]. We perceive this scenario emphasises the need for efficient resampling: were, as is often the case, the likelihood, dynamics and proposal were computationally demanding, the relative merits of different resampling schemes would be less apparent. Our evaluation focused on specific aspects of the implementation, which are described as follows:

1. We start, in section 6.1, by providing evidence that, in contrast to a naïve implementation, the particle filter we have developed can exploit multi-core architectures while having deterministic run-time.
2. In section 6.2, as a precursor to a detailed evaluation and analysis, we analyse the overall profile of the particle filtering algorithm for implementations on a single core, using Hadoop and using Spark.
3. Then, in section 6.3, for both the Spark and Hadoop implementations, we compare the performance of our new algorithms relative to a single mapper and a single reducer. In doing so, we not only compare the overall performance, but we also compare the fundamental building blocks of the particle filtering algorithm. This section provides a thorough understanding of these algorithms' performance on two key frameworks that support MapReduce.
4. Given that the Spark implementation (unsurprisingly) outperforms the Hadoop implementation, we then focus on the Spark implementation. In section 6.4 we then compare the two versions of the redistribution algorithm described in sections 4.8.1 and 4.8.2 as a function of the numbers

of particles and cores. The intent is that this detailed comparison provides insight into the performance that is achievable using the original and proposed variants of the redistribution algorithm.

5. Finally, in section 6.5, we perform a detailed analysis on the speedup and scalability of the redistribution and the overall particle filter.

In performing these evaluations, a basic parameter that we found useful in assessing the algorithmic performance is the capability to process large amount of data, which directly translates to the number particles that can be processed per unit time, the number of Particles Processed per Second (PPS).

6.1 Worst Case Runtime Performance

6.1.1 Baseline Redistribution Algorithm

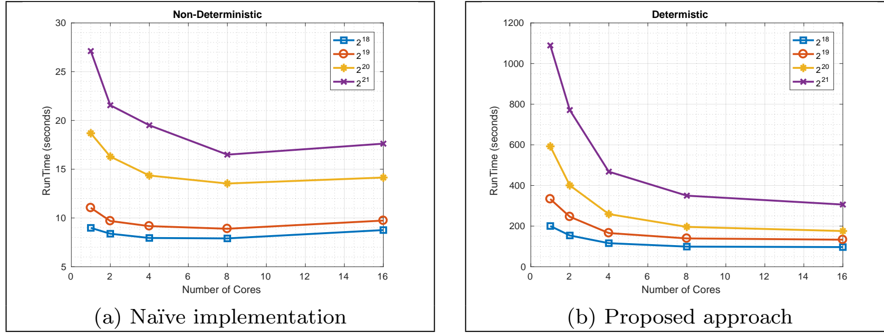
We will compare performance against a naïve baseline implementation of the redistribution component. This implementation involves calculation (in parallel) of a cumulative sum of the number of copies. Once this cumulative sum is calculated (and each element of the sum communicated to be processed along with its neighbour), for each particle in the old population, we know the first and last indices of particles in the new population that will be copies of this particle in the old population. Then, by performing a loop across the particles in the old population, we can populate the new generation of particles.

Note that this algorithm, when running across multiple cores, can be expected to have a runtime complexity that is dependent on the data. To help make this clear, consider the worst case where the redistribution involves making N copies of the ith particle (and zero copies of all other particles). In this case, only one core will actually be populating the new generation of particles.

6.1.2 Runtime Performance

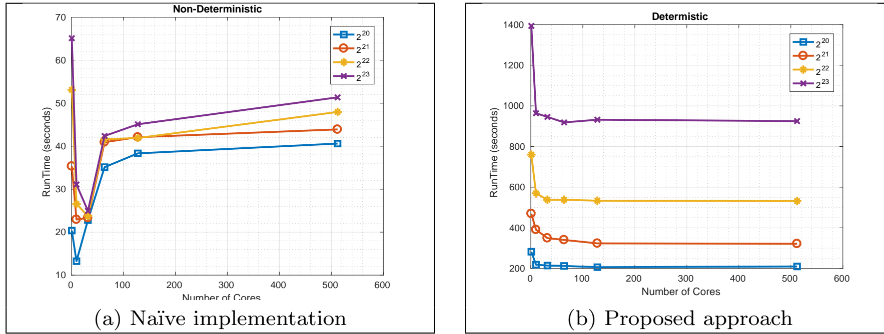
We investigated the worst-case performance of such a naïve parallel implementation of the redistribution component and compared with our proposed implementation (using a Spark implementation). The results are shown in figures 5 and 6 for the worst-case (where the new population of particles are all copies of a single member of the old population). It should be evident that as the number of cores increases, the runtime of the proposed (almost) never increases[22]. In contrast, while the runtime of the naïve implementation initially decreases as the number of cores is increased, it then increases (i.e., such that it is faster in absolute terms to use 8 not 16 cores with Platform 1 and such that it is faster to use less than 50 cores not 512 cores with Platform 2). The reason for the decrease is that the map-reduce framework can use the extra cores to more rapidly process the (many) zeros in the vector describing the

[22] In subsequent sections, we will investigate how and when the decrease in runtime occurs in more detail.



(a) Naïve implementation (b) Proposed approach

Fig. 5 Worst-case performance of Redistribution: Platform 1.



(a) Naïve implementation (b) Proposed approach

Fig. 6 Worst-case performance of Redistribution: Platform 2.

number of copies. The reason for the subsequent increase in processing time is that the additional overhead of having multiple cores becomes increasingly significant if only one of the cores is doing the vast majority of the processing.

It should also be evident that the absolute runtime (on these platforms and with our current Spark implementation) of the deterministic and non-determinsitic variants differ significantly such that the naïve implementation can be approximately 20 times faster (in the contexts of both platforms). This is disappointing and does motivate future work to refine our (initial) implementation. However, we perceive that there are applications where a slower but deterministic runtime is preferable to a faster but data-dependent runtime. In the contexts of such applications, particularly given the scope to improve the implementation, we perceive our algorithm (if not our current implementation) has utility.

6.2 Overall Profile

We now compare performance of three implementations of a particle filter: a sequential implementation (in Java and using quicksort in place of bitonic

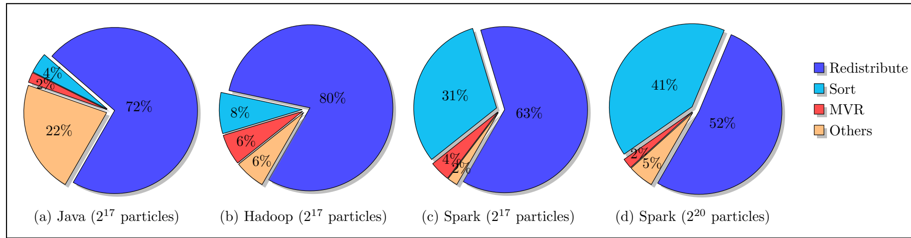


Fig. 7 Overall runtime profile of the particle filtering algorithm for the following implementations: (a) Sequential; (b) Hadoop; (c) Spark with 2^{17} particles; (d) Spark with 2^{20} particles.

sort); an implementation in Hadoop; an implementation in Spark. All implementations involve a single core and Platform 1. Figure 7 shows the proportion of the runtime that is associated with: redistribution; sort; Minimum Variance Resampling (MVR); the remaining components (e.g., sum, cumulative sum, diff, scaling).

As can be observed from figure 7, the majority of the time taken is devoted to the redistribution component. Note that, for the Spark implementation, a significant fraction of the remaining time is spent on the sorting component and the fraction of time devoted to redistribution and sorting increases as the number of particles is increased.

6.3 Comparison of Hadoop and Spark

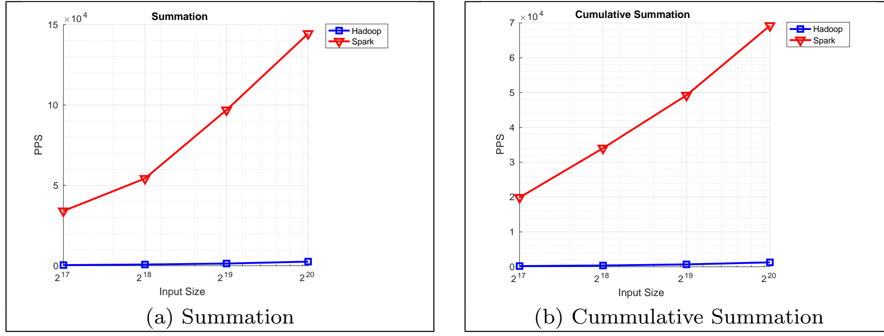
We next investigate how the choice of middleware impacts performance in the context of the components of the algorithm and in the context of the entire particle filter algorithm. All implementations involve a single core and Platform 1.

6.3.1 Sum and Cumulative Sum

Figure 8 shows the comparative performance of the sum and cumulative sum components in these two key frameworks.

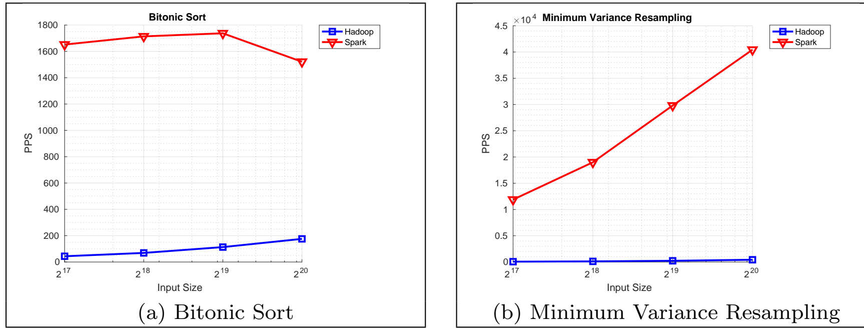
With respect to the number of particles processed per second (PPS), the performance using Spark is far superior to that achieved using Hadoop. This stems from the issues discussed in section 2: Spark uses RDDs to makes use of memory (and lazy evaluation) whereas Hadoop only uses the file system (HDFS) to transfer data from the output of one operation to the input of the next.

It is apparent in both frameworks (and particularly apparent in the context of Spark) that, as the number of particles increases, the number of particle processed per second also increases. This is because with more particles, the overheads associated with setting up (and tearing down) the mappers and reducers are increasingly offset by the parallel operations that make use of the



(a) Summation (b) Cummulative Summation

Fig. 8 Summation and Cumulative Summation on Spark and Hadoop.



(a) Bitonic Sort (b) Minimum Variance Resampling

Fig. 9 Bitonic Sort and Minimum Variance Resampling on Spark and Hadoop.

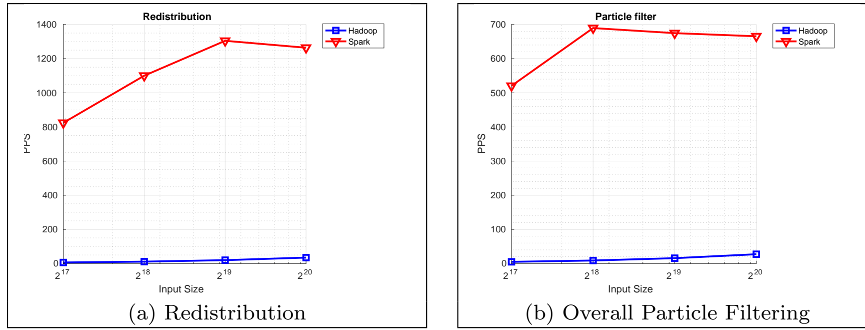
mappers and reducers. The limited extent to which this effect is observed in the context of Hadoop highlights that the overheads associated with opening files in HDFS are significant.

Since, as explained in section 4, calculating a summation involves one adder tree and cumulative sum involves two such trees, we should expect the number of particles per second for the cumulative sum to be approximately half that for the summation. A comparison of the two graphs in figure 8 makes clear that this is indeed (approximately) the case for both frameworks and for all input sizes.

6.3.2 Bitonic Sort and Minimum Variance Resampling

Figure 9 shows the performance for two independent components, *bitonic sort* and *minimum variance resampling*. The performance of *minimum variance resampling* is relatively close to the performance of the cumulative sum (see Figure 8). This is expected since, as explained in section 4, *minimum variance resampling* includes a cumulative sum.

Once again and for the same reasons as discussed in section 6.3.1, we notice the same difference in performance between the Spark and Hadoop implementations. As one might expect and as before, for *minimum variance resampling*,



(a) Redistribution (b) Overall Particle Filtering

Fig. 10 Redistribution and the Overall Particle Filtering on Spark and Hadoop.

the number of particles per second increases with the number of particles. However, it is noteworthy that, for bitonic sort with Spark, the number of particles per second decreases for large numbers of particles. On investigating this in some detail, we observed that the *lineages* used to facilitate the lazy evaluation in Spark[23] become very large with large numbers of particles. This appears to cause Spark to become less efficient when the number of particles becomes large.

6.3.3 Redistribution and Overall Performance

Finally, figure 10 shows the comparative performance of the redistribution algorithm (as described in algorithm 3) and the overall particle filtering algorithm.

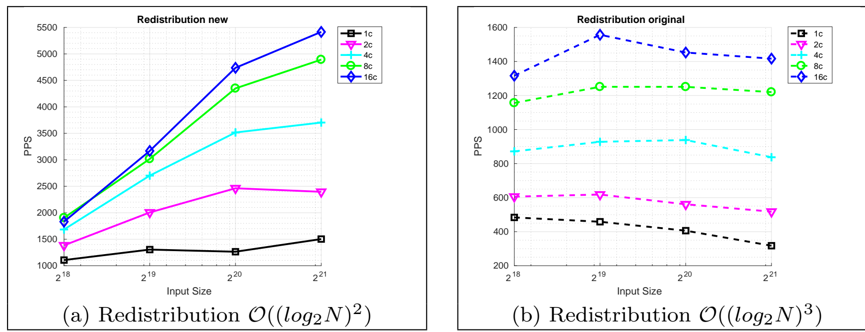
Once again, we notice the same differences between Hadoop and Spark. In the context of the overall particle filter and for the largest number of particles considered, these differences are manifest in Spark, relative to Hadoop, offering a considerable speedup (approximately 25-fold[24]).

The overall performance of the particle filtering algorithm, when implemented in Spark, decreases for large numbers of particles. Again, on investigation, this appears to be caused by large lineages associated with the large number of particles. Finally, we note that the bitonic sort and redistribution components appear to be limiting the number of particles per second that can be processed by the overall particle filtering algorithm.

6.4 Impact of Using Multiple Cores

We now focus on the Spark implementation (with Platform 1) and compare the performance of the two variants of the redistribution component in iso-

[23] Since Hadoop does not attempt lazy evaluation or use such lineages for another purpose, the same phenomenon is not observed in the context of Hadoop.
[24] In the particle filter the resampling is executed in every iteration. Thus the aforementioned figures correspond to a worst-case speedup.



(a) Redistribution $\mathcal{O}((log_2 N)^2)$

(b) Redistribution $\mathcal{O}((log_2 N)^3)$

Fig. 11 Performance of the two variants of the Redistribution Component (using Spark).

lation and in the context of the overall performance of a particle filter. More specifically, we investigate how performance scales with the number of cores and the number of particles.

6.4.1 Redistribution Component in Isolation

Figure 11 compares the performance of the two versions of the redistribution component as a function of the number of particles and number of cores.

On a core-to-core basis, the $\mathcal{O}((\log_2 N)^2)$ redistribution component outperforms the $\mathcal{O}((\log_2 N)^3)$ component across all numbers of particles by a margin of up to a factor of approximately 4 (for 16 cores).

For all numbers of particles, increasing the number of cores improves performance for both variants of the redistribution component. However, in the context of both variants, the improvement in performance when considered as a ratio is less than the ratio of the number of cores.

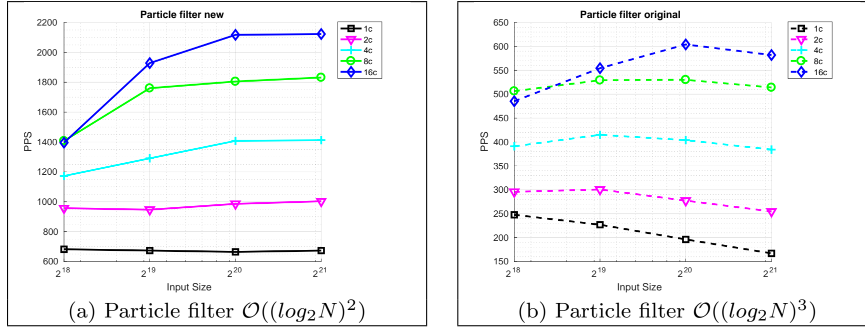
In the context of the $\mathcal{O}((\log_2 N)^3)$ variant, increasing the number of particles for a fixed number of cores can significantly reduce the number of particles processed per second. This is not the case for the $\mathcal{O}((\log_2 N)^2)$ variant.

For the $\mathcal{O}((\log_2 N)^2)$ variant, increasing the number of particles while keeping the number of cores constant improves the number of particle processed per second. However, in the context of the $\mathcal{O}((\log_2 N)^3)$ variant, increasing the number of particles for a fixed number of cores can reduce the number of particles processed per second.

6.4.2 Resulting Overall Particle Filter Performance

Figure 12 compares the performance of the original particle filtering algorithm when using the two variants of the redistribution component.

The comparative performance that was observed in the context of the redistribution component in isolation is also evident when comparing the performance of the overall particle filter. Indeed, the use of the $\mathcal{O}((log_2 N)^2)$ variant of redistribution results in (approximately) a fourfold increase in the number



(a) Particle filter $\mathcal{O}((log_2 N)^2)$ (b) Particle filter $\mathcal{O}((log_2 N)^3)$

Fig. 12 Performance of the overall particle filter using the two variants of the redistribution component.

of particles processed per second. The trends that were observed in the context of the redistribution component in isolation are also apparent in the context of the overall particle filter.

6.5 Speedup and Scalability Analysis

We now focus on the speedup that the $\mathcal{O}((log_2 N)^2)$ variant of the redistribution component offers relative to the $\mathcal{O}((log_2 N)^3)$ variant and the scalability of the $\mathcal{O}((log_2 N)^2)$ variant, i.e., the extent to which using more cores improves performance.

We quantify speedup as the ratio of the number of particles per second for a fixed number of particles and number of cores. We quantify scalability, in the context of a fixed number of particles[25], as the ratio of the number of particles per second with N cores relative to the number of particles per second with a single core.

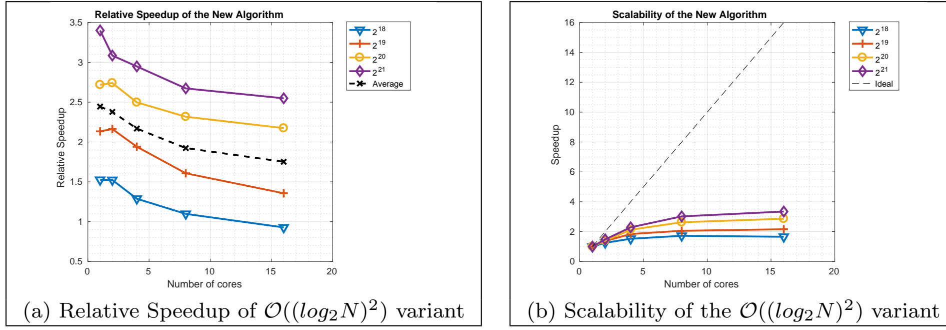
We compare performance in the context of both platforms for various different numbers of particles.

6.5.1 Redistribution Component in Isolation

Figures 13 and 14 describe the speedup and scalability of the $\mathcal{O}((log_2 N)^2)$ redistribution component in the context of platforms 1 and 2 respectively.

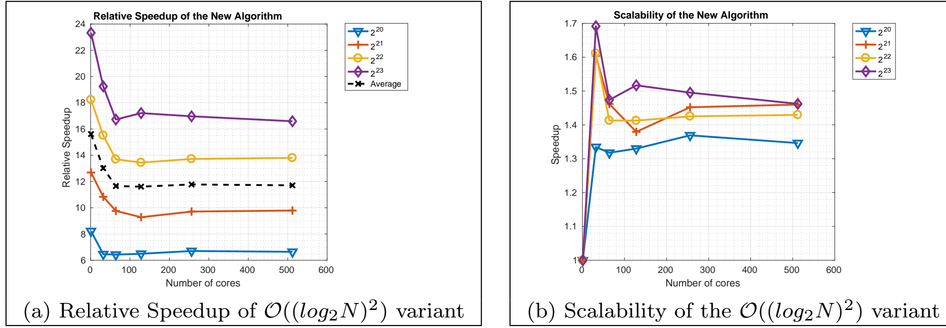
We note that the relative speedup of the $\mathcal{O}((log_2 N)^2)$ variant of the redistribution component (relative to the $\mathcal{O}((log_2 N)^3)$ variant) is significant in all cases: between 2 (on Platform 1) and 24 (on Platform 2). For both platforms, this speedup increases as the number of particles is increased. However, we also note that, with Platform 1 (which has a single node such that all cores share memory), the speedup decreases as the number of cores is increased for a fixed number of particles. In contrast, with platform 2, the speedup is broadly constant for large numbers of cores.

[25] Since the problem size remains fixed, we are actually quantifying *strong scaling* [23].



(a) Relative Speedup of $\mathcal{O}((log_2 N)^2)$ variant (b) Scalability of the $\mathcal{O}((log_2 N)^2)$ variant

Fig. 13 Relative Speedup and Scalability of the $\mathcal{O}((log_2 N)^2)$ variant of the Redistribution component on Platform 1.



(a) Relative Speedup of $\mathcal{O}((log_2 N)^2)$ variant (b) Scalability of the $\mathcal{O}((log_2 N)^2)$ variant

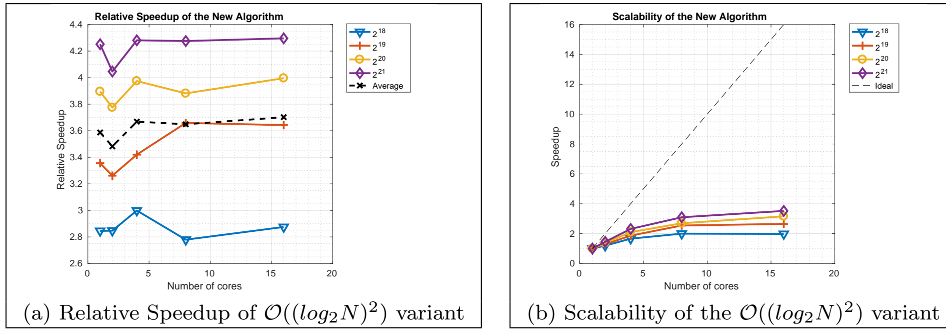
Fig. 14 Relative Speedup and Scalability of the $\mathcal{O}((log_2 N)^2)$ variant of the Redistribution component on Platform 2.

We also note that the scalability of the $\mathcal{O}((log_2 N)^2)$ variant of the redistribution component is far from ideal: increasing the number of cores culminates in minimal (if any) improvements in performance. This occurs because, in the context of both Platforms, it is the communication, and not the computation, that is limiting performance. This also explains why Platform 2's larger number of cores does not offer improved scalability relative to Platform 1: in Platform 2, the processors are distributed across multiple nodes and communicate across a network, whereas Platform 1's processors are all part of the same node and so communicate using shared memory.

6.5.2 Resulting Overall Particle Filter Performance

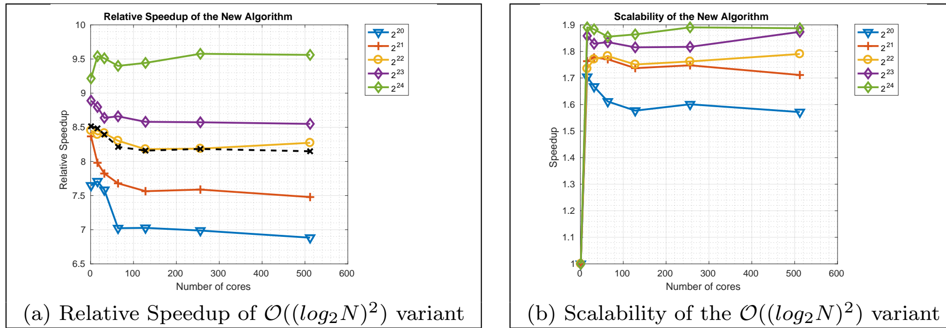
Figures 15 and 16 describe the speedup and scalability of the overall particle filter using the $\mathcal{O}((log_2 N)^2)$ redistribution component in the context of platforms 1 and 2 respectively.

The speedups, as measured in the context of the overall particle filter algorithm are between 3 and 9.5. Again, for both platforms, the speedup increases with the number of particles. Again, the scalability is far from ideal.



(a) Relative Speedup of $\mathcal{O}((log_2 N)^2)$ variant (b) Scalability of the $\mathcal{O}((log_2 N)^2)$ variant

Fig. 15 Relative Speedup and Scalability of the overall particle filter algorithm using the $\mathcal{O}((log_2 N)^2)$ variant of the Redistribution component on Platform 1.



(a) Relative Speedup of $\mathcal{O}((log_2 N)^2)$ variant (b) Scalability of the $\mathcal{O}((log_2 N)^2)$ variant

Fig. 16 Relative Speedup and Scalability of the overall particle filter algorithm using the $\mathcal{O}((log_2 N)^2)$ variant of the Redistribution component on Platform 2.

7 Related Work

A review of different resampling techniques is provided in [32]. This review makes clear that, at first sight, some of the key components of a particle filter, notably cumulative sum and redistribution, are inherently sequential[26].

Indeed, this thinking has motivated research (e.g., as described in [13]) into approaches where a (small) number of Processing Elements (PEs) each perform local resampling and then communicate via a central process that, for example, allocates the particles to the PEs (a process that, as demonstrated in section 6, results in non-deterministic run-time). In contrast to the approaches involving communication between PEs, this paper is focused on a fully distributed algorithm (with no explicit central process and so no implicit assumption of a small number of PEs).

[26] The review also highlights challenges associated with, for example, multiple processors generating independent random number sequences, discusses the relative merits of using floating-point and fixed-point numbers and points to papers discussing architecture-specific issues (e.g., in [20, 21, 26, 27]).

The detailed comparison of different (single processor implementations of) resampling algorithms provided in [25] highlights that systematic resampling offers the best performance amongst the approaches considered. One strategy for parallel implementation (discussed in [13] and explored in more detail elsewhere [35]) is to deliberately choose an alternative resampling algorithm such that the alternative algorithm is more amenable to parallel implementation. This paper focuses on systematic resampling specifically.

Another approach that [32] highlights involves each particle performing resampling using only information from its local neighbours (e.g., as described in [34], which, in the view of the authors, does not make obvious that, if the resampling is performed locally then the weight after resampling should be proportional to the local normalising constant[27]). In contrast to approaches based on considering only local neighbours, this paper describes approaches that provide exactly the same output as a single processor would have generated.

Research not explicitly covered in the aformentioned review includes the implementation described in [33] and which this paper explicitly builds upon. That implementation achieves $\mathcal{O}((\log N)^3)$ time-complexity with N parallel processors (and achieves a run-time that is not data dependent). Other related research includes (in [40]) a more complex, parallelised particle filter that uses a context-aware scheduling algorithm. They address the load imbalance arising from the naïve parallelisation of the particle filtering by using a custom (but reusable) scheduler. In this paper, we replace the use of such a scheduler at run-time by algorithmic development at design-time.

There has been previous work on implementing particle filters in a MapReduce context (e.g., in [9, 10]). However, this research has focused on using Hadoop and has not included a similar analysis to that documented in section 6 of this paper. Our analysis in that section of this paper indicates that substantial improvements are possible using Spark but also highlights that the speed-up offered using MapReduce and large numbers of processors is somewhat disappointing.

8 Conclusions

In this paper we have developed an improved parallel particle filtering algorithm. The core novelty is a novel redistribution component. The component provides deterministic run-time and a time-complexity of $\mathcal{O}((\log N)^2)$ (with

[27] More mathematically, assume the ith particle has a weight (before resampling) of w_i and the jth member of the new population is resampled as a copy of the ith particle with probability of $\frac{w_i}{\sum_{i' \in I_j} w_{i'}}$ where I_j is the set of particles that are local to the jth particle. The (unnormalised) weight after resampling (based on considering the resampling process in terms of importance sampling) is $w_i \times \frac{\sum_{i' \in I_j} w_{i'}}{w_i} = \sum_{i' \in I_j} w_{i'}$. The normalised weight would then be proportional to this unnormalised weight, but scaled such that the normalised weight sums to one over all particles.

N particles and N processors). This improves on a previous approach that achieved a time-complexity of $\mathcal{O}((\log N)^3)$.

A particle filter (including both the previous and new redistribution components) has been implemented using two Big Data frameworks, Hadoop and Spark. Extensive performance evaluation has been conducted. Our new component outperforms the original version in isolation and when considering a particle filter that uses the new component in place of the original version. Our results indicate that, in the context of a particle filter, Spark's ability to perform calculations in memory enable it to offer a 25-fold improvement in run-time relative to Hadoop. Using Spark and our new component, we go on to show that, as the number of particles increases, so does the implementation efficiency.

The implementation we evaluated is limited by the communications overhead necessarily associated with giving each particle a unique key in the MapReduce framework: as a result, while we can achieve a speed-up of 3-fold with 16 cores in a single node, with 512 cores spread across 28 nodes, we only achieve a speed-up of approximately 1.4 (i.e., less). Furthermore, our implementation is outperformed by a naïve implementation by a factor of approximately 20. Put simply, using our current implementation, we cannot yet outperform an (optimised) single processor resampling algorithm.

Of course, there will be applications where resampling is a small fraction of the total computational cost of the particle filter. In such contexts, the proposal, likelihood and/or dynamic model will be computationally demanding to calculate. These components of the particle filter are trivial to parallelise. Our future work will aim to broaden the applicability of our results beyond those applications. More specifically, we plan to focus on architectures involving a single key being related to multiple particles, explicitly minimising the need for data movement and removing the large lineages that appear to be limiting the performance possible using Spark.

Finally, we note that we have made our implementations available for public access via an OpenSource repository at GitHub as `particlefilter` [6].

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Competing interests

The authors declare that they have no competing interests.

Authors contributions

Simon Maskell proposed the novel algorithm for redistribution in $\mathcal{O}((\log N)^2)$ time. Jeyan Thiyagalingam led on defining the strategy for MapReduce implementation. Lykourgos Kekempanos conducted the detailed implementation and ran the simulations. All authors contributed to the drafting of the manuscript and approved the final versions.

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