Massively Parallel Construction of Radix Tree Forests for the Efficient Sampling of Discrete Probability Distributions

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Abstract We compare different methods for sampling from discrete probability distributions and introduce a new algorithm which is especially efficient on massively parallel processors, such as GPUs. The scheme preserves the distribution properties of the input sequence, exposes constant time complexity on the average, and significantly lowers the average number of operations for certain distributions when sampling is performed in a parallel algorithm that requires synchronization afterwards. Avoiding load balancing issues of naïve approaches, a very efficient massively parallel construction algorithm for the required auxiliary data structure is complemented.

1 Introduction

In many applications, samples need to be drawn according to a given discrete probability density

\[ p := (p_1, p_2, \ldots, p_n), \]

where the \( p_i \) are positive and \( \sum_{i=1}^{n} p_i = 1 \). Defining \( P_0 := 0 \) and the partial sums \( P_k := \sum_{i=1}^{k} p_i \) results in \( 0 = P_0 < P_1 < \cdots < P_n = 1 \), which forms a partition of the unit interval \([0,1)\). Then the inverse cumulative distribution function (CDF)

\[ P^{-1}(x) = i \iff P_{i-1} \leq x < P_i \]

can be used to map realizations of a uniform random variable \( \xi \) on \([0,1)\) to \(\{1,2,\ldots,n\}\) such that

\[ \text{Prob}(\{P_{i-1} \leq \xi < P_i\}) = p_i. \]
Fig. 1: Drawing 1024 samples according to a given discrete probability distribution (left), a monotonic mapping (middle) can preserve uniformity properties of an input sample sequence (middle), while the non-monotonic alias map (right) negatively affects uniformity.

Besides identifying the most efficient such mapping, we are interested in transforming low discrepancy sequences [8] and how such mappings affect the uniformity of the sequence to be transformed. An example for such a sampling process is shown in Figure 1.

The article is organized as follows: After reviewing several algorithms to sample according to a given discrete probability density by transforming uniformly distributed samples in Section 2, massively parallel algorithms to construct auxiliary data structures for the accelerated computation of $P^{-1}$ are introduced in Section 3. The results of the scheme that preserves distribution properties, especially when transforming low discrepancy sequences, are presented in Section 4 and discussed in Section 5 before drawing the conclusions.

2 Sampling from Discrete Probability Densities

In the following we will briefly survey existing methods to evaluate the inverse mapping $P^{-1}$ and compare their properties with respect to computational complexity, memory requirements, memory access patterns, and sampling efficiency.

2.1 Linear Search

A linear search computes the inverse mapping $P^{-1}$ by subsequently checking all intervals for inclusion of the value of the uniformly distributed variable $\xi$. This is simple, does not require additional memory, achieves very good performance for a
small number \( n \) of values, and scans the memory in linear order. However, its average and worst case complexity of \( \mathcal{O}(n) \) makes it unsuitable for large \( n \). In the example in Figure 2, four comparison operations are required to identify the interval \( i = 3 \) that includes \( \xi \).

![Fig. 2: Linearly searching through all intervals until the interval containing the variable \( \xi \) is found, requires \( \mathcal{O}(n) \) steps on the average. In this example four comparisons are required.](image)

### 2.2 Binary Search

Binary search lowers the average and worst case complexity of the inverse mapping \( P^{-1} \) to \( \mathcal{O}(\log_2 n) \) by performing bisection. Again, no additional memory is required, but memory no longer is accessed in linear order. Figure 3 shows binary search for the given example, where \( \xi = 0.5 \) is found to be included in the interval \( i = 3 \).

![Fig. 3: Binary search bisects the list of potential intervals in each step and hence has an average case and worst case complexity of \( \mathcal{O}(\log_2 n) \). In this example two comparisons are required.](image)
2.3 Binary Trees

While the average case and worst case complexity of performing the inverse mapping \( P^{-1} \) with an explicitly stored tree does not get below \( \mathcal{O}(\log_2 n) \), allowing for arbitrary tree structures enables further optimization over the fixed structure induced by bisection with binary search. Again, memory access is not in linear order, but due to the information required to identify the two children of each node in the tree, \( \mathcal{O}(n) \) additional memory must be allocated and transferred. It is important to note that the worst case complexity may be as high as \( \mathcal{O}(n) \) if the tree is completely unbalanced.

2.4 \( k \)-ary Trees

In practice it can be beneficial to use trees with a branching factor higher than two, even though in theory more memory is transferred and more comparisons are performed on the average, as due to the higher branching factor larger chunks of memory are loaded. These access patterns are beneficial on most hardware architectures, since the smallest granularity of memory transfer is almost always larger than what would be needed to perform a single comparison and get the index of one or the other child. The average case complexity for a branching factor \( k \) is \( \mathcal{O}(\log_k n) \), but the number of comparisons is either increased to \( \log_2 k \) (binary search in children) or even \( k - 1 \) (linear scan over children) in each step, and therefore either equal or greater than for binary trees on the average.

Fig. 4: The Cutpoint Method uses a guide table that uniformly partitions the unit interval and stores the first interval that overlaps each cell (shown below each cell). These indices are then used as starting points for linear search. In this example only a single lookup is required; in general the average case complexity is \( \mathcal{O}(1) \).
2.5 The Cutpoint Method

By employing additional memory, the indexed search [2], also known as the Cutpoint Method [5], can perform the inverse mapping $P^{-1}$ in $O(1)$ on the average. Therefore, the unit interval is partitioned into $m$ cells of equal size and a *guide table* stores each first interval that overlaps a cell as illustrated in Figure 4. Starting with this interval, linear search is employed to find the one that includes the realization of $\xi$. As shown in [3, Chapter 2.4], the expected number of comparisons is $1 + \frac{n}{m}$. In the worst case all but one interval are located in a single cell and since linear search has a complexity of $O(n)$, the worst case complexity of the Cutpoint Method is also $O(n)$. Sometimes, these worst cases can be avoided by recursively nesting another guide table in cells with many entries. In general, however, the problem persists. If nesting is performed multiple times, the structure of the nested guide tables is similar to a $k$-ary tree (see Section 2.4) with implicit split values defined by the equidistant partitioning.

Another way of improving the worst case performance is using binary search instead of linear search in each cell of the guide table. No additional data needs to be stored since the index of the first interval of the next cell can be conservatively used as the last interval in the current cell. The resulting complexity remains $O(1)$ on the average, but improves to $O(\log_2 n)$ in the worst case.

![Fig. 5: Similar to the Cutpoint Method, the Alias Map uses an additional table that uniformly partitions the unit interval. However, the Alias Map cuts and redistributes the intervals so that each cell contains at most two intervals, the first one being the interval with the same index as the cell and a second one that covers the rest of the range of the cell. Then, by storing the index of the second interval in each cell and the split points $q_j$ of each cell with index $j$, the mapping can always be evaluated in $O(1)$, and in our example, as before, only a single lookup is required to find the interval $i = 3$ including $\xi = 0.5$.](image-url)
2.6 The Alias Map

Using an Alias Map [10, 11], the inverse $P^{-1}$ can be evaluated in $O(1)$ both in the average as well as in the worst case. It avoids the worst case by cutting and reordering the intervals such that each cell contains at most two intervals, and thus neither linear search nor binary search is required. For the example used in this article, a resulting table is shown in Figure 5.

Unfortunately, the reordering of the intervals comes with unpleasant side effects for quasi-Monte Carlo methods [8]. As intervals are reordered, the low discrepancy of a sequence may be destroyed. This especially affects regions with high probabilities (see Figure 7). In such regions, many samples are aliases of samples in low-density regions, which is intrinsic to the construction of the alias map. Hence the resulting set of samples cannot be guaranteed to be of low discrepancy, which may harm convergence speed as shown in Figure 8. As a second example, the one-dimensional distribution in Figure 6 as approximated by the alias map method exposes a high approximation error for regions with high densities.

3 An Efficient Monotonic Inverse Mapping

In the following, a method is introduced that accelerates finding the inverse $P^{-1}$ of the cumulative distribution function and therefore preserves the distribution properties. Similar to the Cutpoint Method with binary search, the mapping can be performed in $O(1)$ on the average and in $O(\log_2 n)$ in the worst case. However, we improve the average case performance by explicitly storing a more optimal hierarchical structure that improves the average case of finding values that can not be immediately identified using the guide table.

Instead of optimizing for the minimal required memory footprint to guarantee access in constant time, we dedicate $O(n)$ additional space for the hierarchical structure and propose to either assign as much memory as affordable for the guide table or to select its size proportional to the size of the discrete probability distribution $P$.

As explained in the previous section, monotonicity of the inverse mapping $P^{-1}$ is an absolute necessity for our quasi-Monte Carlo simulations. At the same time, the massively parallel execution on Graphics Processing Units (GPUs) suffers more from outliers than serial computation since computation is performed by a number of threads organized in groups (“warps”), which need to synchronize and hence only finish after the last thread in this group has terminated. Therefore, lengthy computations that would otherwise be averaged out need to be avoided.

While the Cutpoint Method does preserve monotonicity, and with binary search avoids the worst case, it does not yield good performance for the majority of cases in which an additional search in each cell needs to be performed. Therefore, we combine the Cutpoint Method with a binary tree which especially optimizes these cases.
Radix trees are of special interest since they can be very efficiently built in parallel [1, 6]. Section 3.1 introduces their properties and their efficient parallel construction. Furthermore, their underlying structure that splits intervals in the middle is nearly optimal for this application.

However, as many trees of completely different sizes are required, a naïve implementation that builds these trees in parallel results in severe load balancing issues. In Section 3.2 we therefore introduce a method that builds the entire radix tree forest simultaneously in parallel, but instead of parallelizing over trees, parallelization is uniformly distributed over the data.

Fig. 6: Sampling proportional to a one-dimensional density with the Alias Map often converges significantly slower than sampling the inverse cumulative distribution, especially in regions with high densities. In this example the discrete target probability distribution is the continuous black curve sampled at 64 equidistant steps.
Fig. 7: Due to the reordering of intervals that the Alias Map performs to guarantee a complexity of \( O(1) \) even in the worst case, the uniformity of distribution (white dots) degrades. This is especially bad in regions with a high probability density (grey). In these examples, the two-dimensional target density is shown in the background as a gradient from black (low density) over red and yellow to grey (high density). The low discrepancy Hammersley point set served as sequence of uniformly distributed points to be transformed.
3.1 Massively Parallel Construction of Radix Trees

In a radix tree, also often called compact prefix tree, the value of each leaf node is the concatenation of the values on the path to it from the root of the tree. The number of children of each internal node is always greater than one; otherwise the values of the node and its child can be concatenated already in the node itself. An example of a radix tree is shown in Figure 9.

Radix trees over integers with a radix of two are of particular interest for hardware and software operating on binary numbers. Since by definition each internal node has exactly two children, there exists an enumeration scheme for these trees that determines the index each node only given the range of input values below its children: The index of each node is the lowest data index below its right, or, equivalently, the highest data index below its left child plus one. This information is not only available if the tree is built top-down by recursive bisection, but can also easily be propagated up when building the tree bottom-up. The index of the parent node, implied by this enumeration rule, is then the lowest index below the current node if the current node is a right child and consequently equals the highest index below the current node plus one if it is a right child. Determining whether a node is a left or a right child can be done by comparing the input values at the boundaries to its neighbors outside the range of nodes below it. If the binary distance, determined by taking the bit-wise exclusive or, of the leftmost input value below the node to its left neighbor is smaller
Fig. 9: In a radix tree, or compact prefix tree, values are encoded in the nodes or edges along each path. Each internal node has at least two and at most $r$ children for a radix of $r$. Node indices are shown inside each internal node, data indices are below the input values in the square boxes.

than the distance of the rightmost input value below the node to its right neighbor, it must be a right child. Otherwise it is a left child.

Given this scheme, these trees can be built from bottom up completely in parallel since all information required to perform one merging step can be retrieved without synchronization. The only synchronization required ensures that only one of the children merges further up, and does that after its sibling has already reported the range of nodes below it.

The implementation of the method presented in Algorithm 1 uses an atomic exchange operation ($\text{atomicExch}$) and an array initialized to -1 for this synchronization. The ⊕ operator performs a bitwise exclusive or operation on the floating point representation of the input value. As the ordering of IEEE 754 floating point numbers is equal to the binary ordering, taking the exclusive or of two floating point numbers calculates a value in which the position of the most significant bit set to one indicates the highest level in the implicit tree induced by recursive bisection of the interval $[0, 1)$ on which the two values are not referenced by the same child. Hence, the bitwise exclusive or operation determines the distance of two values in such a tree.

### 3.2 Massively Parallel Construction of Radix Tree Forests

A forest of radix trees can be built in a similar way. Again, parallelization runs over the whole data range, not over the individual trees in the forest. Therefore, perfect load balancing can be achieved. As highlighted in Algorithm 1, the key difference between building a single tree and a forest is that in each merging step it must be
checked whether merging would go over partition boundaries of the forest. Avoiding such a merge operation over a boundary is as simple as setting the distance (again computed using $\oplus$) to the maximum.

Note that node indices for small (sub-) trees are always consecutive by design, which improves cache hit rates, which furthermore can be improved by interleaving the values of the cumulative distribution and the indices of the children.

**Algorithm 1** Parallel constructing a radix tree forest. Omitting the colored parts results in the construction of a radix tree, only.

**Input:** $data \in [0, 1)^n$ in increasing order, number of partitions $m$

**Output:** $n$ nodes, each with indices of the left and right child

$otherBounds \leftarrow (-1, ..., -1) \in \mathbb{Z}^n$

$data[-1] \leftarrow data[n] = 1$

for $i \in [0, n)$ in parallel do

nodeId $\leftarrow \text{leaf}_i$

curCell $\leftarrow [data[i] \cdot m]$

range $\leftarrow (i, i)$

repeat

valueLow $\leftarrow data[range[0]]$

valueHigh $\leftarrow data[range[1]]$

valueNeighborLow $\leftarrow data[range[0] - 1]$

valueNeighborHigh $\leftarrow data[range[1] + 1]$

if $[valueNeighborLow \cdot m] < curCell$ then

$\text{valueNeighborLow} \leftarrow 1$

end if

if $[valueNeighborHigh \cdot m] > curCell$ then

$\text{valueNeighborHigh} \leftarrow 1$

end if

child $\leftarrow \begin{cases} 0 & \text{valueLow} \oplus \text{valueNeighborLow} > \text{valueHigh} \oplus \text{valueNeighborHigh} \\ 1 & \text{otherwise} \end{cases}$

parent $\leftarrow \begin{cases} range[1] + 1 & \text{child} = 0 \\ range[0] & \text{child} = 1 \end{cases}$

$\text{nodes[parent].child[child]} \leftarrow \text{nodeId}$

otherBound $\leftarrow \text{atomicExch} \begin{pmatrix} otherBounds[parent] \\ range[0] \quad child = 0 \\ range[1] \quad child = 1 \end{pmatrix}$

if $\text{otherBound} \neq -1$ then

range[1 - child] $\leftarrow$ otherBound

nodeId $\leftarrow$ parent

end if

until otherBound = -1

end for

We indicate that a cell in the guide table is only overlapped by a single interval by setting its reference to the two’s complement of the index of the interval. Then, a most significant bit set to one identifies such an interval, and one unnecessary indirection is avoided. If the size of the distribution is sufficiently small, further information could also be stored in the reference, such as a flag that there are exactly
two intervals that overlap the cell. Then, only one comparison must be performed and there is no need to explicitly store a node.

Building the radix forest is slightly faster than building a radix tree over the entire distribution since merging stops earlier. However, we found the savings to be almost negligible, similarly to the effort required to set the references in the guide table.

4 Results

We evaluate our sampling method in two steps: First, we compare to an Alias Map in order to quantify the impact on convergence speed. Second, we compare to the Cutpoint Method with binary search which performs the identical mapping and therefore allows one to quantify execution speed.

Figure 7 illustrates how sampling is affected by the discontinuities of the Alias Map. Figure 11 shows the result of numerical experiments, where for both the Alias Map and sampling using the inverse cumulative distribution function Hammersley points have been transformed. We measure the sum of the quadratic deviations of the sample density to the target density.
The results indicate that sampling with the Alias Map may indeed be less efficient.

Table 1 details the performance improvement of our method as compared to the Cutpoint Method with binary search for the distributions shown in Figure 12. As expected, the sampling performance of the new method is similar to the Cutpoint Method with binary search, which shares the same primary acceleration data structure, the guide table. For reasonable table sizes both perform almost as good as sampling with an Alias Map, however, do so without affecting the distribution quality.

Sampling densities with a high dynamic range can be efficiently accelerated using the cutpoint method and its guide table. However, since then some of its cells contain many small values with largely different magnitudes, performance suffers from efficiency issues of index bisection. Radix tree forests improve on this aspect by storing an explicit tree (see the parallel Algorithm 1).

Our method only marginally improves the average search time as compared to the cutpoint method with binary search since the overall time is largely dominated by the time required to find large values. For every value that can be directly determined from the guide table – since it is the only one in a cell – this process is already
optimal. In some cases the average search time of our new method can be slightly slower since manually assigning the interval overlapping from the left as the left child of the root node the tree deteriorates overall tree quality (see Table 1, example “4 spikes”). On the other hand, performing bisection to find a value inside a cell that includes many other values does not take the underlying distribution into account and is therefore suboptimal. Still, since these values are sampled with a low probability, the impact on the average sampling time is low.

The optimizations for values with a lower probability become more important in parallel simulations where the slowest simulation determines the run time for every group. The “4 spikes” example is a synthetic bad case for our method: Spikes are efficiently sampled only using the guide table, whereas all other values have uniform probabilities. Therefore binary search is optimal. The explicit tree, on the other hand, always has one sub-optimal first split to account for intervals overlapping from the left, and therefore requires one additional operation.

In practice, parallel execution of the sampling process often requires synchronization, and therefore suffers more from the outliers: Then, the slowest sampling process determines the speed of the entire group that is synchronized. On Graphics Processing Units (GPUs), such groups are typically of size 32. Under these circumstances

Fig. 12: Example distributions for the numerical results in Table 1.
Table 1: Measuring the maximum and average number of memory load operations required for searching as well as the average number of load operations or idle operations if 32 simulations need to be synchronized (average\textsubscript{32}) shows that while the maximum number of load operations is increased, for distributions with a high range the average number of load operations is typically reduced.

\begin{tabular}{llll}
\toprule
$p_i \sim i^{20}$ & maximum & average & average\textsubscript{32} \\

cutpoint method + binary search & 8 & 1.25 & 3.66 \\
cutpoint method + radix forest & 16 & 1.23 & 3.46 \\
\midrule
$p_i \sim (i \mod 32 + 1)^{25}$ & maximum & average & average\textsubscript{32} \\
cutpoint method + binary search & 6 & 1.30 & 4.62 \\
cutpoint method + radix forest & 13 & 1.22 & 3.72 \\
\midrule
$p_i \sim (i \mod 64 + 1)^{35}$ & maximum & average & average\textsubscript{32} \\
cutpoint method + binary search & 7 & 1.19 & 4.33 \\
cutpoint method + radix forest & 13 & 1.11 & 2.46 \\
\midrule
“4 spikes” & maximum & average & average\textsubscript{32} \\
cutpoint method + binary search & 4 & 1.60 & 3.98 \\
cutpoint method + radix forest & 5 & 1.67 & 4.93 \\
\bottomrule
\end{tabular}

our method performs significantly better for distributions with a high dynamic range (see Table 1, third column).

It is important to note that if the maximum execution time is of concern, binary search almost always achieves the best worst case performance. Then explicit tree structures can only improve the average time if the maximum depth does not exceed the number of comparisons required for binary search, which is the binary logarithm of the number of elements.

5 Discussion

A multi-dimensional inversion method proceeds component by component; the two-dimensional distributions in Figure 7 have been sampled by first calculating the cumulative density function of the image rows and one cumulative density function for each row. Then, after selecting a row its cumulative density is sampled to select the column. Finally, as distributions are considered piecewise constant, a sub-pixel position is required. Therefore, the relative position in the pixel is calculated by rescaling the relative position in the row/column to the unit interval. Other approximations, such as piecewise linear or piecewise quadratic require an additional, simple transformation of the relative position [4].

Building multiple tables and trees simultaneously, e.g. for two-dimensional distributions, is as simple as adding yet another criterion to the extended check in
Algorithm 1: If the index of the left or right neighbor goes beyond the index boundary of a row, it is a leftmost or a rightmost node, respectively.

Algorithm 1 constructs binary trees. Due to memory access granularity, it may be beneficial to construct 4-ary or even wider trees. A higher branching factor simply results by just collapsing two (or more) levels of the binary trees.

For reasonable table sizes, the cutpoint method with binary search preserves the properties of the input samples at a memory footprint comparable to the one required for the Alias Map. Radix forest trees require additional memory to reference two children for each value $p_i$ of the distribution.

Depending on the application and space constraints, it may be beneficial to use balanced trees instead of radix trees. Balanced trees do not need to be built; their structure is implicitly defined, and for each cell we only need to determine the first and last interval that overlap it. Then, the implicit balanced tree is traversed by consecutive bisection of the index interval.

6 Conclusion

Radix tree forests trade additional memory for faster average case search and come with a massively parallel construction algorithm with optimal load balancing independent of the probability density function $p$.

While the performance of evaluating the inverse cumulative distribution function $P^{-1}$ is improved for highly nonuniform distributions $p$ with a high dynamic range, performance is slightly worse on distributions which can already be efficiently sampled using the cutpoint method with binary search. Furthermore, the improvement of the average case comes at the price of worsening the worst case performance.

Thus the choice of the best sampling algorithm depends on the actual application. For example, using high dynamic range video environment maps to illuminate computer generated scenes greatly benefits from the efficient parallel construction and sampling of radix tree forests.

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