Abstract
The probability Jaccard similarity was recently proposed as a natural generalization of the Jaccard similarity to measure the proximity of sets whose elements are associated with relative frequencies or probabilities. In combination with a hash algorithm that maps those weighted sets to compact signatures which allow fast estimation of pairwise similarities, it constitutes a valuable method for big data applications such as near-duplicate detection, nearest neighbor search, or clustering. This paper introduces a class of locality-sensitive one-pass hash algorithms that are orders of magnitude faster than the original approach. The performance gain is achieved by calculating signature components not independently, but collectively. Four different algorithms are proposed based on this idea. Two of them are statistically equivalent to the original approach and can be used as direct replacements. The other two may even improve the estimation error by breaking the statistical independence of signature components. Moreover, the presented techniques can be specialized for the conventional Jaccard similarity, resulting in highly efficient algorithms that outperform traditional minwise hashing.

1 Introduction

The calculation of pairwise object similarities is an important task for clustering, near-duplicate detection, or nearest neighbor search. Big data applications require sophisticated algorithms to overcome time and space constraints. A widely used technique to reduce costs for pairwise similarity computations is minwise hashing (MinHash) [3]. It allows the calculation of signatures for individual objects that can be represented as sets of features. Using only the corresponding signatures, the Jaccard similarity can be estimated from the number of equal signature components.

The Jaccard similarity \( J \) of two sets \( A \) and \( B \) is defined as
\[
J = \frac{|A \cap B|}{|A \cup B|}
\]

Minwise hashing maps a set \( S \) to an \( m \)-dimensional signature vector \( z(S) = (z_1(S), z_2(S), \ldots, z_m(S)) \) with statistically independent components that are defined as
\[
z_k(S) := \arg \min_{d \in S} h_k(d) \tag{1}
\]

where \( h_k \) are independent hash functions with identically distributed output. If hash collisions of \( h_k \) are very unlikely and can be ignored, the probability that the same signature components of two different sets \( A \) and \( B \) have the identical value is equal to the Jaccard similarity
\[
\Pr(z_k(A) = z_k(B)) = J. \tag{2}
\]

This property allows unbiased estimation of \( J \) using the estimator
\[
\hat{J}(z(A), z(B)) = \frac{1}{m} \sum_{k=1}^{m} 1(z_k(A) = z_k(B)) \tag{3}
\]

where \( 1 \) denotes the indicator function. The variance of this estimator is
\[
\text{Var}(\hat{J}(z(A), z(B))) = \frac{J(1 - J)}{m}, \tag{4}
\]

because the signature components are independent according to (1) and the number of equal components in \( z(A) \) and \( z(B) \) is binomially distributed with success probability \( J \).

1.1 Incorporating Weights

Describing objects as feature sets is not always appropriate. Sometimes features are associated with some weight. For example, text documents can be represented as bag of words weighted according to their term frequency-inverse document frequency [13]. Multiple approaches have been proposed to generalize the Jaccard similarity to weighted sets. For the mathematical representation of weighted sets we use weight functions. A weight function gives for each element its associated nonnegative weight. It can be extended to a mapping from the universe of all possible elements \( D \), if elements not belonging to the corresponding weighted set are considered to have zero weight.

The weighted Jaccard similarity \( J_W \) is one way to generalize the Jaccard similarity \( J \) and is defined as
\[
J_W = \frac{\sum_{d \in D} \min(w_A(d), w_B(d))}{\sum_{d \in D} \max(w_A(d), w_B(d))}.
\]

Here \( w_A \) and \( w_B \) are the weight functions for weighted sets \( A \) and \( B \), respectively. \( J \) and \( J_W \) are identical for a set, whose elements have weight equal to 1 while all remaining elements of the universe \( D \) have weight 0. Various hash algorithms have been developed to calculate signatures that allow the estimation of \( J_W \) using estimator (3) [8, 11, 29].

Sometimes the scale of feature weights is not important. This is for example the case if they describe relative frequencies or probabilities. A simple solution is the normalization of weights before calculating \( J_W \) to achieve scale-invariance [14, 32]. This leads to the normalized weighted Jaccard similarity
\[
J_N = \frac{\sum_{d \in D} \min \left( \frac{w_A(d)}{\sum_{d' \in D} w_A(d')}, \frac{w_B(d)}{\sum_{d' \in D} w_B(d')} \right)}{\sum_{d \in D} \max \left( \frac{w_A(d)}{\sum_{d' \in D} w_A(d')}, \frac{w_B(d)}{\sum_{d' \in D} w_B(d')} \right)}.
\]
However, a more natural extension of $J$ to discrete probability distributions is the probability Jaccard similarity

$$J_p = \frac{\sum_{d \in D} \max \left( \frac{w_A(d')}{w_A(d)}, \frac{w_B(d')}{w_B(d)} \right)}{\sum_{d \in D} \max \left( \frac{w_A(d')}{w_A(d)}, \frac{w_B(d')}{w_B(d)} \right)}$$

which is scale-invariant by definition and which was proposed recently together with an appropriate locality-sensitive hash algorithm [21]. The algorithm uses the hash functions

$$h_k(d) := y_k(d)/w(d),$$

for the signature computation given by (1), where

$$y_k(d) \sim \text{Exp}(\lambda)$$

are hash functions with an exponentially distributed output. The rate parameter $\lambda$ is a free parameter and has no influence on the signature. The resulting signature satisfies $\Pr(z_k(A) = z_k(B)) = J_p$ and therefore allows unbiased estimation of $J_p$ from the proportion of equal components using estimator (3). If $y_k(d)$ for all $k \in \{1, 2, \ldots, m\}$ are independent, the signature components will be independent as well and the variance of the estimator will be $J_p(1 - J_p)/m$ analogous to (4). As $J_N$, $J_P$ corresponds to $J$ in case of binary weights $w(d) \in \{0, 1\}$ and can therefore be regarded as generalization of the Jaccard similarity $J$. In this case, the corresponding signature is equivalent to the MinHash signature (1), because the outputs of hash functions $h_k(d)$ given by (5) are identically distributed for $w(d) = 1$.

The signature definition (1) together with hash functions (5) can be straightforwardly translated into an algorithm called P-MinHash [21] shown as Algorithm 1. Instead of using $m$ independent hash functions, we use a pseudorandom number generator (PRNG) $R$ seeded with a hash value of $d$ to generate independent and exponentially distributed values. Since the rate parameter of the exponential distributed random values in (6) is a free parameter, $\lambda = 1$ is used for simplicity. $R[\text{Exp}(\lambda)]$ denotes the generation of an exponentially distributed random value with rate parameter $\lambda$ using random bits taken from $R$. Since floating-point divisions are more expensive than multiplications, it makes sense to pre-calculate the reciprocal weight $w_{inv}$ as done in Algorithm 1.

### 1.2 Related Work

Interestingly, hash algorithms with collision probabilities equal to $J_P$ have already been unintentionally presented before $J_P$ was actually discovered and thoroughly analyzed in [21]. In [32] a data structure called HistoSketch was proposed to calculate signatures for $J_N$. The derivation started from 0-bit consistent weighted sampling (0-bit CWS) [14], which was proposed as simplification of improved consistent weighted sampling (ICWS) [11]. While the collision probability for ICWS equals $J_N$, it is actually not known for 0-bit CWS and may be far off from $J_N$ [8]. For example, consider two weighted sets, both consisting of the same single element. 0-bit CWS will always have 100% collision probability regardless of the actual weights. Therefore, choosing this algorithm with unknown behavior as starting point for the derivation of a new algorithm is questionable. Nevertheless, after some simplifications and thanks to a nonequivalent transformation that eliminated the scale dependence, the final HistoSketch algorithm had a collision probability equal to $J_P$ instead of the originally desired $J_N$. Without awareness of the correct collision probability, the same authors simplified the HistoSketch algorithm [33] and finally obtained an algorithm that was equivalent to P-MinHash [21]. The successful application of HistoSketch to the calculation of graph embeddings [34] or microbiome analytics [28] prove the usefulness of $J_P$ and corresponding locality-sensitive hash algorithms.

Another but similar attempt to derive a simplified algorithm from 0-bit CWS is given in [26]. However, the use of a slightly different nonequivalent transformation also led to a slightly different hashing algorithm. Even though the algorithm is scale-invariant, the hash collision probability is neither equal to $J_N$ nor equal to $J_P$.

The straightforward implementation of signatures based on (1) leads to time complexities of $\mathcal{O}(nm)$, where $m$ denotes the signature size and $n$ is the set size or the number of elements with nonzero weight $n = \{|d : w(d) > 0|\}$ in the weighted case. A lot of effort was done to break this $\mathcal{O}(nm)$ barrier. By calculating all $m$ signature components in a more collective fashion, much better time complexities of kind $\mathcal{O}(n + m \log^2(m))$ are possible. In case of the conventional Jaccard similarity $J$, One Permutation Hashing (OPH) [16, 18, 30, 31], Fast Similarity Sketching (FSS) [5], or the SuperMinHash algorithm [7] are representatives of such algorithms. They have in common that signature components are not statistically independent. Because of that, the latter two algorithms even have the property that estimation errors are significantly reduced, if $n$ is not much larger than $m$.

As example, the SuperMinHash algorithm defines the hash functions $h_k$ as

$$h_k(d) := u_k(d) + \pi_k(d)$$

in (1). Here $u_k$ is uniformly distributed over $[0, 1)$ and $\pi_k(d)$ are the elements of a random permutation of values $\{0, 1, 2, \ldots, m-1\}$. The corresponding signature satisfies

![Figure 1: The function $\alpha(m, u)$ over $u := |A \cup B|$ for different values of $m$.](image-url)
We propose four different ways to generate exponentially distributed random variables as needed in (5), which then can be directly translated into four new one-pass algorithms called ProbMinHash1, ProbMinHash2, ProbMinHash3, and ProbMinHash4, respectively. All of them are orders of magnitude faster than the original P-MinHash algorithm with the exception of very small input sizes \( n \). The first two are statistically equivalent to the original approach. As our experimental results will show, the latter two are even able to reduce the estimation error due to the statistical dependence of individual signature components. Similar to the SuperMinHash algorithm the variance of estimator (3) is decreased by up to a factor of two for input sizes \( n \) smaller than the signature size \( m \).

We also present a performance optimization for ProbMinHash1 and ProbMinHash3 leading to corresponding equivalent algorithms ProbMinHash1a and ProbMinHash3a, respectively. The interleaved processing of input elements by using an additional buffer can significantly improve performance for medium-sized inputs.

We investigated specializations of all our algorithms for the conventional Jaccard similarity \( J \) which corresponds to the case of binary weights. In this case, ProbMinHash1 and ProbMinHash2 are statistically equivalent to the original minwise hashing approach and can be used as direct replacements. Particularly interesting is the specialization of ProbMinHash3a, which results in a very fast algorithm for \( J \) with a time complexity of \( \mathcal{O}(n + m \log m) \) and a space complexity of \( \mathcal{O}(m \log m) \).

We conducted rigorous experiments using synthetic data to investigate the runtime behavior as well as the estimation error for different input and signature sizes. The results also confirm our theoretical considerations. All source code required to reproduce the results presented in this paper has been published on GitHub at https://github.com/oertl/probminhash.

### 2 Methodology

The computation of signatures for \( J_P \) as defined by (1) and (5) involves \( nm \) independent exponentially distributed random values \( \{z_i\} \). \( m \) hash values, one for each signature component, must be calculated per element. The elements with the smallest hash value finally define the signature. Therefore, while processing elements, the minimum hash values seen so far must be kept for each signature component. In this paper we were able to track this limit efficiently over time, and at the same time, if we were able to generate hash values of an element in ascending order, processing of that element could be stopped as soon as its hash value breached \( q_{\text{max}} \).

Let us consider a positive monotonic increasing random sequence \( X(d) = (x_1(d), x_2(d), \ldots) \) of points. Furthermore, assume the points are randomly labeled with values from \( \{1, 2, \ldots, m\} \). Let \( l_i(d) \) be the label for point \( x_i(d) \). The corresponding random sequence of labels is denoted by \( L(d) = (l_1(d), l_2(d), \ldots) \). If the random sequences \( X(d) \) and

\begin{align}
(2) \quad \text{and the variance of the estimator (3) is}
\end{align}

\begin{align}
\text{Var}(\hat{J}) &= J(1 - J)\alpha(m, u) \quad (7)
\end{align}

where \( u := |A \cup B| \) denotes the union cardinality. \( \alpha(m, u) \) is given by

\begin{align}
\alpha(m, u) &= \frac{1 - \sum_{l=1}^{m-1} \left( l + 1 \right)^u + (l - 1)^u - 2^u}{\left( m - 1 \right)^u m^u (u - 1)} \quad (8)
\end{align}

and shown in Figure 1 for different values of \( m \) [7]. For \( u < m \), the function value tends to be in the range of 0.5, and therefore, the variance (7) is significantly smaller than for the original MinHash algorithm.

The first algorithm for the conventional Jaccard similarity \( J \) that has overcome the \( \mathcal{O}(nm) \) barrier with provable independent signature components was presented in [8] as a special case of the BagMinHash algorithm. More generally, BagMinHash is the first algorithm that has overcome the \( \mathcal{O}(nm) \) barrier for \( J_{1/2} \). For special cases with beforehand known universe and upper bounds for weights another fast approach was presented in [29].

A time complexity proportional to \( nm \) would not be an issue, if both \( n \) and \( m \) were small. However, real world problems often have large feature sizes \( n \). Moreover, it is common that the signature size \( m \) is in the hundreds or even thousands [11, 14, 22, 23, 28, 31]. In particular, indexing techniques like locality-sensitive hashing [2, 10, 17], which enable sublinear nearest neighbor lookups, require many signature components to increase sensitivity and specificity.

Even larger signature sizes are needed, if \( b \)-bit minwise hashing is used [15]. This technique reduces each signature component to only a few bits. The loss of information must be compensated by increasing the number of components in order to achieve the same estimation error. Nevertheless, this approach can significantly reduce the total space requirements of signatures, especially if one is mainly interested in high similarities. Any signature can be easily reduced to a \( b \)-bit signature using Algorithm 2 which transforms each component by taking \( b \) bits from a hash value calculated from the component itself and its index. Since \( b \)-bit values of different elements will collide with high probability, estimator (3) will have a bias that must be accounted for. Moreover, to avoid correlated collisions of different elements over multiple signature components, it is crucial that the hash computation also incorporates the component index.

### 1.3 Our Contributions

Motivated by the recently developed algorithms SuperMinHash [7] and BagMinHash [8], which achieved superior performance by calculating signature components in a collective fashion instead of calculating them independently, we applied the same principle to design new minwise-hashing algorithms for the probability Jaccard similarity \( J_P \).
The recursion can be equivalently written as
\[ \lambda \text{ obtained by adding a value drawn from an exponential distribution } \]
with rate \( \lambda/\tau \). Therefore, \( y_\lambda(d) \) is exponentially distributed with rate \( \lambda \) as required.

For the correlated approach we consider the probability
\[ p_i := \Pr(\min(\{j : l_j(d) = k\}) = i) \]
that the \( i \text{-th} \) trial yields a certain value \( k \in \{1, 2, \ldots, m\} \) for the first time. This means that \( l_j(d) \neq k \) for \( j < i \) and \( l_i(d) = k \). If we sample without replacement from \( I_i \), this probability is given by
\[ p_i = \frac{\prod_{j=1}^{i-1} mr - r(j - 1)}{mr - (i - 1)} \]  
(11)
where \( p_i \) is zero for \( i > mr - r + 1 \), because last after sampling \( mr - r + 1 \) values without replacement from \( I_i \), all values have been sampled at least once. By nature, we have \( \sum_{r=1}^{mr-r+1} p_i = 1 \). We dissect the support of an exponential distribution into subsequent intervals at points \( a_i \), such that \( \Pr(a_{i-1} \leq x < a_i) = p_i \) with \( a_0 := 0 \) holds for an exponentially distributed \( x \sim \text{Exp}(\lambda) \). As a consequence, if \( x_i(d) \) is sampled from the two-sided truncated exponential distribution \( \text{Exp}(\lambda; a_{i-1}, a_i) \) with rate \( \lambda \) and support \( [a_{i-1}, a_i] \), \( y_\lambda(d) \) will be exponentially distributed with rate \( \lambda \). Since \( y_\lambda(d) \) for \( k \in \{1, 2, \ldots, m\} \) are all sampled from different intervals, they are not independent and the variance of estimator (3) will differ from (4), in contrast to uncorrelated generation of \( X(d) \).

Algorithm 3: Basic structure of ProbMinHash algorithms.

Input: \( w \)
Output: \( l \)
forall \( (x_k, y_k, \ldots, y_m) \in (\infty, \infty, \ldots, \infty) \)
\[ \forall w \in \text{PRNG with seed } d \]
\[ R \leftarrow \text{new PRNG with seed } d \]
x \( \leftarrow \) generate first element of \( X(d) \) using \( R \)
\[ h \leftarrow \text{uniform } x \]
\[ r \leftarrow 1 \]
while \( h < q_{\text{max}} \) do
\[ k \leftarrow \text{generate } i \text{-th element of } L(d) \text{ using } R \]
\[ q_i \leftarrow k \]
\[ r_{\text{max}} \leftarrow \text{max } q_i \]
\[ r = \text{max } r_{\text{max}}, q_i \]
\[ r \leftarrow r + 1 \]
x \( \leftarrow \) generate \( i \text{-th element of } X(d) \) using \( R \)
\[ h \leftarrow \text{uniform } x \]
end do

L(d) are chosen in such a way that the first points with a certain label \( k \) given by
\[ y_k(d) := x_{\text{min}(i : l_k(d) = k)}(d) = \min_{i : l_k(d) = k} x_i(d), \]  
(9)
are exponentially and identically distributed satisfying (6), then \( X(d) \) and \( L(d) \) can be used to generate exponentially distributed random values in ascending order as needed for (5).

Algorithm 3 shows the signature calculation using this idea. Elements of sequences \( X(d) \) and \( L(d) \) are lazily generated using the PRNG \( R \) which is initialized using \( d \) as seed. As soon as elements from \( X(d) \) are greater than or equal to \( q_{\text{max}} \) processing of element \( d \) can be stopped. For the very first element \( d \), when \( q_{\text{max}} \) is still infinite, this stop condition is satisfied as soon as all values from \( \{1, 2, \ldots, m\} \) have appeared at least once in \( L(d) \). For further elements, \( q_{\text{max}} \) has already become smaller and the stop condition will likely be satisfied earlier. If \( n > m \), \( q_{\text{max}} \) will get very small such that the whole-loop can be entirely skipped for most elements and a huge speedup factor in the order of \( m \) can be expected compared to Algorithm 1.

According to requirement (6) \( y_k(d) \) must be identically distributed for all \( k \), which implies \( p(1; k) = \frac{1}{m} \). This can be achieved by sampling the labels \( l_k(d) \) either from the multiset \( I_i := \{1^2, 2^2, \ldots, m^2\} \) without replacement or from \( \{1, 2, \ldots, m\} \) with replacement. In the following, sampling with replacement is treated as a special case of sampling without replacement where \( r \to \infty \). Given \( I_i \) used for generating \( L(d) \) we need to find an appropriate monotonic increasing random sequence \( X(d) \) such that (6) is satisfied.

We propose two different methods which we refer to as uncorrelated and correlated generation of \( X(d) \), respectively.

The uncorrelated approach uses the idea of ordered sample generation as described in [6], which allows sampling of \( mr \) independent random values from an exponential distribution with rate parameter \( \lambda/\tau \) in ascending order by using the recursion
\[ x_i(d) \sim x_{i-1}(d) + \frac{r}{\lambda(mr - (i - 1))} \text{ Exp}(1). \]  
(10)
for the correlated approach we consider the probability
value of a parent node is defined to be the maximum of the values of both children. By definition, the value of the root node will be $q_{\text{max}}$. If some value $q_k$ is replaced by some smaller hash value $q_i$, Algorithm 4 can be used to update the tree including $q_{\text{max}}$. Starting from the modified leaf node, the algorithm makes a bottom-up tree traversal until no further change is necessary. It is a slightly modified but equivalent version of the algorithm presented in [8].

Clearly, the worst case time complexity is $O(\log m)$. However, for ProbMinHash where the values of labels $l_i(d)$ are equally frequent, the expected time complexity is $O(1)$, which can be explained as follows: Assume $l_i(d) = k$ and hence $q_k$ has been chosen to be potentially updated by $x_i(d)$. Obviously, the probability that the value of $q_k$ is actually changed is at most $1/k$. The probability that the value of $q_k$ is modified, is at most $1/2$, because it is equally likely that the parent value, which is the maximum of the values of its two children, is given by the sibling of $q_k$. Decrementing the value of $q_k$ has no impact on the parent in this case.

Continuation of this argumentation shows that the expected number of node updates must be bounded by the geometric series $1 + 1/2 + 1/4 + \ldots = 2$ and therefore takes amortized constant time.

### 2.1 ProbMinHash1

Sampling with replacement ($r \to \infty$) for $L(d)$ together with uncorrelated sampling for $X(d)$ are the ingredients for the ProbMinHash1 algorithm, $r \to \infty$ and the choice $\lambda := \frac{2}{m}$ for the free parameter $\lambda$ simplifies the recursion (10) to $x_i(d) \sim x_{i-1}(d) + \frac{m}{m+1} \text{Exp}(1)$ such that the multiplication can be avoided for the very first and most frequently calculated point which is then given by $x_1(d) \sim \text{Exp}(1)$. The remaining factors $\frac{m}{m+1}$ can be precomputed to avoid the costly floating-point divisions.

### 2.2 ProbMinHash2

Our second algorithm uses sampling without replacement ($r = 1$) for $L(d)$ and uncorrelated sampling for $X(d)$. Unfortunately, sampling without replacement is more expensive than sampling with replacement. It is usually done using Fisher-Yates shuffling which requires an array $g = (g_1, g_2, \ldots, g_m)$ of size $m$ with initial values $g_i = i$ [9]. Due to the stop condition, ProbMinHash only needs the labels of a few points for most input elements. Since the $O(m)$ allocation and initialization costs would lead to a $O(nm)$ algorithm, we propose Algorithm 6, a variant of Fisher-Yates shuffling. It reuses the array $g$ to amortize allocation costs. Furthermore, it applies lazy initialization by using a permutation counter $c$ and an additional array $v$ that indicates already initialized elements of $g$ for the current permutation. $v_i = i$ means that $g_i$ has already been initialized. Otherwise, $g_i$ is considered to be equal to its initial value $i$. To start a new permutation for the next input element $d_i$ it is sufficient to increment the counter which is just an $O(1)$ operation.

The free parameter in (10) is chosen as $\lambda := \frac{1}{m}$. In this way the recursion simplifies together with $r = 1$ to $x_i(d) \sim x_{i-1}(d) + \frac{m}{m+1} \text{Exp}(1)$ such that the multiplication can be avoided for the very first and most frequently calculated point which is then given by $x_1(d) \sim \text{Exp}(1)$.

The number of generated points per element is limited to $m$ which gives a total of $nm$. Therefore, ProbMinHash2 has a worst case complexity of $O(nm)$ which is also the complexity of the original P-MinHash algorithm. In contrast, there is labels have appeared in $L(d_i)$. As this corresponds to the coupon collector’s problem [4], this takes $mH_m$ iterations on average, where $H_m := 1 + \frac{1}{2} + \ldots + \frac{1}{m}$ denotes the $m$-th harmonic number. Processing of the second element $d_2$ already takes less time, because $q_{\text{max}}$ has decreased and is no longer infinite. Consider the point sequence obtained by combining and sorting $X(d_1)$ and $X(d_2)$ together with the corresponding common label sequence given by $L(d_1)$ and $L(d_2)$. Again, the stop condition is satisfied as soon as all possible labels have shown up in the combined label sequence. As before, the expected sequence length is $H_m m$. However, since the density of points that come from $X(d_1)$ and $X(d_2)$ is proportional to $w(d_1) + w(d_2)$, respectively, we expect that the proportion of points originating from $d_2$ is $w(d_2)/(w(d_1) + w(d_2))$.

Continuing in this way leads to $mH_m w(d_1)/\sum_{i=1}^m w(d_i)$ for $d_i$. If we assume that elements are not processed in any particular order with respect to their weights, the expectation of $w(d_1)/\sum_{i=1}^m w(d_i)$ is equal to $1/m$. Summation over all $n$ input elements yields the expected total number of inner loop iterations which is $mH_m H_n$. Using $H_m = O(\log m)$ and incorporating the fixed costs $O(n)$ associated with each of all $n$ processed elements, the amortized overall time complexity is $O(n + m(\log m)(\log n)) \leq O(n + m \log^2 m)$.

---

**Algorithm 4:** Maintenance of stop limit $q_{\text{max}} := \max(q_1, q_2, \ldots, q_m)$

$q_{\text{max}}$ is the parent of $q_i$ if a leaf node $q_i$, with $i \in \{1, 2, \ldots, m\}$ is replaced by a smaller value $h < q_i$, following procedure updates the root node $q_{\text{max}}$ which is equal to $q_{\text{max}}$.

**Input:** $h, k$

while $h < q_i$
do $q_i \leftarrow h$
  index of parent
  if $i > 2m$ then break
  $l := (k - 3(i-1) + 1)$ + 1
  index of sibling $\oplus$ denotes bitwise XOR operation
  if $q_l \geq q_i$ then break
  if $h < q_i$ then $h \leftarrow q_i$
  $k \leftarrow 2$

**Algorithm 5:** ProbMinHash1

**Output:** $v$

forall $d \in D$ such that $w(d) > 0$ do
  $v_{\text{root}} \leftarrow 1/w(d)$
  $R \leftarrow$ new PRNG with seed $h$
  $h \leftarrow v_{\text{root}} \cdot \text{Exp}(1)$
  while $h < q_{\text{max}}$
do $k := \text{Uniform}(1, 2, \ldots, m))$
  if $h < q_k$, then
    $q_k \leftarrow h$
    $z_k \leftarrow v$
    update $q_{\text{max}}$ using Algorithm 4
  if $h \geq q_{\text{max}}$ then break
  $h \leftarrow h + v_{\text{max}} \cdot \text{Exp}(1)$

---
no such upper bound for ProbMinHash1.

### 2.3 ProbMinHash3

The third algorithm combines sampling with replacement $(r \to \infty)$ for label generation and the correlated sampling approach for $X(d)$. According to (11) $p_i = \frac{1}{m} \left(\frac{m-i}{m}\right)^{-1}$ as $r \to \infty$. The interval boundaries are given by $a_i = \frac{1}{r} \log(1 + \frac{m-i}{m})$. By choosing $\lambda := \log(1 + \frac{1}{m-i})$, which requires $m \geq 2$, we have $a_i = i$ and the points can be generated using $x_i(d) \sim \text{Exp}(\lambda)$ for $i \to \infty$-th hash value. If this limit is not less than $q_{\text{max}}$, the iteration can be terminated immediately, since all other hash values are greater than $q_{\text{max}}$. The points can be generated using $x_i(d) \sim \text{Exp}(\lambda)$ for $i \to \infty$ and $\text{Exp}(0, 1)$ for $i = m$. The following algorithm is shown as Algorithm 8. In contrast to ProbMinHash1 and ProbMinHash2, an additional stop condition within the inner loop makes use of the fact that the $(i+1)$-th point originates from $[a_i, a_{i+1})$ by using a corresponding additional stop condition. Analogous to ProbMinHash2, Algorithm 6 is used for sampling without replacement and the time complexity is bounded by $O(nm)$.

### 2.4 ProbMinHash4

The fourth variant combines sampling without replacement $(r = 1)$ for label generation and correlated sampling for $X(d)$. This case (11) simplifies to $p_i = \frac{1}{m}$ and the interval boundaries are given by $a_i = \frac{1}{m} \log(1 + \frac{m-i}{m})$. For $i < m$, the points can be generated using $x_i(d) \sim \text{Exp}(\lambda; a_{i-1}, a_i) \sim a_{i-1} + (a_i - a_{i-1}) \cdot \text{Exp}(\lambda; 0, 1)$ with $\lambda := \log(1 + \frac{1}{m-i})$. For $i = m$, we get $x_i(d) \sim a_{m-1} + \text{Exp}(\lambda)$ for $i > m$. Setting again $\lambda := \log(1 + \frac{1}{m-i})$, the iteration can be terminated immediately when reaching the first stop condi-
A common approach is to store an array of length \( m \) for each element in the buffer as needed by shuffling algorithms. Therefore, a more complex data structure like a hash table that only stores initialized elements of that array is needed. We did a couple of experiments using hash tables, but found that the additional hash table lookups destroy the performance gain by interleaved processing. Therefore, we focused on ProbMinHash1 and ProbMinHash3 which are both based on sampling without replacement and which do not rely on the sampling history. ProbMinHash1 and ProbMinHash3 are the corresponding logically equivalent algorithms using interleaved processing and are shown as Algorithm 10 and Algorithm 11, respectively.

For the space complexity analysis we assume that elements \( d_i \) are not sorted with regard to their weights. As a consequence, the first hash values \( h = x_j(d_i)/w(d_i) \) of different elements \( d_i \) can be considered to be identically distributed, because the weight \( w(d_i) \) and also the first point \( x_j(d_i) \) are both identically distributed. The expected maximum buffer size is given by the sum of individual probabilities that an element is added to the buffer during the first pass.

For ProbMinHash1 an element is added to the buffer, if its first hash value is smaller than \( q_{\text{max}} \). Since it takes \( m_{H_{\text{max}}} \) elements on average, according to the coupon collector’s problem [4], until the labels of their first points cover all possible label values \( \{1, 2, \ldots, m\} \), \( q_{\text{max}} \) is roughly given by the \( m_{H_{\text{max}}} \)-th smallest hash value seen so far. The probability that the first hash value of the \( l \)-th element is among the \( m_{H_{\text{max}}} \) smallest hash values, is given by \( \min(1, m_{H_{\text{max}}}/l) \). As this corresponds to the probability that the first hash value is smaller than \( q_{\text{max}} \) and that the corresponding element is inserted into the buffer, summation of these probabilities for all \( n \) elements finally yields the expected buffer size \( \sum_{l=1}^{m_{H_{\text{max}}}} \min(1, m_{H_{\text{max}}}/l) = O(m(\log m)(\log n)) \). Since

---

**Algorithm 10: ProbMinHash1**

Input: \( w \)

Output: \( x_1, x_2, \ldots, x_n \)

\( (q_1, q_2, \ldots, q_k) \leftarrow (\infty, \infty, \ldots, \infty) \)

\( b \leftarrow \) empty dynamic array

\( s \leftarrow \) number of elements in buffer

forall \( d_i \in D \) such that \( w(d_i) > 0 \) do

\( i_{\text{max}} \leftarrow 1/w(d_i) \)

\( R \leftarrow \) new PRNG with seed \( d \)

\( h \leftarrow w_{\text{max}} \cdot R[\text{Exp}(1)] \)

if \( h < q_{\text{max}} \) then continue

\( k \leftarrow R[\text{Uniform}(1, \ldots, m)] \)

if \( h < q_k \) then

\( q_k \leftarrow h \)

\( z_k \leftarrow d \)

update \( q_{\text{max}} \) using Algorithm 4

if \( h > q_{\text{max}} \) then continue

\( s \leftarrow s + 1 \)

\( b_s \leftarrow (d, w_{\text{max}}, R, h) \)

while \( s > 0 \) do

\( s \leftarrow s - 1 \)

for \( l = 1, 2, \ldots, s \) do

\( (d_{l, w_{\text{max}}}, R, h) \leftarrow (l) \)

if \( h > q_{\text{max}} \) then continue

\( h \leftarrow h + w_{\text{max}} \cdot R[\text{Exp}(1)] \)

if \( h > q_{\text{max}} \) then continue

\( k \leftarrow R[\text{Uniform}(1, \ldots, m)] \)

if \( h < k \) then

\( q_k \leftarrow h \)

\( z_k \leftarrow d \)

update \( q_{\text{max}} \) using Algorithm 4

if \( h > q_{\text{max}} \) then continue

\( t \leftarrow t + 1 \)

\( b_t \leftarrow (d, w_{\text{max}}, R, h) \)

\( s \leftarrow s \)

**Algorithm 11: ProbMinHash3**

Input: \( w \)

Output: \( x_1, x_2, \ldots, x_n \)

\( (q_1, q_2, \ldots, q_k) \leftarrow (\infty, \infty, \ldots, \infty) \)

\( b \leftarrow \) empty dynamic array

\( s \leftarrow \) number of elements in buffer

forall \( d_i \in D \) such that \( w(d_i) > 0 \) do

\( i_{\text{max}} \leftarrow 1/w(d_i) \)

\( R \leftarrow \) new PRNG with seed \( d \)

\( h \leftarrow w_{\text{max}} \cdot R[\text{Exp}(\lambda, 0, 1)] \)

if \( h > q_{\text{max}} \) then continue

\( k \leftarrow R[\text{Uniform}(1, \ldots, m)] \)

if \( h < q_k \) then

\( q_k \leftarrow h \)

\( z_k \leftarrow d \)

update \( q_{\text{max}} \) using Algorithm 4

if \( w_{\text{max}} \geq q_{\text{max}} \) then continue

\( s \leftarrow s + 1 \)

\( b_s \leftarrow (d, w_{\text{max}}, R) \)

\( s \leftarrow s \)
the space complexity and the number of input elements \( n \) are lower bounds for the time complexity, it is \( \mathcal{O}(n + m(\log m)\log n) \) for ProbMinHash1.

For ProbMinHash3a we first consider the unweighted case where all weights are equal to one. Again, \( q_{\text{max}} \) is approximately given by the \( mH_n \)-th smallest hash value. Thus the stop condition is fulfilled roughly after generating the \( mH_n \) smallest hash values. Since ProbMinHash3a calculates hash values of elements chunk-wise in ascending order, meaning that the \( i \)-th pass gives all hash values in the range \([i-1,i] \), the stop condition is satisfied after the calculation of \( \mathcal{O}(n \log m) \) hash values. The processing time of the remaining elements, which will then immediately fulfill the stop condition, is bounded by \( \mathcal{O}(n) \) giving a total of \( \mathcal{O}(n + m\log m) \) for the time complexity. The expected maximum number of elements in the buffer is given by \( \min(n,mH_n) = \mathcal{O}(m \log m) \). It is noteworthy that the space complexity is not dependent on the input size \( n \) in contrast to ProbMinHash1a.

In the general case with arbitrary weights, the space complexity of ProbMinHash3a depends on the distribution of weights. However, supported by our experimental results presented later, we presume that there is an upper bound that is independent of \( n \) as long as the distribution of weights \( F_w(w) \) has a power-tail with an index \( \eta > 1 \). Hence, \( 1 - F_w(w) \sim w^{-\eta} \) as \( w \to 0 \). \( \eta > 1 \) means that the bound is finite. Our assumption can be made plausible by making the following considerations. \( q_{\text{max}} \) is approximately given by the \( mH_n \)-th smallest hash value. The probability that the first hash value of the \( l \)-th input element is among them is given by \( \min(1,mH_n/l) \). Therefore, for \( l \to \infty \), \( q_{\text{max}} \) is approximately given by \( q_{\text{max}} \approx \mathcal{F}^{-1}(mH_n/l) \) where \( F_w \) is the distribution of hash values \( h = x_1/w \) with \( x_1 \) drawn from \( \text{Exp}(\lambda;0,1) \) and \( w \) distributed according to \( F_w \). For the distribution of \( h \) we have \( F_h(h) = \int_0^h (1 - e^{-\lambda w})/(1 - e^{-\lambda w}) \cdot dF_w(w) \geq h^{-1/l} \cdot dF_w(w) \sim h E[w] \) as \( h \to 0 \). Here \( E[w] \) denotes the expected weight. Therefore, \( q_{\text{max}} \approx mH_n/(lE[w]) \). The probability that an element needs to be added to the buffer is \( \text{Pr}(1/w < q_{\text{max}}) = 1 - F_w(1/q_{\text{max}}) \leq 1 - F_w(1E[w]/(mH_n)) \approx l^{-\eta} \). Since the hyperharmonic series \( \sum_{i=1}^{\infty} l^{-\eta} \) converges for \( \eta > 1 \), the sum of probabilities that elements are added to the buffer will be independent of \( n \).

### 2.6 Truncated Exponential Sampling

For ProbMinHash3 and ProbMinHash4 we need to generate many random values that are distributed according to the truncated exponential distribution \( \text{Exp}(\lambda;0,1) \). The straightforward approach, inverse transform sampling, requires the evaluation of a logarithm. We have not found any other more efficient method in literature that avoids, like the ziggurat method for the exponential distribution [20], expensive function calls. Therefore, we have developed our own method based on rejection sampling.

Figure 2 shows the probability density function (PDF) \( \rho(x) = e^{-\lambda x} \) for an exponential distribution with rate \( \lambda \) for \( x \in [0,1] \). Clearly, if we sample points uniformly from the region below this PDF, its \( x \)-coordinate will be distributed as \( \text{Exp}(\lambda;0,1) \). The region is split into \( A_1 = [0,1] \times [0, e^{-\lambda}] \) and the remaining part \( A_2 \). As a first step, we randomly decide whether the point should be drawn from \( A_1 \) or \( A_2 \) according to their areas \(|A_1| = e^{-\lambda} \) and \(|A_2| = (1 - e^{-\lambda})/\lambda - |A_1| \), respectively. This is done by generating a uniformly distributed random value \( x \in [0,1] \) with \( c_1 := (|A_1| + |A_2|)/|A_1| = (e^{-1} - 1)/\lambda \). Since \( \text{Pr}(x < 1) = |A_1|/(|A_1| + |A_2|) \), we sample the point from \( A_1 \) if \( x < 1 \). In this case the \( x \)-coordinate is uniformly distributed on \([0,1]\) and can therefore directly used as coordinate. Because \( A_1 \) is an axis-aligned rectangle, we can omit the generation of the \( y \)-coordinate and return \( x \) in any case.

If \( x \geq 1 \), we introduce a different \( y \)-scale defined by the transformation \( \tilde{y} = (y - e^{-\lambda - \lambda x})/(1 - e^{-\lambda}) \) for simplicity. Instead of sampling a point from \( A_2 \), we draw a point from the triangle \( A_3 \cup A_4 \cup A_6 \) (see Figure 2) and reject points that are not below the PDF. To do that we sample from the rectangle \( A_3 \cup A_4 \cup A_6 = [0,1] \times [0,0.5] \) which has the same area as the triangle, because \(|A_3| = |A_5| \). In case the sampled point belongs to \( A_3 \) the point is mapped to \( A_6 \) by reflection at point \((0.5,0.5)\). Next we need to test whether the sampled point is below the PDF. In order to avoid the expensive exponential function evaluation, we do first the cheap tests whether the point is either below the tangent at \( 0 \) or the tangent at \( 1 \). In both cases, the sampled point can be accepted immediately. Otherwise, we need to test against the PDF. In any case, if the point gets accepted, its \( x \)-coordinate is returned as result. An additional performance optimization was introduced when sampling from the rectangle. We first sample its \( x \)-coordinate from \([0,1]\). If it is less than \( c_2 := \log(2/(1 + e^{-\lambda}))/\lambda \), the point belongs to \( A_3 \). Since \( A_3 \) is entirely below the PDF all points in \( A_3 \) are accepted and the generation of the corresponding \( y \)-coordinate can be omitted.

The whole procedure is shown as Algorithm 12. The algorithm is especially efficient for small \( \lambda \), because then the first if-condition \( x < 1 \) is satisfied with high probability and the algorithm can be terminated immediately.
For all points in ProbMinHash3 and the first points in ProbMinHash4 we have \( \lambda = \log(1 + \frac{1}{m^2}) \) and therefore \( \Pr(x < 1) = e^{-(m-1)} \log(1+\frac{1}{m^2}) \approx 1 - \frac{1}{2m^2} \) as \( m \to \infty \). Since \( m \) is typically in the hundreds or even greater, drawing a value from \( \exp(\lambda) \) is almost as cheap as the generation of a random uniform value followed by a floating-point multiplication. For ProbMinHash4 \( \lambda \) increases with the number of generated points and finally gets \( \lambda = \log(2) \) for the second last point. Even in this worst case chances are still high that the first if-condition is satisfied as \( \Pr(x < 1) = \log(2) \approx 69.3\% \).

### 2.7 Conventional Jaccard Similarity

It is obvious that the presented algorithms can be specialized for the conventional Jaccard similarity \( J \). In this case \( w(d) \in \{0, 1\} \) holds for all input elements \( d \). For ProbMinHash1 and ProbMinHash2 this means that the weight inversion and a couple of floating-point multiplications can be saved. In addition ProbMinHash1a benefits from a smaller memory footprint, because \( w(d) \) is not needed to be stored in the buffer. Since ProbMinHash1, ProbMinHash1a, and ProbMinHash2a are all based on uncorrelated point generation (compare Section 2) they are statistically equivalent to the original MinHash algorithm and can therefore be used as faster substitutes.

ProbMinHash3 and ProbMinHash4, which use correlated point generation, benefit much more from the restriction to binary weights. The hash values of different elements with equal weights are drawn exactly from the same subsequent intervals. Since only the relative order of hash values is important, we can exchange the (truncated) exponential distributions used for point generation by any other continuous distributions over subsequent intervals. For the sake of simplicity and also for performance reasons we use the uniform distribution. This means, we replace \( R[\exp(\lambda; 0, 1)] \) by \( R[\text{Uniform}(0, 1)] \) in ProbMinHash3 and ProbMinHash3a. In ProbMinHash4 we set \( a_i = i \) and substitute both \( R[\exp(\lambda; 0, 1)] \) and \( c \cdot R[\exp(1)] \) by \( R[\text{Uniform}(0, 1)] \).

Some of these specialized algorithms relate to other known algorithms. ProbMinHash1 corresponds to the BagMinHash algorithm [8] if fully specialized for the unweighted case. ProbMinHash1a has some similarities to BagMinHash2 which uses a min-heap for buffering elements that are still able to contribute to the signature. Elements are processed in ascending order of their last hash values. In contrast, ProbMinHash1a calculates the \( i \)-th smallest hash values of all relevant elements in the \( i \)-th pass regardless of the preceding hash values.

The unweighted version of ProbMinHash3a has similarities to FSS [5] and OPH [16]. The first part of Algorithm 11 consisting of the first for-loop is almost identical to the first pass of FSS and OPH, respectively. For large input sizes, where further passes are often not necessary, they are almost equivalent. The only difference is that ProbMinHash3a additionally tracks \( q_{\text{max}} \) which allows an early termination if the stop condition is satisfied. In this way the generation of the label that determines the signature component can often be avoided. The second part of ProbMinHash3a consisting of the while-loop can be regarded as new densification scheme as needed for OPH in case of small input sizes \( n \). At the expense of a buffer of size \( O(m \log m) \), the estimation error for \( J \) is reduced for small input sizes as our experimental results will show.

ProbMinHash4 for the unweighted case corresponds to the SuperMinHash algorithm [7]. The main difference is again the stop condition. SuperMinHash only tracks a histogram of hash values which only allows discrete stop limits. ProbMinHash4 keeps track of \( q_{\text{max}} \), which is slightly more expensive. However, it pays off for larger input sizes, because the stop limit can go below 1. As a consequence, the label generation can be avoided in many cases leading to a slightly better performance. As ProbMinHash4 is logically equivalent to the SuperMinHash algorithm it also shares the theoretically proven better variance of the Jaccard similarity estimator (7) for input sizes small compared to the signature size.

### 3 Experiments

The implementations of all algorithms have been written in C++. The corresponding source code and the scripts to produce the results and figures shown in the following are available on Github at https://github.com/oertl/probminhash. The PRNG, which is used by the presented algorithms, is particularly important for good performance, since it is called in the innermost loops. For our theoretical considerations we have assumed an ideal random number generator. Therefore, the output of the chosen PRNG should be indistinguishable from that. Poor randomness would lead to estimation errors significantly different from the theoretical predictions. We used the Wyrand algorithm (version 1) which was recently developed and published on GitHub [95]. It is very fast, has a state of 64 bits, and passes a series of statistical quality tests. Seeded with a 64-bit hash value of the input element, it can be used to produce random bit sequences of arbitrary lengths. Strictly speaking, Wyrand always generates 64 bits at once. However, we consume random bits very economically. For example, to generate a double-precision floating-point number from \( [0, 1) \) 53 random bits corresponding to the signifcant precision are sufficient. Only if all 64 bits have been consumed, the next bunch of 64 bits will be generated.

We have implemented all algorithms including the original P-MinHash algorithm with the same methods of random value generation to allow a fair comparison. We used the ziggurat method [20] for the generation of exponentially distributed random values. Its implementation is based on that of the Boost C++ libraries [1]. For the truncated exponential and uniform integer distributions we used Algorithm 12 and the algorithm given in [12], respectively.

Our experiments have been all carried out using synthetic data. The reason is that realistic data sets usually do not contain enough different pairs of sets that have exactly the same predefined similarity. However, this is fundamental to confirm the theoretically predicted distribution of estimation errors. Furthermore, synthetic data facilitate the reproducibility of the results. The test data are sets of random 64-bit integers. This is reasonable, because realistic elements can always be hashed to 64-bit integers first. When using a good hash function, the corresponding hash values are indistinguishable from the random elements in the synthetically generated sets in practice.
Figure 3: The empirical mean squared error (MSE) relative to $J_P (1 - J_P) / m$ over the signature size $m$ for different multisets of weight pairs $W$. Each data point is calculated from 10,000 pairs of randomly generated sets with weight functions satisfying $W = \bigcup_{d,w_A(d) > 0} \{ (w_A(d), w_B(d)) \}$. The gray band covers the middle 99.99% of all z-scores.

3.1 Verification

We considered 12 different cases for the verification of the proposed algorithms. Each case is characterized by a multiset $W$ of pairs of weight values. Each pair represents the weights of some random element in two different sets, respectively. Given $W$, arbitrary many pairs of weighted sets $A$ and $B$ can be generated whose weight functions satisfy $W = \bigcup_{d,w_A(d) > 0} \{ (w_A(d), w_B(d)) \}$. This is done by drawing a random element for each pair of weight values in $W$, which is then added to sets $A$ and $B$ together with the corresponding weights, respectively. The resulting pairs of weighted sets will always have the same probability Jaccard similarity $J_P$ as it is uniquely defined by $W$.

10,000 different pairs of such weighted random sets have been generated for each case and for signatures sizes $m \in \{1,2,4,\ldots,2^{14}\}$. After computing the corresponding signatures using different algorithms, the similarity was estimated using (3), and the empirical MSE with respect to the true $J_P$ was calculated. Since the expected empirical MSEs for P-MinHash and for the statistically equivalent algorithms ProbMinHash1 and ProbMinHash2 are equal to $J_P (1 - J_P) / m$, we considered the corresponding relative empirical MSE which was finally plotted over the signature size $m$ for all 12 different cases in Figure 3. The regions covering the middle 99.99% of the expected z-scores are also shown to indicate realistic deviations from the expected empirical MSE. The z-score is obtained from the empirical MSE by normalization. The expectation and the variance of the empirical MSE are given by $J_P (1 - J_P) / m$ and $J_P^2 (1 - J_P)^2 (2 - \frac{6}{m}) + J_P (1 - J_P)$, respectively [8], where $c = 10000$ is the sample size. The results show perfect agreement with the theory for P-MinHash, ProbMinHash1, and ProbMinHash2. However, for ProbMinHash3 and ProbMinHash4 the error is significantly smaller, especially if the signature size exceeds the quantity size. As both algorithms are not defined for $m = 1$ the corresponding points are missing in Figure 3. Dependent on the case, the correlated generation of hash values is able to reduce the empirical MSE by up to a factor of two. We also observed that the empirical MSE of ProbMinHash1 is slightly smaller than that of ProbMinHash3 for tiny sets as can be seen for the cases $W = \{ (3,20),(30,7) \}$ and $W = \{ (0,1),(1,0),(1,1) \}$.

The last column of Figure 3 shows results for three different cases with binary weights. For those examples we used the unweighted variants of the ProbMinHash algorithms. Furthermore, we included the MinHash and SuperMinHash algorithms. For the latter, the theoretical relative MSE is known and given by (8). Since ProbMinHash4 corresponds to the SuperMinHash algorithm in the unweighted case, we observed a perfect match with the theory. ProbMinHash1 and ProbMinHash3a have also been covered by our experiments. However, the logical equivalence to ProbMinHash1 and ProbMinHash3, respectively, led to identical results which were therefore omitted in Figure 3.

3.2 Performance

All performance measurements have been carried out on a Dell Precision 5530 notebook with an Intel Core i9-8950HK.
Figure 4: The average calculation time for signatures of size $m$ and for different assumed distributions of $w(d)$ over the input size $n$.

Figure 5: The average maximum buffer size as a function of the number of input elements $n$ for ProbMinHash1a and ProbMinHash3a. The shown bands cover the middle 99% of the observed values.
processor and 32 GB of memory. The average calculation time for a single signature was measured for signature sizes 256, 1024, and 4096, and different assumed weight distributions. The results plotted over input sizes \( n \) varying from 1 to \( 10^6 \) are shown in Figure 4. For each data point we first generated 100 randomly weighted sets and stored them in main memory. Then the actual measurement calculated the corresponding signatures for all of them.

The calculation time of P-MinHash which has a linear scaling with \( n \) was our reference. We see that all ProbMinHash variants are orders of magnitude faster for very large \( n \). The maximum speedup factor is roughly given by \( n \), because for most elements only a single hash value has to be calculated compared to the \( m \) hash values for P-MinHash. ProbMinHash3 and ProbMinHash4 are even slightly faster, because random value generation is cheaper for the truncated than for the regular exponential distribution. The break even points lie in the range from \( m = 20 \) to \( m = 100 \). Only for very small \( n \), which is not the typical use case of such algorithms though, P-MinHash performs better. For \( n = 1 \) all ProbMinHash variants using sampling with replacement exhibit a \( \mathcal{O}(m \log m) \) time complexity, which explains their significant worse performance. In contrast, ProbMinHash2 and ProbMinHash4, both based on sampling without replacement, perform better but still are about a factor of 3 slower.

The last column in Figure 4 presents the results for the unweighted case. There we used the unweighted specializations of all ProbMinHash algorithms and also considered the MinHash and the SuperMinHash algorithms. P-MinHash is about an order of magnitude slower than MinHash. The reason is the more expensive random value generation for exponential than for uniform distributions. When comparing the ProbMinHash algorithms to MinHash, the break even points range roughly from \( m = 50 \) to \( m = 1000 \). For large input sizes the unweighted specializations of ProbMinHash3, ProbMinHash3a, and ProbMinHash4 are faster than the SuperMinHash algorithm which comes from the more adaptive stop limit as discussed in Section 2.7. Due to their performance ProbMinHash1a and ProbMinHash3a are very interesting candidates for the unweighted case. ProbMinHash3a offers the best performance and potentially improves the estimation error. ProbMinHash1a is slightly slower, but it can replace MinHash equivalently due to its statistically independent signature components.

The performance improvement of ProbMinHash1a and ProbMinHash3a over ProbMinHash1 and ProbMinHash3, respectively, depends on the distribution of weights. As shown in the second column of Figure 4, where we assumed Pareto(1, 0.5)-distributed weights, which is maybe not a realistic scenario as the mean does not exist, interleaved processing did not improve the calculation time.

We also analyzed the buffer size distribution over \( n \) for ProbMinHash1a and ProbMinHash3a. Figure 5 shows the average as well as the band covering the middle 99% of all observed buffer sizes. The results are based on 10 000 random examples per data point. There is a perfect match with our theoretical considerations in Section 2.5. Contrary to ProbMinHash1a, ProbMinHash3a has a dependence on the weight distribution. As assumed, the average buffer size reaches a plateau except for the Pareto(1, 0.5)-distribution which has a tail with index smaller than 1. For the unweighted cases shown in the last column of Figure 5 we could also confirm the predicted level of this plateau.

4 Outlook

There are some other metrics that might also benefit from the presented ideas. For example, there is the Lempel-Ziv Jaccard distance which can be used as generic similarity measure. It is defined on the set of binary subsequences resulting during Lempel-Ziv compression [23, 24] and is able to incorporate weights [25]. Another approach is the OrderMinHash algorithm which was recently proposed as locality-sensitive hash algorithm for the edit similarity between sequences [19]. The signature calculation requires for each component the smallest \( l \) hash values (instead of only the smallest as with the Jaccard distance). We already implemented statistically equivalent algorithms called FastOrderMinHash1/1a/2 based on ProbMinHash1/1a/2, respectively. The results shown in Figure 6 look very promising as we have been able to reduce the calculation time by an order of magnitude for longer sequences. There are many more applications of minwise-hashing worth to be considered in future.

Apart from that, there are some open theoretical questions. We have not yet been able to mathematically prove that the variance of ProbMinHash3/4 is never worse than that of P-MinHash. The only exception is the unweighted case of ProbMinHash4, which corresponds to the SuperMinHash algorithm and for which the variance is given by (7). Moreover, we are interested in the required characteristics of the weight distribution such that the complexity of the expected space requirements is independent of the input size \( n \) and the time complexity is \( \mathcal{O}(n \log m) \). In our analysis we assumed that elements are unordered with respect to their weights. Processing elements in descending order of their weights would be more efficient as the stop limit \( q_{\text{MAX}} \) would decrease more quickly. It would be interesting to see if sorting could improve the overall performance in practice despite the additional \( \mathcal{O}(n \log n) \) effort.

5 Conclusion

We have presented new location-sensitive algorithms for the probability and the conventional Jaccard similarity, which can accelerate existing applications and open up new application possibilities due to their significantly better performance compared to the conventional methods. We therefore expect that our algorithms will soon be used in practice.
References

[1] Boost C++ Libraries. http://www.boost.org/.

[2] M. Bawa, T. Condie, and P. Ganesan. LSH forest: Self-tuning indexes for similarity search. In Proceedings of the 14th International Conference on World Wide Web (WWW), pages 651–660, 2005.

[3] A. Z. Broder. On the resemblance and containment of documents. In Proceedings of Compression and Complexity of Sequences, pages 21–29, 1997.

[4] T. H. Cormen, C. E. Leiserson, R. L. Rivest, and C. Stein. Introduction to Algorithms. MIT Press, 3rd edition, 2013.

[5] S. Dahlgaard, M. B. T. Knudsen, and M. Thorup. Fast similarity sketching. In Proceedings of the 58th Annual IEEE Symposium on Foundations of Computer Science (FOCS), pages 663–671, 2017.

[6] L. Devroye. Non-Uniform Random Variate Generation. Springer, New York, 1986.

[7] O. Ertl. SuperMinHash – A new minwise hashing algorithm for Jaccard similarity estimation. arXiv:1706.05698 [cs.DS], 2017.

[8] O. Ertl. BagMinHash – Minwise hashing algorithm for weighted sets. In Proceedings of the ACM SIGKDD 24th International Conference on Knowledge Discovery and Data Mining (KDD), pages 1368–1377, 2018.

[9] R. A. Fisher and F. Yates. Statistical Tables for Biological, Agricultural and Medical Research. Oliver & Boyd, London, 1938.

[10] P. Indyk and R. Motwani. Approximate nearest neighbors: Towards removing the curse of dimensionality. In Proceedings of the 30th Annual ACM Symposium on Theory of Computing (STOC), pages 604–613, 1998.

[11] S. Ioffe. Improved consistent sampling, weighted minhash and L1 sketching. In Proceedings of the IEEE 10th International Conference on Data Mining (ICDM), pages 246–255, 2010.

[12] D. Lemire. Fast random integer generation in an interval. ACM Transactions on Modeling and Computer Simulation, 29(1):3:1–3:12, 2019.

[13] J. Leskovec, A. Rajaraman, and J. D. Ullman. Mining Massive Datasets. Cambridge University Press, 2014.

[14] P. Li. 0-bit consistent weighted sampling. In Proceedings of the 21th ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD), pages 665–674, 2015.

[15] P. Li and A. C. König. b-bit minwise hashing. In Proceedings of the 19th International Conference on World Wide Web (WWW), pages 671–680, 2010.

[16] P. Li, A. Owen, and C. Zhang. One permutation hashing. In Proceedings of the 56th Conference on Neural Information Processing Systems (NIPS), pages 3113–3121, 2012.

[17] Q. Lv, W. Josephson, Z. Wang, M. Charikar, and K. Li. Multi-probe LSH: Efficient indexing for high-dimensional similarity search. In Proceedings of the 33rd International Conference on Very Large Data Bases (VLDB), pages 950–961, 2007.

[18] T. Mai, A. Rao, M. Kapilevich, R. A. Rossi, Y. Abbasi-Yadkori, and R. Sinha. On densification for minwise hashing. In Proceedings of the 35th Conference on Uncertainty in Artificial Intelligence (UAI), 2019.

[19] G. Marcais, D. DeBlasio, P. Pandey, and C. Kingsford. Locality-sensitive hashing for the edit distance. Bioinformatics, 35(14):i127–i135, 2019.

[20] G. Marsaglia and W. W. Tsang. The ziggurat method for generating random variables. Journal of Statistical Software, 5(8):1–7, 2000.

[21] R. Moulton and Y. Jiang. Maximally consistent sampling and the Jaccard index of probability distributions. In Proceedings of the 6th ICDM Workshop on High Dimensional Data Mining (HDM), pages 347–356, 2018.

[22] A. Z. Broder. On the resemblance and containment of documents. In Proceedings of the 14th International Conference on World Wide Web (WWW), pages 651–660, 2005.

[23] Q. Lv, W. Josephson, Z. Wang, M. Charikar, and K. Li. Multi-probe LSH: Efficient indexing for high-dimensional similarity search. In Proceedings of the 33rd International Conference on Very Large Data Bases (VLDB), pages 950–961, 2007.

[24] T. Mai, A. Rao, M. Kapilevich, R. A. Rossi, Y. Abbasi-Yadkori, and R. Sinha. On densification for minwise hashing. In Proceedings of the 35th Conference on Uncertainty in Artificial Intelligence (UAI), 2019.

[25] G. Marcais, D. DeBlasio, P. Pandey, and C. Kingsford. Locality-sensitive hashing for the edit distance. Bioinformatics, 35(14):i127–i135, 2019.

[26] G. Marsaglia and W. W. Tsang. The ziggurat method for generating random variables. Journal of Statistical Software, 5(8):1–7, 2000.

[27] R. Moulton and Y. Jiang. Maximally consistent sampling and the Jaccard index of probability distributions. In Proceedings of the 6th ICDM Workshop on High Dimensional Data Mining (HDM), pages 347–356, 2018.

[28] A. Z. Broder. On the resemblance and containment of documents. In Proceedings of the 14th International Conference on World Wide Web (WWW), pages 651–660, 2005.
[29] A. Shrivastava. Simple and efficient weighted minwise hashing. In *Proceedings of the 30th Conference on Neural Information Processing Systems (NIPS)*, pages 1498–1506, 2016.

[30] A. Shrivastava. Optimal densification for fast and accurate minwise hashing. In *Proceedings of the 34th International Conference on Machine Learning (ICML)*, pages 3154–3163, 2017.

[31] A. Shrivastava and P. Li. Improved densification of one permutation hashing. *Proceedings of the 30th Conference on Uncertainty in Artificial Intelligence (UAI)*, 2014.

[32] D. Yang, B. Li, L. Rettig, and P. Cudré-Mauroux. HistoSketch: Fast similarity-preserving sketching of streaming histograms with concept drift. In *Proceedings of the 17th IEEE International Conference on Data Mining (ICDM)*, pages 545–554, 2017.

[33] D. Yang, B. Li, L. Rettig, and P. Cudré-Mauroux. D²HistoSketch: Discriminative and dynamic similarity-preserving sketching of streaming histograms. *IEEE Transactions on Knowledge and Data Engineering*, 31(10):1898–1911, 2019.

[34] D. Yang, P. Rosso, B. Li, and P. Cudré-Mauroux. Nodesketch: Highly-efficient graph embeddings via recursive sketching. In *Proceedings of the ACM SIGKDD 25th International Conference on Knowledge Discovery and Data Mining (KDD)*, pages 1162–1172, 2019.

[35] W. Yi. Wyhash. https://github.com/wangyi-fudan/wyhash, 2019.