Linear-Time Algorithms for Computing Maximum-Density Sequence Segments with Bioinformatics Applications

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Abstract

We study an abstract optimization problem arising from biomolecular sequence analysis. For a sequence $A$ of pairs $(a_i, w_i)$ for $i = 1, \ldots, n$ and $w_i > 0$, a segment $A(i, j)$ is a consecutive subsequence of $A$ starting with index $i$ and ending with index $j$. The width of $A(i, j)$ is $w(i, j) = \sum_{i \leq k \leq j} w_k$, and the density is $((\sum_{i \leq k \leq j} a_k)/w(i, j))$. The maximum-density segment problem takes $A$ and two values $L$ and $U$ as input and asks for a segment of $A$ with the largest possible density among those of width at least $L$ and at most $U$. When $U$ is unbounded, we provide a relatively simple, $O(n)$-time algorithm, improving upon the $O(n \log L)$-time algorithm by Lin, Jiang and Chao. When both $L$ and $U$ are specified, there are no previous nontrivial results. We solve the problem in $O(n)$ time if $w_i = 1$ for all $i$, and more generally in $O(n + n \log(U - L + 1))$ time when $w_i \geq 1$ for all $i$.

Key words: bioinformatics, sequences, density

1 Introduction

Non-uniformity of nucleotide composition within genomic sequences was first revealed through thermal melting and gradient centrifugation [Inm66,MTB76]. The GC content of the DNA sequences in all organisms varies from 25% to 75%. GC-ratios have the greatest variations among bacteria’s DNA sequences, while the typical GC-ratios of mammalian genomes stay in 45-50%. The GC content of human DNA varies widely throughout the genome, ranging between 30% and 60%. Despite intensive research effort in the past two decades, the underlying causes of the observed heterogeneity remain contested [Bar00,BB86,Cha94,EW92,EW93,Fil87,FO99,Hol92,Sue88,WSL89]. Researchers [NL00,SFR+99] observed that the compositional heterogeneity is highly correlated to the GC content of the genomic sequences. Other investigations showed that gene length [DMG95], gene density [ZCB96], patterns of codon usage [SAL+95], distribution of different classes of repetitive elements [DMG95,SMRB83], number of isochores [Bar00], lengths of isochores [NL00], and recombination rate within chromosomes [FCC01] are all correlated with GC content. More research exists related to GC-rich segments [GGA+98,HHJ+97,IAY+96,JFN97,MHL01,MRO97,SA93,WLOG02,WSE+99].

Although GC-rich segments of DNA sequences are important in gene recognition and comparative genomics, only a couple of algorithms for identifying GC-rich segments appeared in the literature. A widely used window-based approach is based upon the GC-content statistics of a fixed-length window [FS90,HDV+91,NL00,RLB00]. Due to the fixed length of windows, these practically fast approaches are likely to miss GC-rich segments that
span more than one window. Huang [Hua94] proposed an algorithm to accommodate windows with variable lengths. Specifically, by assigning \(-p\) points to each AT-pair and \(1 - p\) points to each GC-pair, where \(p\) is a number with \(0 \leq p \leq 1\), Huang gave a linear-time algorithm for computing a segment of length no less than \(L\) whose score is maximized. As observed by Huang, however, this approach tends to output segments that are significantly longer than the given \(L\).

In this paper, we study the following abstraction of the problem. Let \(A\) be a sequence of pairs \((a_i, w_i)\) for \(i = 1, \ldots, n\) and \(w_i > 0\). A segment \(A(i, j)\) is a consecutive subsequence of \(A\) starting with index \(i\) and ending with index \(j\). The width of \(A(i, j)\) is \(w(i, j) = \sum_{i \leq k \leq j} w_k\), and the density is \((\sum_{i \leq k \leq j} a_k) / w(i, j)\).

Let \(L\) and \(U\) be positive values with \(L \leq U\). The maximum-density segment problem takes \(A\), \(L\), and \(U\) as input and asks for a segment of \(A\) with the largest possible density among those of width at least \(L\) and at most \(U\). This generalizes a previously studied model, which we term the uniform model, in which \(w_i = 1\) for all \(i\). All of the previous work discussed in this section involves the uniform model. We introduce the generalized model as it might be used to compress a sequence \(A\) of real numbers to reduce its sequence length and thus its density analysis time in practice or theory.

In its most basic form, the sequence \(A\) corresponds to the given DNA sequence, where \(a_i = 1\) if the corresponding nucleotide in the DNA sequence is \(G\) or \(C\); and \(a_i = 0\) otherwise. In the work of Huang, sequence entries took on values of \(p\) and \(1 - p\) for some real number \(0 \leq p \leq 1\). More generally, we can look for regions where a given set of patterns occur very often. In such applications, \(a_i\) could be the relative frequency with which the corresponding DNA character appears in the given patterns. Further natural applications of this problem can be designed for sophisticated sequence analyses such as mismatch density [Sel84], ungapped local alignments [AS98], and annotated multiple sequence alignments [SFR+99].

Nekrutendo and Li [NL00], and Rice, Longden and Bleasby [RLB00] employed algorithms for the case where \(L = U\). This case is trivially solvable in \(O(n)\) time using a sliding window of the appropriate length. More generally, when \(L \neq U\), this yields a trivial \(O(n(U - L + 1))\) algorithm. Huang [Hua94] studied the case where \(U = n\), i.e., there is effectively no upper bound on the width of the desired maximum-density segments. He observed that an optimal segment exists with width at most \(2L - 1\). Therefore, this case is equivalent to the case with \(U = 2L - 1\) and thus can be solved in \(O(nL)\) time. Recently, Lin, Jiang, and Chao [LJC02] gave an \(O(n \log L)\)-time algorithm for this case based on the introduction of right-skew partitions of a sequence.

In this paper, we present an \(O(n)\)-time algorithm which solves the maximum-density segment problem in the absence of upper bound \(U\). When both lower
and upper bounds, \( L \) and \( U \), are specified, we provide an \( O(n) \)-time algorithm for the uniform case, and an \( O(n + n \log(U - L + 1)) \)-time algorithm when \( w_i \geq 1 \) for all \( i \). Our results exploit the structure of locally optimal segments to improve upon the \( O(n \log L) \)-time algorithm of Lin, Jiang, and Chao [LJC02] and to extend the results to arbitrary values of \( U \). The remainder of this paper is organized as follows. Section 2 introduces some notation and definitions. In Section 3, we carefully review the previous work of Lin, Jiang and Chao, in which they introduce the concept of right-skew partitions. Our main results are presented in Section 4.

Other related works include algorithms for the problem of computing a segment \( \langle a_i, \ldots, a_j \rangle \) with a maximum sum \( a_i + \cdots + a_j \) as opposed to a maximum density. Bentley [Ben86] gave an \( O(n) \)-time algorithm for the case where \( L = 0 \) and \( U = n \). Within the same linear time complexity, Huang [Hua94] solved the case with arbitrary \( L \) yet unbounded \( U \). More recently, Lin, Jiang, and Chao [LJC02] solved the case with arbitrary \( L \) and \( U \).

2 Notation and Preliminaries

We consider \( A \) to be a sequence of \( n \) objects, where each object is represented by a pair of two real numbers \( (a_i, w_i) \) for \( i = 1, \ldots, n \) and \( w_i > 0 \). For \( i \leq j \), we let \( A(i, j) \) denote that segment of \( A \) which begins at index \( i \) and ends with index \( j \). We let \( w(i, j) \) denote the width of \( A(i, j) \), defined as \( w(i, j) = \sum_{i \leq k \leq j} w_k \). We let \( \mu(i, j) \) denote the density of \( A(i, j) \), defined as

\[
\mu(i, j) = \frac{\left( \sum_{i \leq k \leq j} a_k \right)}{w(i, j)}.
\]

We note that the prefix sums of the input sequence can be precomputed in \( O(n) \) time. With these, the values of \( w(i, j) \) and \( \mu(i, j) \) can be computed in \( O(1) \) time for any \( (i, j) \) using the following formulas,

\[
w(i, j) = \sum_{1 \leq k \leq j} w_k - \sum_{1 \leq k \leq i - 1} w_k,
\]

\[
\mu(i, j) = \left( \sum_{1 \leq k \leq j} a_k - \sum_{1 \leq k \leq i - 1} a_k \right)/w(i, j).
\]

The maximum-density segment problem is to find a segment \( A(i, j) \) of maximum density, subject to \( L \leq w(i, j) \leq U \). Without loss of generality, we assume that \( w_i \leq U \) for all \( i \), as items with larger width could not be used in a solution. If \( w_i = 1 \) for all \( i \), we denote this as the uniform model.
For a given index $i$, we introduce the notation $L_i$ for the minimum index such that $w(i, L_i) \geq L$ if such an index exists, and we let $U_i$ denote the maximum index such that $U_i \geq i$ and $w(i, U_i) \leq U$. A direct consequence of these definitions is that segment $A(i, j)$ has width satisfying $L \leq w(i, j) \leq U$ if and only if $L_i$ is well-defined and $L_i \leq j \leq U_i$.

In the uniform model, the set of all such values is easily calculated in $O(n)$ time, as $L_i = i + L - 1$ for $i \leq n - L + 1$ and $U_i = \min(i + U - 1, n)$. In general, the full set of $L_i$ and $U_i$ values can be precomputed in $O(n)$ time by a simple sweep-line technique. The precomputation of the $U_i$ values is shown in Figure 1; a similar technique can be used for computing $L_i$ values. It is not difficult to verify the correctness and efficiency of these computations.

### 3 Right-Skew Segments

For the uniform model, Lin, Jiang and Chao [LJC02] define segment $A(i, k)$ to be right-skew if and only if $\mu(i, j) \leq \mu(j + 1, k)$ for all $i \leq j < k$. They define a partition of a sequence $A$ into segments $A_1 A_2 \ldots A_m$ to be a decreasingly right-skew partition if it is the case that each $A_i$ is right-skew, and that $\mu(A_x) > \mu(A_y)$ for any $x < y$. The prove the following Lemma.

**Lemma 1** Every sequence $A$ has a unique decreasingly right-skew partition.

We denote this unique partition as $\text{DRSP}(A)$. Within the proof of the above lemma, the authors implicitly demonstrate the following fact.

**Lemma 2** If segment $A(x, y)$ is not right-skew, then $\text{DRSP}(A(x, y))$ is precisely equal to the union of $A(x, k)$ and $\text{DRSP}(A(k + 1, y))$ where $A(x, k)$ is the longest possible right-skew segment begining with index $x$.

Because of this structural property, the decreasingly right-skew partitions of all suffixes of $A(1, n)$ can be simultaneously represented by keeping a right-skew pointer, $p[i]$, for each $1 \leq i \leq n$. The pointer is such that $A(i, p[i])$ is
the first right-skew segment of $\text{DRSP}(A(i,n))$. They implicitly use dynamic programming to construct all such right-skew pointers in $O(n)$ time.

In order to find a maximum-density segment of width at least $L$, they proceed by independently searching for the “good partner” of each index $i$. The good partner of $i$ is the index $i'$ that maximizes $\mu(i,i')$ while satisfying $w(i,i') \geq L$. In order to find each good partner, they make use of versions of the following three lemmas.

**Lemma 3 (Atomic)** Let $B$, $C$ and $D$ be sequences with $\mu(B) \leq \mu(C) \leq \mu(D)$. Then $\mu(BC) \leq \mu(BCD)$.

**Lemma 4 (Bitonic)** Let $B$ be a sequence and let $\text{DRSP}(C) = C_1C_2\cdots C_m$ for sequence $C$ which immediately follows $B$. Let $k$ be the greatest index $i \in [0,m]$ that maximizes $\mu(BC_1C_2\cdots C_i)$. Then $\mu(BC_1C_2\cdots C_i) > \mu(BC_1C_2\cdots C_{i+1})$ if and only if $i \geq k$.

**Lemma 5** Given a sequence $B$, let $C$ denote the shortest segment of $B$ realizing the maximum density for those segments of width at least $L$. Then the width of $C$ is at most $2L - 1$.

Without any upper bound on the desired segment length, the consequence of these lemmas is an $O(\log L)$-time algorithm for finding a good partner for arbitrary index $i$. Since only segments of width $L$ or greater are of interest, the segment $A(i,L_i)$ must be included. If considering the possible inclusion of further elements, Lemma 3 assures that if part of a right-skew segment increases the density, including that entire segment is just as helpful (in the application of that lemma $C$ represents part of a right-skew segment $CD$). Therefore, the good partner for $i$ must be $L_i$ or else the right endpoint of one of the right-skew segments from $\text{DRSP}(A(L_i + 1,n))$. Lemma 4 shows that the inclusion of each successive right-skew segment leads to a bitonic sequence of densities, thus binary search can be used to locate the good partner. Finally, Lemma 5 assures that at most $L$ right-skew segments need be considered for inclusion, and thus the binary search for a given $i$ runs in $O(\log L)$ time. The result is an $O(n \log L)$-time algorithm for arbitrary $L$, with $U = n$.

Though presented in terms of the uniform model, the definition of a right-skew segment involves only the densities of segments and so it applies equally to our more general model. Lemmas 1–4 remain valid in the general model. A variant of Lemma 5 can be achieved with the additional restriction that $w_i \geq 1$ for all $i$, and thus their $O(n \log L)$-time algorithm applies subject to this additional restriction.
4 Improved Algorithms

Our techniques are built upon the use of decreasingly right-skew partitions, as reviewed in Section 3. Our improvements are based upon the following observation. An exact good partner for an index \( i \) need not be found if it can be determined that such a partner would result in density no greater than that of a segment already considered. This observation allows us to use a sweep-line technique to replace the \( O(\log L) \)-time binary searches used by Lin, Jiang and Chao [LJC02] with sequential searches that run with an *amortized* time of \( O(1) \). In particular, we make use of the following key lemma.

**Lemma 6** For a given \( j \), assume \( A(j, j') \) is a maximum-density segment of those starting with index \( j \), having \( L \leq w(j, j') \leq U \), and ending with index in a given range \([x, y]\). For a given \( i < j \), assume \( A(i, i') \) is a maximum-density segment of those starting with index \( i \), having \( L \leq w(i, i') \leq U \) and ending in range \([x, y]\). If \( i' > j' \), then \( \mu(j, j') \geq \mu(i, i') \).

**PROOF.** A typical such configuration is shown in Figure 2. By assumption, both indices \( i' \) and \( j' \) lie within the range \([x, y]\). Since \( L \leq w(j, j') < w(j, i') \leq w(i, i') \leq U \), the optimality of \( A(j, j') \) guarantees that \( \mu(j, j') \geq \mu(j, i') \). This implies that \( \mu(j, j') \geq \mu(j, i') \geq \mu(j' + 1, i') \). Since \( L \leq w(j, j') < w(i, j') \leq w(i, i') \leq U \), the optimality of \( A(i, i') \) guarantees that \( \mu(i, i') \geq \mu(i, j') \), which in turn implies \( \mu(j' + 1, i') \geq \mu(i, i') \geq \mu(i, j') \). Combining these inequalities, \( \mu(j, j') \geq \mu(j, i') \geq \mu(j' + 1, i') \geq \mu(i, i') \), thus proving the claim that \( \mu(j, j') \geq \mu(i, i') \).  

Our high level approach is thus to find good partners for each left endpoint \( i \), considering those indices in decreasing order. However, rather than finding the true good partner for each \( i \), our algorithm considers only matching indices which are less than or equal to all previously found good partners, in accordance with Lemma 6. In this way, as we sweep from right to left over the left endpoints \( i \), we also sweep from right to left over the relevant matching indices.
4.1 Maximum-Density Segment with Width at Least $L$

In this section, we consider the problem of finding a segment with the maximum possible density among those of width at least $L$. We begin by introducing a sweep-line data structure which helps manage the search for good partners.

4.1.1 A Sweep-Line Data Structure

The data structure developed in this section is designed to answer queries of the following type for a given range $[x, y]$, specified upon initialization. For left index $i$, the goal is to return a matching right index $i'$ such that $\mu(i, i')$ is maximized, subject to the constraints that $i' \in [x, y]$ and that $w(i, i') \geq L$. No upper bound on the segment length is considered by this structure.

In order to achieve improved efficiency, the searches are limited in the following two ways:

1. The structure can be used to find matches for many different left indices, however such queries must be made in decreasing order.
2. When asked to find the match for a left index, the structure only finds the true good partner in the case that the good partner has index less than or equal to all previously returned indices.

Our data structure augments the right-skew pointers for a given interval with additional information used to speed up searches for good partners. The structure contains the following state information, relative to given parameters $1 \leq x \leq y \leq n$:

- A (static) array, $p[k]$ for $x + 1 \leq k \leq y$, where $A(k, p[k])$ is the leftmost segment of $\text{DRSP}(A(k, y))$.
- A (static) sorted list, $S[k]$, for each $x + 1 \leq k \leq y$, containing all indices $j$ for which $p[j] = k$.
- Two indices $\ell$ and $u$ (for “lower” and “upper”), whose values are non-increasing as the algorithm progresses.
- A variable, $b$ (for “bridge”), which is maintained so that $A(b, p[b])$ is the segment of $\text{DRSP}(A(\ell, y))$ which contains index $u$.

These data structures are initialized with procedure $\text{InitializeL}(x, y)$, given in Figure 3. An example of an initialized structure is given in Figure 4. Lines 1–8 of $\text{InitializeL}$ set the values $p[k]$ as was done in the algorithm of Lin, Jiang and Chao [LJC02]. Therefore, we state the following fact, proven in that preceding paper.
procedure InitializeL(x, y)  
assumes 1 ≤ x ≤ y ≤ n
for i ← y downto x + 1 do
  S[i] ← ∅
  p[i] ← i
  while ((p[i] < y) and (µ(i, p[i]) ≤ µ(p[i] + 1, p[p[i] + 1]))) do
    p[i] ← p[p[i] + 1]
  end while
  Insert i at beginning of S[p[i]]
end for
ℓ ← y; u ← y; b ← y

Fig. 3. InitializeL operation.

\begin{tabular}{cccccccccccc}
1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 & 12 & 13 & 14 \\
\hline
\end{tabular}

\begin{tabular}{c|ccccccc}
 & 1 & 4 & 1 & 5 & 4 & 5 & 4 \\
\hline
a_i & 1 & 4 & 1 & 5 & 4 & 5 & 4 \\
p[i] & 2 & 7 & 4 & 6 & 6 & 7 & 9 & 9 & 14 & 11 & 13 & 13 & 14 \\
S[i] & 2 & 4 & 5 & 3 & 8 & 11 & 12 & 10 & 6 & 7 & 9 & 13 & 14 \\
\end{tabular}

Fig. 4. Example of data structure after InitializeL(1, 14), with w_i = 1 for all i.

**Lemma 7** After a call to InitializeL(x, y), p[k] is set for all x + 1 ≤ k ≤ y such that A(k, p[k]) is the leftmost segment of DRSP(A(k, y)).

We also prove the following nesting property of decreasingly right-skew partitions.

**Lemma 8** Consider two segments A(x_1, y) and A(x_2, y) with a common right endpoint. Let A(k, k') be a segment of DRSP(A(x_1, y)) and let A(m, m') be a segment of DRSP(A(x_2, y)). It cannot be the case that k < m ≤ k' < m'.

**Proof.** If A(k, k') is a segment of DRSP(A(x_1, y)), a repeated application of Lemma 2 assures that A(k, k') is the leftmost segment of DRSP(A(k, y)) and that A(k, k') is the longest possible right-skew segment of those starting with index k.

We assume for contradiction that k < m ≤ k' < m', and consider the following three non-empty segments, A(k, m - 1), A(m, k') and A(k' + 1, m'). Since A(k, k') is right-skew, it must be that µ(k, m - 1) ≤ µ(m, k'). Since A(m, m') is right-skew, it must be that µ(m, k') ≤ µ(k' + 1, m'). In this case, it must be that the combined segment A(k, m') is right-skew (this fact can be explicitly proven by application of Lin, Jiang and Chao’s Lemma 4 [LJC02]). Therefore
procedure FindMatchL(i)
1. while (ℓ > 1 + max(x, L_i)) do  // decrease ℓ
2. ℓ ← ℓ − 1
3. if (p[ℓ] ≥ u) then
4. b ← ℓ
5. end if
6. end while
7. while (u ≥ ℓ) and (µ(i, b − 1) > µ(i, p[b])) do  // bitonic search
8. u ← b − 1
9. if (u ≥ ℓ) then
10. b ← minimum k ∈ S[u] such that k ≥ ℓ
11. end if
12. end while
13. return u

Fig. 5. FindMatchL(i) operation.

the existence of right-skew segment A(k, m') contradicts the assumption that A(k, k') is the longest right-skew segment beginning with index k. □

Corollary 9 There cannot exist indices k and m such that k < m ≤ p[k] < p[m].

PROOF. A direct result of Lemmas 7–8. □

We introduce the main query routine, FindMatchL, given in Figure 5.

Lemma 10 If b is the minimum value satisfying ℓ ≤ b ≤ u ≤ p[b], then A(b, p[b]) is the segment of DRSP(A(ℓ, y)) which contains index u.

PROOF. By Lemma 7, A(b, p[b]) is the leftmost segment of DRSP(A(b, y)), and as b ≤ u ≤ p[b], A(p, p[b]) contains index u.

By repeated application of Lemma 2, DRSP(A(ℓ, y)) equals A(ℓ, p[ℓ]), A(p[ℓ] + 1, p[p[ℓ] + 1]), and so on, until reaching right endpoint y. We claim that A(b, p[b]) must be part of that partition. If not, there must be some other A(m, p[m]) with m < b ≤ p[m]. By Lemma 8, it must be that p[m] ≥ p[b], yet then we have m < b ≤ u ≤ p[b] ≤ p[m]. Such an m violates the assumed minimality of b. □

Lemma 11 Whenever line 7 of FindMatchL() is evaluated, b is the minimum value satisfying ℓ ≤ b ≤ u ≤ p[b], if such a value exists.
PROOF. We show this by induction over time. When initialized, \( \ell = b = u = p[b] = y \), and thus \( b \) is the only satisfying value. The only time this invariant can be broken is when the value of \( \ell \) or \( u \) changes. \( \ell \) is changed only when decremented at line 2 of \texttt{FindMatchL}. The only possible violation of the invariant would be if the new index \( \ell \) satisfies \( \ell \leq u \leq p[\ell] \). This is exactly the condition handled by lines 3–4.

Secondly, \( u \) is modified only at line 8 of \texttt{FindMatchL}. Immediately before this line is executed the invariant holds. At this point, we claim that \( p[k] \leq b - 1 \) for any values of \( k \) such that \( \ell \leq k < b \). For \( k < b \), Corollary 9 implies that either \( p[k] < b \) or \( p[k] \geq p[b] \). If it were the case that \( p[k] \geq p[b] \geq u \) this would violate the minimality of \( b \) assumed at line 7. Therefore, it must be that \( p[k] \leq b - 1 \) for all \( \ell \leq k \leq b - 1 \). As \( u \) is reset to \( b - 1 \), the only possible values for the new bridge \( b \) are those indices \( k \) with \( p[k] = u \), which is precisely the set \( S[b - 1] \) considered at line 10 of \texttt{FindMatchL}.

Lemma 12 Assume \texttt{FindMatchL}(i) is called with a value \( i \) less than that of all previous invocations and such that \( L_i < y \). Let \( m_0 \) be the most recently returned value from \texttt{FindMatchL}() or \( y \) if this is the first such call. Let \( A(i, m) \) be a maximum-density segment of those starting with \( i \), having width at least \( L \), and ending with \( m \in [x, y] \). Then \texttt{FindMatchL}(i) returns the value \( \min(m, m_0) \).

PROOF. All segments which start with \( i \), having width at least \( L \) and ending with \( m \in [x, y] \) must include interval \( A(i, \max(x, L_i)) \). The loop starting at line 1 ensures that variable \( \ell = 1 + \max(x, L_i) \) upon the loop’s exit. As discussed in Section 3, the optimal such \( m \) must either be \( \ell - 1 \) or else among the right endpoints of \( \text{DRSP}(A(\ell, y)) \).

Since \( u \) is only set within \texttt{FindMatchL}, it must be that \( u = m_0 \) upon entering the procedure. By Lemmas 10–11, \( A(b, p[b]) \) is the right-skew segment containing index \( u \) in \( \text{DRSP}(A(\ell, y)) \). If \( \mu(i, b - 1) \leq \mu(i, p[b]) \), the good partner must have index at least \( p[b] \geq u \), by Lemma 4. In this case, the while loop is never entered, and the procedure returns \( m_0 = \min(m, m_0) \).

In any other case, the true good partner for \( i \) is less than or equal to \( m_0 \), and this good partner is found by the while loop of line 1, in accordance with Lemmas 3–4. \( \square \)

Lemma 13 If \texttt{FindMatchL}(i) returns value \( i' \), it must be the case that for some \( j \geq i \), segment \( A(j, i') \) is a maximum-density segment of those starting with \( j \), having width at least \( L \), and ending in \([x, y]\).

PROOF. We prove this by induction over the number of previous calls to \texttt{FindMatchL}. \( i' = m \), as defined in the statement of Lemma 12, then this claim
is trivially true for \( j = i \). Otherwise, \( i' \) is equal to the same value returned by the previous call to \text{FindMatchL} \), and by induction, there is some \( j \geq i \) such that segment \( A(j,i') \) is such a maximum-density segment. 

**Lemma 14** The data structure supports its operations with amortized running times of \( O(y-x+1) \) for \( \text{InitializeL}(x,y) \), and \( O(1) \) for \( \text{FindMatchL}(i) \).

**PROOF.** With the exception of lines 2, 7 and 9, the initialization procedure is simply a restatement of the algorithm given by Lin, Jiang and Chao [LJC02] for constructing the right-skew pointers. An \( O(y-x+1) \)-time worst-case bound was proven by those authors.

In analyzing the cost of \( \text{FindMatchL} \) we note that variables \( \ell \) and \( u \) are initialized to value \( y \) at line 9 of \( \text{InitializeL} \). Variable \( \ell \) is modified only when decremented at line 2 of \( \text{FindMatchL} \) and remains at least \( x+1 \) due to the condition at line 1. Therefore, the loop of lines 1–6 executes at most \( y-x+1 \) times and this cost can be amortized against the initialization cost. Variable \( u \) is modified only at line 8. By Lemma 11, \( x < \ell \leq b \leq u \leq p[b] \), and so this line results in a strict decrease in the value of \( u \) yet \( u \) remains at least \( x \). Therefore, the while loop of lines 7–12 executes \( O(y-x+1) \) times. The only step within that loop which cannot be bounded by \( O(1) \) in the worst case is that of line 10. However, since each \( k \) appears in list \( S[u] \) for a distinct value of \( u \), the overall cost associated with line 10 is bounded by \( O(y-x+1) \). Therefore the cost of this while loop can be amortized as well against the initialization cost. An \( O(1) \) amortized cost per call can account for all remaining instructions outside of the loops. 

**4.1.2 An \( O(n) \)-time Algorithm**

In Figure 6, we present a linear-time algorithm for the maximum-density segment problem subject only to a lower bound of \( L \) on the segment width. The algorithm makes use of the data structure developed in Section 4.1.1.

**Theorem 15** Given a sequence \( A \), the algorithm \( \text{MaximumDensitySegmentL} \) finds the maximum-density segment of those with width at least \( L \).

**PROOF.** To prove the correctness, assume that \( \hat{\mu} \) is the density of an optimal such segment. First, we note that for any value \( i \), Lemma 12 assures that \( g[i] \) is set such that \( g[i] \geq L_i \). Therefore, \( \mu(k,g[k]) \leq \hat{\mu} \) for all \( k \) for which \( g[k] \) was defined.

We claim that for some \( k \), value \( g[k] \) is set such that \( \mu(k,g[k]) \geq \hat{\mu} \). Assume that the maximum density \( \hat{\mu} \) is achieved by some segment \( A(i,i') \). Since it
Fig. 6. Algorithm for finding maximum-density segment with width at least \( L \)
must be that \( L_i \) is well-defined, we consider the pass of the loop starting at line 4 for such an \( i \). Lemma 13 assures us that if \( \text{FindMatchL} \) is called, it either returns \( i' \) or else it must be the case that for some \( j > i \), \( g[j] < i' \). In this case, as \( U \) is unbounded, Lemma 6 assures us that \( \mu(j, g[j]) \geq \mu(i, i') = \hat{\mu} \). And thus \( \text{MaximumDensitySegmentL} \) returns a segment with density \( \hat{\mu} \). □

**Theorem 16** Given a sequence \( A \) of length \( n \), \( \text{MaximumDensitySegmentL} \) runs in \( O(n) \) time.

**PROOF.** This is a direct consequence of Lemma 14. □

### 4.2 Maximum-Density Segment with Width at Least \( L \) and at Most \( U \)

In this section, we consider the problem of finding a segment with the maximum possible density among those of width at least \( L \) and at most \( U \). At first glance, the sweeping of variable \( u \) in the previous algorithm appears similar to placing an explicit upper bound on the width of the segments of interest for a given left index \( i \). In locating the good partner for \( i \), a sequential search is performed over right-skew segments of \( \text{DRSP}(A(L_i + 1, n)) \). The repeated decision of whether it is advantageous to include the bridge segment \( A(b, p[b]) \) is determined in accordance with the bitonic property of Lemma 4.

The reason that this technique does not immediately apply to the case with an explicit upper bound of \( U \) is the following. If the right endpoint of the bridge, \( p[b] \), is strictly greater than \( U_i \), considering the effect of including the entire bridge may not be relevant. To properly apply Lemmas 3–4, we must consider segments of \( \text{DRSP}(A(L_i + 1, U_i)) \) as opposed to \( \text{DRSP}(A(L_i + 1, n)) \).
procedure InitializeU(x, y)  \text{assumes } 1 \leq x \leq y \leq n

1  \text{for } i \leftarrow x + 1 \text{ to } y \text{ do}
2       q[i] \leftarrow i
3    \text{while } ((q[i] > x) \text{ and } (\mu(q[i] - 1), q[i] - 1) \leq \mu(q[i], i)) \text{ do}
4        q[i] \leftarrow q[q[i] - 1]
5  \text{end while}
6  \text{end for}
7  u \leftarrow y

Fig. 7. InitializeU operation.

| a_i | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 |
|-----|---|---|---|---|---|---|---|---|---|----|----|----|----|----|
| q[i]| 2 | 3 | 3 | 3 | 3 | 3 | 8 | 8 | 10 | 10 | 10 | 10 | 10 | 10 |

Fig. 8. Example of data structure after InitializeU(1, 14), with \( w_i = 1 \) for all \( i \).

4.2.1 Another Sweep-Line Data Structure

Recall that the structure of Section 4.1.1 focused on finding segments beginning with \( i \), ending in \([x, y]\) and subject to a lower bound on the resulting segment width. Therefore, as \( i \) was decreased, the effective lower bound, \( L_i \), on the matching endpoint can only decrease. The decomposition of interest was \( \text{DRSP}(A(L_i, y)) \), and such decompositions were simultaneously represented for all possible values of \( L_i \) by the right-skew pointers, \( p[k] \).

In this section, we develop another sweep-line data structure that we used to locate segments beginning with \( i \), ending in \([x, y]\) and subject to an upper bound on the resulting segment width (but with no explicit lower bound). For a given \( i \), the decomposition of interest is \( \text{DRSP}(A(x + 1, U_i)) \). However, since \( U_i \) decreases with \( i \), our new structure is based on representing the decreasingly right-skew partitions for all prefixes of \( A(x + 1, y) \), rather than all suffixes. We assign values \( q[k] \) for \( x + 1 \leq k \leq y \) such that \( A(q[k], k) \) is the rightmost segment of \( \text{DRSP}(A(x + 1, k)) \). Though there are clear symmetries between this section and Section 4.1.1, there is not a perfect symmetry; in fact the structure introduced in this section is considerably simpler. The lack of perfect symmetry is because the concept of right-skew segments, used in both sections, is oriented.

The initialization routine for this new structure is presented in Figure 7. An example of an initialized structure is given in Figure 8. The redesign of the initialization routine relies on a simple duality when compared with the corresponding routine of Section 4.1.1. One can easily verify that an execution of this routine on a segment \( A(x, y) \) sets the values of array \( q \) precisely as
procedure FindMatchU(i)
1   while (u > Ui) do // decrease u
2      u ← u - 1
3   end while
4   while (u > x) and (µ(i,q[u] - 1) > µ(i,u)) do // bitonic search
5      u ← q[u] - 1
6   end while
7   return u

Fig. 9. FindMatchU(i) operation.

the original version would set the values of array p if run on a reversed and negated copy of A(x, y). Based on this relationship, we claim the following dual of Lemma 7 without further proof.

Lemma 17 Immediately after InitializeU(x, y), the segment A(q[k], k) is the rightmost segment of DRSP(A(x + 1, k)), for all k in the range [x + 1, y].

We now present the main query routine, FindMatchU, given in Figure 9, and discuss its behavior.

Lemma 18 Assume FindMatchU(i) is called with a value i less than that of all previous invocations and such that x ≤ Ui ≤ y. Let m₀ be the most recently returned value from FindMatchU() or y if this is the first such call. Let A(i, m) be a maximum-density segment of those starting with i, having width at most U, and ending with m ∈ [x, m₀]. Then FindMatchU(i) returns the value m.

PROOF. Combining the constraints that w(i, m) ≤ U and that m ∈ [x, m₀], it must be that m ≤ min(Uᵢ, m₀). When entering the procedure, the variable u has value Uᵢ. The loop starting at line 1 ensures that variable u = min(Uᵢ, m₀) upon the loop’s exit. The discussion in Section 3 assures us that the optimal m ∈ [x, u] must either be x or else among the right endpoints of DRSP(A(x + 1, u)). Based on Lemma 17, A(q[u], u) is the rightmost segment of DRSP(A(x + 1, u)) and so the loop condition at line 4 of FindMatchU is a direct application of Lemma 4.

Lemma 19 The data structure supports its operations with amortized running times of O(y - x + 1) for InitializeU(x, y), and O(1) for FindMatchU(i), so long as Ui ≥ x for all i.

PROOF. The initialization procedure has an O(y - x + 1)-time worst-case bound, as was the case for the similar routine in Section 4.1.1.
To account for the cost of \texttt{FindMatchU}, we note that \( u \) is initialized to value \( y \) at line 7 of \texttt{InitializeU}. It is only modified by lines 2 and 5 of the routine, and we claim that both lines strictly decrease the value. This is obvious for line 2, and for line 5, it follows for \texttt{FindMatchU}, since \( q[u] \leq u \) in accordance with Lemma 17. We also claim that \( u \) is never set less than \( x \). Within the loop of lines 1–3, this is due to the assumption that \( U_i \geq x \). For the loop of lines 4–7, it is true because \( q[u] \geq x + 1 \) in accordance with Lemma 17. Therefore, these loops execute at most \( O(y - x + 1) \) times combined and this cost can be amortized against the initialization cost. An \( O(1) \) amortized cost per call can account for checking the initial test condition before entering either loop.

\[ \square \]

4.2.2 An \( O(n) \)-time Algorithm for the Uniform Model

In this section, we present a linear-time algorithm for the uniform maximum-density segment problem subject to both a lower bound \( L \) and an upper bound \( U \) on the segment width, with \( L < U \).

Our strategy is as follows. We pre-process the original sequence by breaking it into blocks of cardinality exactly \( U - L \) (except, possibly for the last block). For each such block, we maintain two sweep-line data structures, one as in Section 4.1.1 and one as in Section 4.2.1.

For a given left index \( i \), a valid good partner must lie in the range \([L_i, U_i]\). Because we consider the uniform model, such an interval had cardinality precisely \((U - L + 1)\) and thus overlaps exactly two of the pre-processed blocks. For \( \alpha = (U - L)[L_i/(U - L)] \), we search for a potential partner in the range \([L_i, \alpha]\) using the data structure of Section 4.1.1, and for a potential partner in the range \([\alpha + 1, U_i]\) using the data structure of Section 4.2.1. Though we are not assured of finding the true good partner for each \( i \), we again find the global optimum, in accordance with Lemma 6. Our complete algorithm is given in Figure 10.

**Theorem 20** Given a sequence \( A \) of length \( n \) for which \( w_i = 1 \) for all \( i \), and parameters \( L < U \), the algorithm \texttt{MaximumDensitySegmentLU} finds the maximum-density segment of those with width at least \( L \) and at most \( U \).

**Proof.** Because \( w_i = 1 \) for all \( i \), the interval \([L_i, U_i]\) has cardinality precisely \((U - L + 1)\). We note that \( z \) is chosen at line 12 so that \( L_i \) lies within \texttt{BlockL}[z] and that \( U_i \) lies within \texttt{BlockU}[z + 1].

To prove the correctness, assume that \( \hat{\mu} \) is the density of an optimal such segment. First, we claim that \( L \leq w(i, q[i]) \leq U \) for any \( i \) and thus that the algorithm cannot possibly return a density greater than \( \hat{\mu} \). This is a direct
procedure MaximumDensitySegmentLU\((A, L, U)\)
1 \[\text{[calculate values } L_i \text{ and } U_i \text{, as discussed in Section 2]}\]
2 \(\text{leftend} \leftarrow 1\)
3 \(\text{while } (\text{leftend} < n) \) do // initialize blocks
4 \(\text{rightend} \leftarrow \min(n, \text{leftend} + (U - L) - 1)\)
5 \(z \leftarrow (\text{leftend} - 1)/(U - L)\)
6 \(\text{Block}_{L}[z] \leftarrow \text{InitializeL}(\text{leftend}, \text{rightend})\)
7 \(\text{Block}_{U}[z] \leftarrow \text{InitializeU}(\text{leftend}, \text{rightend})\)
8 \(\text{leftend} \leftarrow \text{leftend} + (U - L)\)
9 \(\text{end while}\)
10 \(i_0 \leftarrow \text{maximum index such that } L_{i_0} \text{ is well-defined}\)
11 \(\text{for } i \leftarrow i_0 \text{ downto } 1 \) do
12 \(z \leftarrow [L_i/(U - L)]\) // determine which blocks to search
13 \(g_{L}[i] \leftarrow \text{FindMatchL}(i) \text{ for Block}_{L}[z]\)
14 \(g_{U}[i] \leftarrow \text{FindMatchU}(i) \text{ for Block}_{U}[z + 1]\)
15 \(\text{if } (\mu(i, g_{L}[i]) \geq \mu(i, g_{U}[i])) \) then
16 \(g[i] \leftarrow g_{L}[i]\)
17 \(\text{else}\)
18 \(g[i] \leftarrow g_{U}[i]\)
19 \(\text{end if}\)
20 \(\text{end for}\)
21 \(\text{return } (k, g[k]) \text{ which maximizes } \mu(k, g[k]) \text{ for } 1 \leq k \leq i_0\)

Fig. 10. Algorithm for finding maximum-density segment with width at least \(L\) and at most \(U\) result of Lemma 12 in regard to the block searched at line 13 and Lemma 18 in regard to the block searched at line 14.

We then claim that for some \(k\), value \(g[k]\) is set such that \(\mu(k, g[k]) \geq \hat{\mu}\). Assume that the maximum density \(\hat{\mu}\) is achieved by some segment \(A(i, i')\). Since it must be that \(L_i\) is well-defined, we consider the pass of the loop starting at line 11 for such an \(i\). We show that either \(g[i] = i'\) or else there exists some \(j > i\) such that \(\mu(j, g[j]) \geq \mu(i, i')\). If \(i'\) lies within \(\text{Block}_{L}[z]\) then we apply the same reasoning about the call to \text{FindMatchL} at line 13, as we did in the proof of Theorem 15. If \(i'\) lies within \(\text{Block}_{U}[z + 1]\) then we consider the behavior of the call to \text{FindMatchU}(i) at line 14. If that call does not return \(i'\) then it must be that \(i' > m_0\) as defined in Lemma 18. Since the return values of this method are non-increasing, we let \(j\) be the largest index for which the returned \(g[j] < i'\). At the onset of that call to \text{FindMatchU} it must have been that \(m_0 \geq i'\) and therefore we can apply Lemma 6 to deduce that \(\mu(j, g[j]) \geq \mu(i, i')\). Thus \text{MaximumDensitySegmentLU} returns a segment with density \(\hat{\mu}\). \(\square\)

**Theorem 21** Given a sequence \(A\) of length \(n\) for which \(w_i = 1\) for all \(i\), the
algorithm MaximumDensitySegmentLU runs in \( O(n) \) time.

**PROOF.** This is a consequence of Lemmas 14 and 19. The calls to the initialization routines in the loop of lines 3–9 runs in \( O(n) \) time, as each initialization routine is called for a set of blocks which partition the original sequence. Similarly, the cost of all the calls to FindMatchL and FindMatchU in the loop of lines 11–20 can be amortized against the corresponding initializations. \( \square \)

4.2.3 An \( O(n + n \log(U - L + 1)) \)-time Algorithm for a More General Model

With general values of \( w_i \), the algorithm in Section 4.2.2 is insufficient for one of two reasons. If values of \( w_i > 1 \) are allowed, it may be that an entire interval \([L_i, U_i]\) falls in a single block, in which case neither of the sweep-line data structures suffice. Alternatively, if values of \( w_i < 1 \) are allowed, then an interval \([L_i, U_i]\) might span an arbitrary number of blocks. Always searching all such blocks might result in \( \omega(n) \) overall calls to FindMatchL or FindMatchU.

In this section, we partially address the general case, providing an \( O(n + n \log(U - L + 1)) \)-time algorithm when \( w_i \geq 1 \) for all \( i \). This condition assures us that the interval \([L_i, U_i]\) has cardinality at most \( U - L + 1 \). Rather than rely on a single partition of the original sequence into fixed-sized blocks, we will create \( O(\log(U - L + 1)) \) partitions, each of which uses fixed-sized blocks, for varying sizes. Then we show that the interval \([L_i, U_i]\) can be covered with a collection of smaller blocks in which we can search.

For ease of notation, we assume, without loss of generality, that the overall sequence \( A \) is padded with values so that it has length \( n \) which is a power of two. We consider \( n \) blocks of size 1, \( n/2 \) blocks of size 2, \( n/4 \) blocks of size 4, and so on until \( n/2^\beta \) blocks of size \( 2^\beta \), where \( \beta = \lfloor \log_2(U - L + 1) \rfloor \).

Specifically, we define block \( B_{j,k} = A(1 + j * 2^k, (j + 1) * 2^k) \) for all \( 0 \leq k \leq \beta \) and \( 0 \leq j < n/2^k \). We begin with the following lemma.

**Lemma 22** For any interval \( A(p, q) \) with cardinality at most \( U - L + 1 \), we can compute, in \( O(1 + \beta) \) time, a collection of \( O(1 + \beta) \) disjoint blocks such that \( A(p, q) \) equals the union of the blocks.

The algorithm CollectBlocks is given in Figure 11, and a sample result is shown in Figure 12. It is not difficult to verify the claim.

**Theorem 23** Given a sequence \( A \) of length \( n \) for which \( w_i \geq 1 \) for all \( i \), a maximum-density segment of those with width at least \( L \) and at most \( U \) can be found in \( O(n + n \log(U - L + 1)) \) time.
procedure CollectBlocks(p, q)
1       s ← p; k ← 0;
2     while \(2^k + s - 1 \leq q\) do
3       while \(2^{k+1} + s - 1 \leq q\) do
4         k ← k + 1
5     end while
6       j ← \([s/2^k]\) - 1
7       Add block \(B_{j,k}\) to the collection
8       k ← k + 1
9   end while
10  while \(s \leq q\) do
11     while \(2^k + s - 1 > q\) do
12       k ← k - 1
13   end while
14       j ← \([s/2^k]\) - 1
15       Add block \(B_{j,k}\) to the collection
16       k ← k - 1
17  end while

Fig. 11. Algorithm for finding collection of blocks to cover an interval

Fig. 12. A collection of blocks for a given interval

PROOF. The algorithm is given in Figure 13. First, we discuss the correctness. Assume that the global maximum is achieved by \(A(i, i')\). We must simply show that this pair, or one with equal density, was considered at line 14. By Lemma 22, \(i'\) must lie in some \(B_{j,k}\) returned by \text{CollectBlocks}(L_i, U_i). Because \(\mu(i, i')\) is a global maximum, the combination of Lemmas 6 and 12 assures us that \text{FindMatchL}() at line 10 will return \(i'\) or else some earlier pair which was found has density at least as great.

We conclude by showing that the running time is \(O(n + n\beta)\). Notice that for a fixed \(k\), blocks \(B_{j,k}\) for \(0 \leq j < n/2^k - 1\) comprise a partition of the original input \(A\), and thus the sum of their cardinalities is \(O(n)\). Therefore, for a fixed \(k\), lines 4–6 run in \(O(n)\) time by Lemma 14, and overall lines 3–7 run in \(O(n\beta)\) time. Each call to \text{CollectBlocks} from line 9 runs in \(O(1 + \beta)\) time by Lemma 22, and produces \(O(1 + \beta)\) blocks. Therefore, the body of that loop, lines 9–14, executes \(O(n + n\beta)\) times over the course of the entire algorithm.
procedure MaximumDensitySegmentLU2(A, L, U)
1  [calculate values $L_i$ and $U_i$, as discussed in Section 2]
2  $\beta \leftarrow \lfloor \log_2(U - L + 1) \rfloor$; $\mu_{\text{max}} \leftarrow -\infty$;
3  for $k \leftarrow 0$ to $\beta$ do
4      for $j \leftarrow 0$ to $n/2^k - 1$ do
5          $B_{j,k} \leftarrow \text{InitializeL}(1 + j \ast 2^k, (j + 1) \ast 2^k)$
6      end for
7  end for
8  $i_0 \leftarrow$ maximum index such that $L_i$ is defined
9  foreach $B_{j,k}$ in CollectBlocks($L_i, U_i$) do
10     $\text{temp} \leftarrow \text{FindMatchL}(i)$
11     if $\mu(i, \text{temp}) > \mu_{\text{max}}$ then
12        $\mu_{\text{max}} \leftarrow \mu(i, \text{temp})$; record endpoints $(i, \text{temp})$
13     end if
14  endforeach
15 end for

Fig. 13. Algorithm for maximum-density segment with width at least $L$, at most $U$

Finally, we must account for the time spent in all calls to FindMatchL from line 10. Rather than analyze these costs chronologically, we account for these calls by considering each block $B_{j,k}$ over the course of the algorithm. By Lemma 14, each of these calls has an amortized cost of $O(1)$, where that cost is amortized over the initialization cost for that block. □

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