Optimal Field Splitting for Large Intensity-Modulated Fields

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Abstract.

The multileaf travel range limitations on some linear accelerators require the splitting of a large intensity-modulated field into two or more adjacent abutting intensitymodulated sub-fields. The abutting sub-fields are then delivered as separate treatment fields. This work-around not only increases the treatment delivery time but it also increases the total monitor units (MU) delivered to the patient for a given prescribed dose. It is imperative that the cumulative intensity map of the sub-fields is exactly the same as the intensity map of the large field generated by the dose optimization algorithm, while satisfying hardware constraints of the delivery system. In this work, we describe field splitting algorithms that split a large intensity-modulated field into two or more intensity-modulated sub-fields with and without feathering, with optimal MU efficiency while satisfying the hardware constraints. Compared to a field splitting technique (without feathering) used in a commercial planning system, our field splitting algorithm (without feathering) shows a decrease in total MU of up to 26% on clinical cases and up to 63% on synthetic cases.

Submitted to: Medical Physics

1. Introduction

Intensity modulated radiation therapy (IMRT) is increasingly used to treat large volumes because of its ability to deliver more conformal radiation while sparing the surrounding normal $tissue^{1-4}$. Most IMRT treatments are delivered with conventional multileaf collimators (MLC) that are now available on all commercial linear accelerators. The MLC systems vary in design and each one of them has certain mechanical limitations, which require some clinical work-around. Maximum leaf spread for leaves on the same leaf bank is one such limitation, which necessitates a large field to be split into two or more adjacent abutting sub-fields. This is true for the Varian MLCs (Varian Medical Systems, Palo Alto, CA), which has a field size limitation of about 15 cm. The abutting sub-fields are then delivered as separate treatment fields. This often results in longer delivery times, poor MU efficiency, and field matching problems. Dogan et. al.⁵ point out that the uncertainties in leaf and carriage positions cause errors in the delivered dose (hot or cold spots) along the match line of the abutting sub-fields. They observed dose differences of up to 10% along the field split line when the split line crossed through the center of the target for all the fields. The problem of dosimetric perturbation along the field split line has been addressed in several recent publications^{1,5,6}. The solutions included automatic feathering of split-fields by modifying the split line position for each gantry position^{1,5} or by dynamically changing radiation intensity in the overlap region of the split fields. None of the field splitting techniques reported in the literature has addressed the issue of treatment delivery and MU efficiency. We believe that it is equally important to address this issue.

In our recent publications^{7,8}, we have reported on leaf sequencing algorithms that are optimal for MU efficiency while satisfying most of the hardware constraints for step-and-shoot IMRT delivery. Our optimal field splitting algorithms with and without feathering may be integrated into our previously developed leaf sequencing algorithms to optimally account for interdigitation and tongue-and-groove effect of some multileaf collimators. We provide rigorous mathematical proofs that the proposed schemes for

field splitting are optimal in MU efficiency. Experimental results show that our optimal field splitting algorithm without feathering reduces total MUs by up to 26% on clinical cases and up to 63% on synthetic cases compared to a commercial planning system that also splits fields without feathering.

2. Field splitting without feathering

2.1. Optimal field splitting for one leaf pair

2.1.1. Intensity map. We consider delivery of intensity map produced by the optimizer. It is important to note that the intensity map from the optimizer is always a discrete matrix. The spatial resolution of this matrix is similar to the smallest beamlet size. The beamlet size typically ranges from 5-10 mm. Let I(x) be the desired intensity profile along x axis. The discretized profile from the optimizer gives the intensity values at sample points x_1, x_2, \ldots, x_m . We assume that the sample points are uniformly spaced and that $\Delta x = x_{i+1} - x_i$, $1 \le i < m$. I(x) is assigned the value $I(x_i)$ for $x_i \le x < x_i + \Delta x$, $1 \le i \le m$. Now, $I(x_i)$ is our desired intensity profile, i.e., $I(x_i)$ is a measure of the number of MUs for which x_i , $1 \le i \le m$, needs to be exposed. In the remainder of this paper, we will refer to a profile $I(x_i)$ simply as profile I. Figure 1 shows a profile, which is the output from the optimizer at discrete sample points x_1, x_2, \ldots, x_m . This profile is delivered either with the Segmental Multileaf Collimation (SMLC) method or with Dynamic Multileaf Collimation (DMLC). In this paper we study delivery with SMLC.

2.1.2. Delivering a profile using one field. Let I be the desired intensity profile. The problem of delivering the exact profile I using a single field has been extensively studied. Ma et. al.⁹ provide an O(m) algorithm for the problem such that the therapy time of the solution is minimized, where m is the number of sample points. Kamath et. al.⁷ also describe the algorithm (Algorithm SINGLEPAIR) and give an alternate proof that it obtains a plan (I_l, I_r) with optimal therapy time for I, where I_l and I_r denote the left and right leaf movement profiles, respectively. The optimal therapy time for I is given

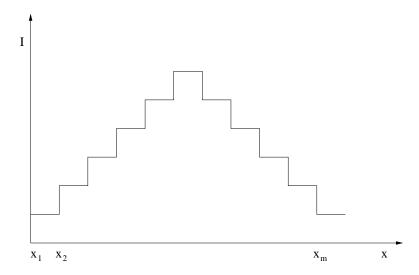


Figure 1. Profile generated by the optimizer

by the following lemma.

Lemma 1 Let inc1, inc2, ..., incq be the indices of the points at which $I(x_i)$ increases, i.e., $I(x_{inci}) > I(x_{inci-1})$. The therapy time for the plan (I_l, I_r) generated by Algorithm SINGLEPAIR is $\sum_{i=1}^{q} [I(x_{inci}) - I(x_{inci-1})]$, where $I(x_{inc1-1}) = 0$.

Algorithm SINGLEPAIR can be directly used to obtain plans when I is deliverable using a single field. Let l be the least index such that $I(x_l) > 0$ and let g be the greatest index such that $I(x_g) > 0$. We will assume without loss of generality that l = 1. So the width of the profile is g sample points, where g can vary for different profiles. Assuming that the maximum allowable field width is w sample points, I is deliverable using one field if $g \le w$; I requires at least two fields for g > w; I requires at least three fields for g > 2w. The case where g > 3w is not studied as it never arises in clinical cases. The objective of field splitting is to split a profile so that each of the resulting profiles is deliverable using a single field. Further, it is desirable that the total therapy time is minimized, i.e., the sum of optimal therapy times of the resulting profiles is minimized. We will call the problem of splitting the profile I of a single leaf pair into 2 profiles each of which is deliverable using one field such that the sum of their optimal therapy times is minimized as the S2 (single pair 2 field split) problem. The sum of the optimal therapy times of the two resulting profiles is denoted by S2(I). S3 and S3(I)

are defined similarly for splits into 3 profiles. The problem S1 is trivial, since the input profile need not be split and is to be delivered using a single field. Note that S1(I) is the optimal therapy time for delivering the profile I in a single field. From Lemma 1 and the fact that the plan generated using Algorithm SINGLEPAIR is optimal in therapy time, $S1(I) = \sum_{i=1}^{q} [I(x_{inci}) - I(x_{inci-1})]$.

2.1.3. Splitting a profile into two. Suppose that a profile I is split into two profiles. Let j be the index at which the profile is split. As a result, we get two profiles, P_j and S_j . $P_j(x_i) = I(x_i)$, $1 \le i < j$, and $P_j(x_i) = 0$, elsewhere. $S_j(x_i) = I(x_i)$, $j \le i \le g$, and $S_j(x_i) = 0$, elsewhere. P_j is a left profile and S_j is a right profile of I.

Lemma 2 Let $S1(P_j)$ and $S1(S_j)$ be the optimal therapy times, respectively, for P_j and S_j . Then $S1(P_j) + S1(S_j) = S1(I) + \hat{I}(x_j)$, where $\hat{I}(x_j) = \min\{I(x_{j-1}), I(x_j)\}$.

Proof: See Appendix.

We illustrate Lemma 2 using the example of Figure 2. The optimal therapy time for the profile I is the sum of increments in intensity values of successive sample points. However, if I is split at x_3 into P_3 and S_3 , an additional therapy time of $\hat{I}(x_3) = \min\{I(x_2), I(x_3)\} = I(x_3)$ is required for treatment. Similarly, if I is split at x_4 into P_4 and S_4 , an additional therapy time of $\hat{I}(x_4) = \min\{I(x_3), I(x_4)\} = I(x_3)$ is required.

Lemma 2 leads to the following O(g) algorithm for S2.

Algorithm S2

- (1) Compute $\hat{I}(x_i) = \min\{I(x_{i-1}), I(x_i)\}, \text{ for } g w < i \le w + 1.$
- (2) Split the field at a point x_j where $\hat{I}(x_j)$ is minimized for $g w < j \le w + 1$.

It is evident from Lemma 2 that if the width of the profile is less than the maximum allowable field width $(g \leq w)$, the profile is best delivered using a single field. If g > 2w two fields are insufficient. So it is useful to apply Algorithm S2 only for $w < g \leq 2w$. Once the profile I is split into two as determined by Algorithm S2,

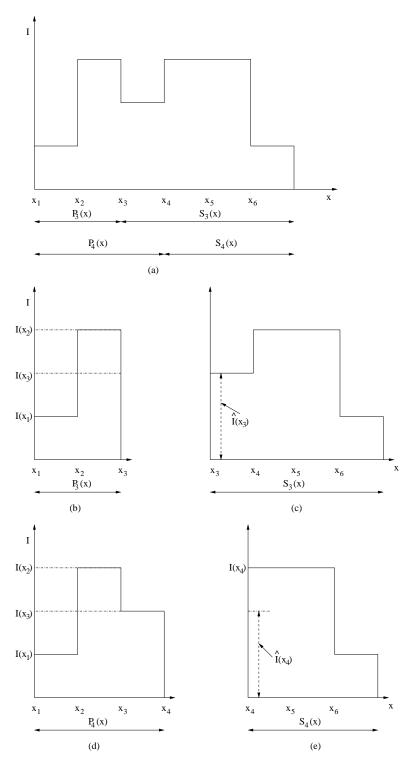


Figure 2. Splitting a profile (a) into two. (b) and (c) show the left and right profiles resulting from a split at x_3 ; (d) and (e) show the left and right profiles resulting from a split at x_4

the left and right profiles are delivered using separate fields. The total therapy time is $S2(I) = S1(P_j) + S1(S_j)$, where j is the split point.

2.1.4. Splitting a profile into three. Suppose that a profile I is split into three profiles. Let j and k, j < k, be the indices at which the profile is split. As a result we get three profiles P_j , $M_{(j,k)}$ and S_k , where $P_j(x_i) = I(x_i)$, $1 \le i < j$, $M_{(j,k)}(x_i) = I(x_i)$, $j \le i < k$, and $S_k(x_i) = I(x_i)$, $k \le i \le g$. P_j , $M_{(j,k)}$ and S_j are zero at all other points. P_j is a left profile, $M_{(j,k)}$ is a middle profile of I and S_k is a right profile.

Lemma 3 Let $S1(P_j)$, $S1(M_{(j,k)})$ and $S1(S_k)$ be the optimal therapy times, respectively, for P_j , $M_{(j,k)}$ and S_k . Then $S1(P_j) + S1(M_{(j,k)}) + S1(S_k) = S1(I) + \min\{I(x_{j-1}), I(x_j)\} + \min\{I(x_{k-1}), I(x_k)\} = S1(I) + \hat{I}(x_j) + \hat{I}(x_k)$.

Proof: Similar to that of Lemma 2

Lemma 3 motivates the following algorithm for S3.

Algorithm S3

- (1) Compute $\hat{I}(x_i) = \min\{I(x_{i-1}), I(x_i)\}, \text{ for } 1 < i \le w+1, g-w < i \le g.$
- (2) Split the field at two points x_j , x_k such that $1 \leq j \leq w+1$, $g-w < k \leq g$, $0 < k-j \leq w$, and $\hat{I}(x_j) + \hat{I}(x_k)$ is minimized.

Note that for Algorithm S3 to split I into three profiles that are each deliverable in one field, it must be the case that $g \leq 3w$. Once the profile I is split into three as determined by Algorithm S3, the resulting profiles are delivered using separate fields. The minimum total therapy time is $S3(I) = S1(P_j) + S1(M_{(j,k)}) + S1(S_k)$. Algorithm S3 examines at most g^2 candidates for (j,k). So the complexity of the algorithm is $O(g^2)$.

2.1.5. Bounds on optimal therapy time ratios. We prove the following bounds on ratios of optimal therapy times.

Lemma 4 (a) $1 \le S2(I)/S1(I) \le 2$

(b)
$$1 \le S3(I)/S1(I) \le 3$$

(c)
$$0.5 < S3(I)/S2(I) < 2$$

Proof: See Appendix.

Lemma 4 tells us that the optimal therapy times can at most increase by factors of 2 and 3, respectively, as a result of a splitting a single leaf pair profile into 2 and 3. Also, the optimal therapy time for a split into 2 can be at most twice that for a split into 3 and vice versa.

2.2. Optimal field splitting for multiple leaf pairs

The input intensity matrix (say I) for the leaf sequencing problem is obtained using the inverse planning technique. The matrix I consists of n rows and m columns. Each row of the matrix specifies the number of monitor units (MUs) that need to be delivered using one leaf pair. Denote the rows of I by I_1, I_2, \ldots, I_n . For the case where I is deliverable using one field, the leaf sequencing problem has been well studied in the past. The algorithm that generates optimal therapy time schedules for multiple leaf pairs (Algorithm MULTIPAIR, Kamath et. al.⁷) applies algorithm SINGLEPAIR independently to each row I_i of I. Without loss of generality assume that the least column index containing a non zero element in I is I and the largest column index containing a non zero element in I is I and the largest column index containing a non zero element in I is I and the profile will need to be split. We define problems I and I and I and I and I are also defined similarly. The optimal therapy times I and I and I and I are also defined similarly.

2.2.1. Splitting a profile into two. Suppose that a profile I is split into two profiles. Let x_j be the column at which the profile is split. This is equivalent to splitting each row profile I_i , $1 \le i \le n$, at j as defined for single leaf pair split. As a result we get two profiles, P_j (left) and S_j (right). P_j has rows $P_j^1, P_j^2, \ldots, P_j^n$ and S_j has rows $S_j^1, S_j^2, \ldots, S_j^n$.

Lemma 5 Suppose I is split into two profiles at x_j . The optimal therapy time for delivering P_j and S_j using separate fields is $\max_i \{S1(P_j^i)\} + \max_i \{S1(S_j^i)\}$.

Proof: The optimal therapy time schedule for P_j and S_j are obtained using Algorithm MULTIPAIR. The therapy times are $\max_i \{S1(P_j^i)\}$ and $\max_i \{S1(S_j^i)\}$ respectively. So the total therapy time is $\max_i \{S1(P_j^i)\} + \max_i \{S1(S_j^i)\}$.

From Lemma 5 it follows that the M2 problem can be solved by finding the index $j, 1 < j \le g$ such that $\max_i \{S1(P_j^i)\} + \max_i \{S1(S_j^i)\}$ is minimized (Algorithm M2). Algorithm M2

- (1) Compute $\max_{i} \{S1(P_{i}^{i})\} + \max_{i} \{S1(S_{i}^{i})\}$ for $g w < j \le w + 1$.
- (2) Split the field at a point x_j where $\max_i \{S1(P_j^i)\} + \max_i \{S1(S_j^i)\}$ is minimized for $g w < j \le w + 1$.

From Lemma 1, $S1(P_j^i) = \sum_{inci \leq j} [I(x_{inci}) - I(x_{inci-1})]$. For each i, $S1(P_1^i)$, $S1(P_2^i)$, ..., $S1(P_g^i)$ can all be computed in a total of O(g) time progressively from left to right. So the computation of S1s (optimal therapy times) of all left profiles of all n rows of I can be done in O(ng) time. The same is true of right profiles. Once these values are computed, step (1) of Algorithm M2 is applied. $\max_i \{S1(P_j^i)\} + \max_i \{S1(S_j^i)\}$ can be found in O(n) time for each j and hence in O(ng) time for all j in the permissible range. So the time complexity of Algorithm M2 is O(ng).

2.2.2. Splitting a profile into three. Suppose that a profile I is split into three profiles. Let j, k, j < k, be the indices at which the profile is split. Once again, this is equivalent to splitting each row profile I_i , $1 \le i \le n$ at j and k as defined for single leaf pair split. As a result we get three profiles P_j , $M_{(j,k)}$ and S_k . P_j has rows $P_j^1, P_j^2, \ldots, P_j^n, M_{(j,k)}$ has rows $M_{(j,k)}^1, M_{(j,k)}^2, \ldots, M_{(j,k)}^n$ and S_k has rows $S_k^1, S_k^2, \ldots, S_k^n$.

Lemma 6 Suppose I is split into three profiles by splitting at x_j and x_k , j < k. The optimal therapy time for delivering P_j , $M_{(j,k)}$ and S_k using separate fields is $\max_i \{S1(P_j^i)\} + \max_i \{S1(M_{(j,k)}^i)\} + \max_i \{S1(S_k^i)\}.$ **Proof:** Similar to that of Lemma 5.

Algorithm M3 solves the M3 problem.

Algorithm M3

- (1) Compute $\max_{i} \{S1(P_{j}^{i})\} + \max_{i} \{S1(M_{(j,k)}^{i})\} + \max_{i} \{S1(S_{k}^{i})\}$ for $1 < j \le w + 1$, $g w < k \le g$, $0 < k j \le w$.
- (2) Split the field at two points x_j , x_k , such that $1 < j \le w + 1$, $g w < k \le g$, $0 < k j \le w$, and $\max_i \{S1(P_j^i)\} + \max_i \{S1(M_{(j,k)}^i)\} + \max_i \{S1(S_k^i)\}$ is minimized.

The complexity analysis is similar to that of Algorithm M2. In this case though, $O(g^2)$ pairs of split points have to be examined. It is easy to see that the time complexity of Algorithm M3 is $O(ng^2)$.

2.2.3. Bounds on optimal therapy time ratios. We prove the following bounds on ratios of optimal therapy times.

Lemma 7 (a) $1 \le M2(I)/M1(I) \le 2$

- (b) $1 \le M3(I)/M1(I) < 3$
- (c) 0.5 < M3(I)/M2(I) < 2

Proof: See Appendix.

Lemma 7 tells us that the optimal therapy times can at most increase by factors of 2 and 3, respectively, as a result of splitting a field into 2 and 3. Also, the optimal therapy time for a split into 2 can be at most twice that for a split into 3 and vice versa. These bounds give us the potential benefits of designing MLCs with larger maximal aperture so that large fields do not need to be split.

2.2.4. Tongue-and-groove effect and interdigitation. Algorithms M2 and M3 may be extended to generate optimal therapy time fields with elimination of tongue-and-groove underdosage and (optionally) the interdigitation constraint on the leaf sequences. Kamath et. al.⁸ present algorithms for delivering an intensity matrix I using a single

field with optimal therapy time, while eliminating the tongue-and-groove underdosage (Algorithm TONGUEANDGROOVE) and also while simultaneously eliminating the tongue-and-groove underdosage and interdigitation constraint violations (Algorithm TONGUEANDGROOVE-ID). Denote these problems by M1' and M1'' respectively (M2', M2'', M3' and M3'' are defined similarly for splits into two and three fields). Let M1'(I) and M1''(I), respectively, denote the optimal therapy times required to deliver I using the leaf sequences generated by these algorithms. To solve problem M2' we need to determine x_j where $M1'(P_j) + M1'(S_j)$ is minimized for $g - w < j \le w + 1$. Note that this is similar to Algorithm M2. Using the fact that M1' can be solved in O(nm) time for an intensity profile with n rows and m columns (Lemma 7, Kamath et. al.⁸), and by computing $M1'(P_j)$ and $M1'(S_j)$ progressively from left to right, it is possible to solve M2' in O(ng) time. In case of M3' we need to find x_j , x_k , such that $1 < j \le w + 1$, $g - w < k \le g$, $0 < k - j \le w$, and $M1'(P_j) + M1'(M_{(j,k)}) + M1'(S_k)$ is minimized. M3' can be solved in $O(ng^2)$ time. The solutions for M2'' and M3'' are now obvious.

3. Field splitting with feathering

One of the problems associated with field splitting is the field matching problem that occurs in the field junction region due to uncertainties in setup and organ motion⁶. To illustrate the problem we use an example. Consider the single leaf pair intensity profile of Figure 3a. Due to width limitations, the profile needs to be split. Suppose that it is split at x_j . Further suppose that the left field is delivered accurately and that the right field is misaligned so that its left end is positioned at x'_j rather than x_j . Due to incorrect field matching the actual profile delivered may be, for example, either of the profiles shown in Figure 3b or Figure 3d, depending on the direction of error. In Figure 3b, the region between x'_j and x'_j gets overdosed and is a hotspot. In Figure 3d, the region between x_j and x'_j gets underdosed and is a coldspot.

One way to partially eliminate the field matching problem is to use the 'feathering'

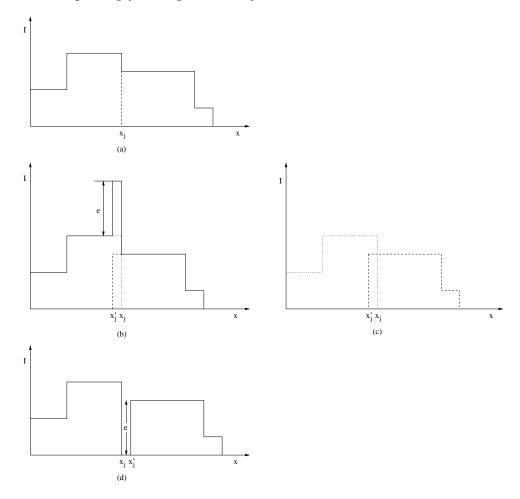


Figure 3. Field matching problem: The profile in (a) is the desired profile. It is split into two fields at x_j . Due to incorrect field matching, the left end of right field is positioned at point x'_j instead of x_j and the fields may overlap as in (c) or may be separated as in (d). In (c), the dotted line shows the left profile and the dashed line shows the right profile. (b) shows these profiles as well as the delivered profile in this case in bold. In (d), the left and right fields are separated and their two profiles together constitute the delivered profile, which is shown in bold. The delivered profiles in these cases, vary significantly from the desired profile in the junction region. e is the maximum intensity error in the junction region, i.e., the maximum deviation of delivered intensity from the desired intensity.

technique⁶. In this technique, the large field is not split at one sample point into two non-overlapping fields. Instead the profiles to be delivered by the two fields resulting from the split, overlap over a central *feathering region*. The beam splitting algorithm proposed by Wu et. al.⁶ splits a large field with feathering, such that in the feathering region the sum of the split fields equals the desired intensity profile. Figure 4a shows a split of the profile of Figure 3 with feathering. Figures 4c and 4d show the effect of

field matching problem on the split with feathering. The extent of field mismatches is the same as those in Figures 3b and 3d, respectively. Note that while the profile delivered in the case with feathering is not the exact profile either, the delivered profile is less sensitive to mismatch compared to the case when it is split without feathering as in Figure 3. In other words, the purpose of feathering is to lower the magnitude of maximum intensity error e in the delivered profile from the desired profile over all sample points in the junction region.

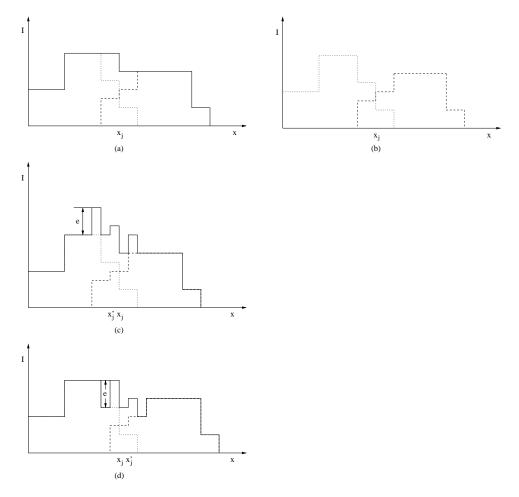


Figure 4. Example of field splitting with feathering: (a) shows a split of the profile of Figure 3 with feathering. The dotted line shows the right part of the left profile and the dashed line shows the left part of the right profile. The left and right profiles are shown separately in (b). (c) and (d) show the effect of field matching problem on the split with feathering. The extent of field mismatches in (c) and (d) are the same as those in Figure 3b and Figure 3d, respectively, ie., the distances between x_j and x'_j are the same as in Figure 3. Note that the maximum intensity error e reduces in both cases with feathering.

In this section, we extend our field splitting algorithms to incorporate feathering.

In order to do so, we define a feathering scheme similar to that of Wu et. al.⁶. However, there are two differences between the splitting algorithm we propose and the algorithm of Wu et. al.⁶. First, our feathering scheme is defined for profiles discretized in space and in MUs as is the profile generated by the optimizer. Second, the feathering scheme we propose defines the profile values in the feathering region, which is centered at some sample point called the *split point* for that split. Thus given a split point, our scheme will specify how to split the large field with a feathering region that is centered at that point. The split point to be used in the actual split will be determined by a splitting algorithm that takes into account the feathering scheme. In contrast, Wu et. al.⁶ always choose the center of the intensity profile as the split point, as they do not optimize the split with respect to any objective.

We study how to split a single leaf pair profile into two (three) fields using our feathering scheme such that the sum of the optimal therapy times of the individual fields is minimized. We will denote this minimization problem by S2F (S3F). The extension of the methods developed for the multiple leaf pairs problems (M2F and M3F) is straightforward and is therefore not discussed separately.

3.1. Splitting a profile into two

Let I be a single leaf pair profile. Let x_j be the split point and let P_j and S_j be the profiles resulting from the split. P_j is a left profile and S_j is a right profile of I. The feathering region spans x_j and d-1 sample points on either side of x_j , i.e., the feathering region stretches from x_{j-d+1} to x_{j+d-1} . P_j and S_j are defined as follows.

$$P_{j}(x_{i}) = \begin{cases} I_{j}(x_{i}) & 1 \leq i \leq j - d \\ \lceil I_{j}(x_{i}) * (j + d - i)/2d \rceil & j - d < i < j + d \\ 0 & j + d \leq i \leq g \end{cases}$$
 (1)

$$S_{j}(x_{i}) = \begin{cases} 0 & 1 \leq i \leq j - d \\ I_{j}(x_{i}) - P_{j}(x_{i}) & j - d < i < j + d \\ I_{j}(x_{i}) & j + d \leq i \leq g \end{cases}$$
 (2)

Note that the profiles overlap over the 2d-1 points $j-d+1, j-d+2, \ldots, j+d-2, j+d-1$. Therefore, for the profile I of width g to be deliverable using two fields, it

must be the case that $g \leq 2w - 2d + 1$. Since P_j needs to be delivered using one field, the split point x_j and at least d-1 points to the right of it should be contained in the first field, i.e., $j+d-1 \leq w \Rightarrow j \leq w-d+1$. Similarly, since S_j has to be delivered using one field $j-(d-1)>g-w \Rightarrow j \geq g-w+d$. These range restrictions on j lead to an algorithm for the S2F problem. Algorithm S2F, which solves problem S2F, is described below. Note that the P_i s and S_i s can all be computed in a single left to right sweep in O(d) time at each i. So the time complexity of Algorithm S2F is O(dg).

Algorithm S2F

- (1) Find P_i and S_i using Equations 1 and 2, for $g w + d \le i \le w d + 1$.
- (2) Split the field at a point x_j where $S1(P_j) + S1(S_j)$ is minimized for $g w + d \le j \le w d + 1$.

3.2. Splitting a profile into three

Suppose that a profile I is split into three profiles with feathering. Let j and k, j < k, be the two split points. As a result we get three profiles P_j , $M_{(j,k)}$ and S_k , where P_j is a left profile, $M_{(j,k)}$ is a middle profile of I and S_k is a right profile. In this case, there are two feathering regions, each of which spans across 2d-1 sample points centered at the corresponding split point. One feathering region stretches from x_{j-d+1} to x_{j+d-1} and the other from x_{k-d+1} to x_{k+d-1} . P_j , $M_{(j,k)}$ and S_j are defined as follows.

$$P_{j}(x_{i}) = \begin{cases} I_{j}(x_{i}) & 1 \leq i \leq j - d \\ \lceil I_{j}(x_{i}) * (j + d - i)/2d \rceil & j - d < i < j + d \\ 0 & j + d \leq i \leq g \end{cases}$$
 (3)

$$M_{(j,k)}(x_i) = \begin{cases} 0 & 1 \le i \le j - d \\ I_j(x_i) - P_j(x_i) & j - d < i < j + d \\ I_j(x_i) & j + d \le i \le k - d \\ \lceil I_k(x_i) * (k + d - i)/2d \rceil & k - d < i < k + d \\ 0 & k + d \le i \le g \end{cases}$$

$$(4)$$

$$S_{j}(x_{i}) = \begin{cases} 0 & 1 \leq i \leq k - d \\ I_{j}(x_{i}) - M_{(j,k)}(x_{i}) & k - d < i < k + d \\ I_{j}(x_{i}) & k + d \leq i \leq g \end{cases}$$

$$(5)$$

The profiles P_j and $M_{(j,k)}$ overlap over 2d-1 points, as do $M_{(j,k)}$ and S_k . For the profile I to be deliverable using three fields, it must be the case that $g \leq 3w-2(2d-1) = 3w-4d+2$. Also, it is undesirable for the two feathering regions to overlap. So $g \geq 4d-2$. For the feathering regions to be well defined and for the split to be useful it can be shown that $g-2w+3d-1 \leq j \leq w-d+1$ and that $g-w+d \leq k \leq 2w-3d+2$. Also, $k-j+1+2(d-1) \leq w \Rightarrow k-j \leq w-2d+1$. Using these ranges for j and k, we arrive at Algorithm S3F, which can be implemented to solve problem S3F in $O(dg^2)$ time.

Algorithm S3F

- (1) Find P_j , $M_{(j,k)}$ and S_k using Equations 3, 4 and 5, for $g-2w+3d-1 \le j \le w-d+1$, $g-w+d \le k \le 2w-3d+2$ and $k-j \le w-2d+1$.
- (2) Split the field at two points x_j , x_k , where $S1(P_j) + S1(M_{(j,k)}) + S1(S_j)$ is minimized, subject to $g 2w + 3d 1 \le j \le w d + 1$, $g w + d \le k \le 2w 3d + 2$ and $k j \le w 2d + 1$.

3.3. Tongue-and-groove effect and interdigitation

The algorithms for M2F and M3F may be further extended to generate optimal therapy time fields with elimination of tongue-and-groove underdosage and (optionally) the interdigitation constraint on the leaf sequences as is done for field splits without feathering in Section 2.2.4. The definitions of problems M2F' (M3F') and M2F'' (M3F''), respectively, for splits into two (three) fields are similar to those made in Section 2.2.4 for splits without feathering.

4. Results

The performance of the Algorithms M2, M3, M2F and M3F was tested using 27 clinical fluence matrices, each of which exceeded the maximum allowable field width w=14, with d=2 for feathering. The fluence matrices were generated with a commercial inverse treatment planning system (CORVUS v5.0, NOMOS Corp., Sewickley, PA) for five clinical cases. Algorithm M2F was used when the profile width was $\leq 2w - 2d + 1 = 25$

and algorithm M2 was used whenever the profile width was $\leq 2w = 28$. Algorithms M3 and M3F were used in all cases. The optimal MUs for the split fields were calculated assuming that the split fields in each case are delivered by sequencing leaves using Algorithm MULTIPAIR (Kamath et. al.⁷). Table 1 displays the resulting total MUs for the field splits obtained using the four algorithms. Also shown are the total MUs obtained using the field split lines as given by the commercial treatment planning system (C(I)). The MUs are normalized to give a maximum pixel value of 100 of a fluence The percent decrease in MUs of $\min\{M2(I), M3(I)\}$ as a result of optimal field splitting over C(I) is also shown in the last column. MU reductions of up to 26% are seen. In about 30% of the cases the reduction was over 20%. The average decrease in MUs is found to be about 11% for the 27 fluence matrices. Note that the application of optimal splitting algorithms with feathering can reduce MU as compared to the optimal algorithms without feathering as a result of the reduction in intensity values in the feathering region in each field resulting from the split. We observe that M2F(I) < M2(I) in over 34% of the cases and M3F(I) < M3(I) in over 40% of the cases. Examination of the optimal split lines from our algorithms shows that the split lines generally occurred in low fluence columns. Figure 5 compares the split line from Algorithm M2 and that from the commercial planning system for one of the fluence matrices. The split line from the commercial planning system occurred at the center of the field, whereas a slight shift in the split line reduces the total MU by 10% in this case (Table 1). For extreme (synthetic) cases, more MU reduction can be achieved. For example, consider an intensity profile each row of which consists of the following nonzero pattern: eight 5s followed by thirteen 100s followed by eight 5s. The commercial treatment planning system split the field into three such that each of the resulting fields had at least one intensity value of 100. As a result, the optimal MUs for delivering this split is 300. However, Algorithm M3 split this field into three fields such that the first and third fields contained only 5s and only the middle field contained 100s (note that w=14). The optimal MUs for this split is 110. The MU reduction is 63% for this case.

| Matrix (I) | Width | C(I) | M2(I) | M3(I) | M2F(I) | M3F(I) | % MU decrease |
|--------------|-------|------|-------|-------|--------|--------|---------------|
| 1 | 15 | 280 | 280 | 330 | 290 | 335 | 0 |
| 2 | 15 | 310 | 310 | 350 | 318 | 350 | 0 |
| 3 | 16 | 300 | 260 | 340 | 260 | 310 | 13.3 |
| 4 | 16 | 400 | 300 | 370 | 290 | 353 | 25 |
| 5 | 16 | 350 | 350 | 380 | 360 | 394 | 0 |
| 6 | 16 | 340 | 310 | 310 | 325 | 382 | 8.8 |
| 7 | 16 | 390 | 310 | 360 | 310 | 338 | 20.5 |
| 8 | 16 | 350 | 320 | 340 | 320 | 357 | 8.6 |
| 9 | 16 | 400 | 300 | 370 | 310 | 365 | 25 |
| 10 | 16 | 440 | 350 | 390 | 322 | 398 | 20.5 |
| 11 | 16 | 320 | 320 | 360 | 310 | 362 | 0 |
| 12 | 16 | 400 | 300 | 340 | 280 | 360 | 25 |
| 13 | 17 | 380 | 280 | 320 | 285 | 323 | 26.3 |
| 14 | 18 | 280 | 240 | 260 | 240 | 280 | 14.3 |
| 15 | 20 | 320 | 320 | 380 | 320 | 375 | 0 |
| 16 | 22 | 400 | 360 | 400 | 360 | 400 | 10 |
| 17 | 22 | 320 | 320 | 360 | 300 | 360 | 0 |
| 18 | 24 | 540 | 480 | 520 | 480 | 500 | 11.1 |
| 19 | 24 | 540 | 500 | 500 | 490 | 500 | 7.4 |
| 20 | 24 | 460 | 420 | 460 | 420 | 425 | 8.7 |
| 21 | 24 | 520 | 520 | 540 | 525 | 545 | 0 |
| 22 | 24 | 560 | 520 | 520 | 505 | 505 | 7.1 |
| 23 | 25 | 360 | 360 | 380 | 340 | 380 | 0 |
| 24 | 26 | 560 | 440 | 460 | - | 430 | 21.4 |
| 25 | 29 | 520 | ı | 480 | - | 445 | 7.7 |
| 26 | 29 | 580 | - | 440 | - | 440 | 24.1 |
| 27 | 32 | 560 | - | 480 | - | 470 | 14.3 |

Table 1. Total MUs for five clinical cases

5. Conclusion

We have developed algorithms to split large intensity-modulated fields into two or three sub-fields. Such a work-around needs to be implemented for MLCs that have a maximum leaf spread limitation, which imposes a field width limitation. We have presented algorithms that split large fields into non-overlapping sub-fields along one or

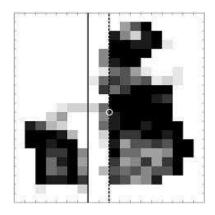


Figure 5. Comparison of the field split line obtained with Algorithm M2 (solid line) with the split line from the commercial planning system (dashed line) for the fluence matrix 8 in Table 1. The isocenter is marked with the solid circle.

two columns. Also presented are algorithms that split fields with feathering. Feathering of split fields helps reduce the effect of the field matching problem that occurs in the field junction region due to uncertainties in setup and organ motion. We have shown that our algorithms result in field splits for which the MU efficiency is optimal. Application of our optimal field splitting algorithms without feathering to clinical data reduced total MUs by up to 26% and on synthetic data up to 63% compared to a commercial planning system that also splits fields without feathering. We have also shown that our algorithms can easily be extended to split fields resulting in maximal MU efficiency when the MLC model is subject to the interdigitation constraint and/or the tongue-and-groove effect is to be eliminated.

Acknowledgments

This work was supported, in part, by the National Library of Medicine under grant LM06659-03.

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Appendix

Proof of Lemma 2

Proof: From Lemma 1, we have $S1(I) = \sum_{i=1}^{q} [I(x_{inci}) - I(x_{inci-1})]$. For the left profile, $S1(P_j) = \sum_{inci < j} [I(x_{inci}) - I(x_{inci-1})]$. The optimal therapy time of the right profile S_j is equal to the sum of the increments in the intensities of successive sample points of the right profile. Adding these increments, we get, $S1(S_j) = S_j(x_j) - S_j(x_{j-1}) + \sum_{inci>j} [I(x_{inci}) - I(x_{inci-1})] = I(x_j) + \sum_{inci>j} [I(x_{inci}) - I(x_{inci-1})]$ (since $S_j(x_{j-1}) = 0$ and $S_j(x_j) = I(x_j)$). If $I(x_j) > I(x_{j-1})$, this can be written as $S1(S_j) = (I(x_j) - I(x_{j-1})) + \sum_{inci>j} [I(x_{inci}) - I(x_{inci-1})] + I(x_{j-1})$. If $I(x_j) \leq I(x_{j-1})$, $S1(S_j) = \sum_{inci>j} [I(x_{inci}) - I(x_{inci-1})] + I(x_j) = \sum_{inci\ge j} [I(x_{inci}) - I(x_{inci-1})] + I(x_j)$. Therefore $S1(S_j) = \sum_{inci\ge j} [I(x_{inci}) - I(x_{inci-1})] + \min\{I(x_{j-1}), I(x_j)\}$. By addition, $S1(P_j) + S1(S_j) = \sum_{i=1}^{q} [I(x_{inci}) - I(x_{inci-1})] + \min\{I(x_{j-1}), I(x_j)\} = S1(I) + \hat{I}(x_i)$.

Proof of Lemma 4

- **Proof:** (a) $S2(I) = \sum_{i=1}^{q} [I(x_{inci}) I(x_{inci-1})] + \min\{I(x_{j-1}), I(x_j)\} = S1(I) + \min\{I(x_{j-1}), I(x_j)\}$, where j is the best point to split the field as determined by Algorithm S2. This implies $S2(I)/S1(I) \geq 1$ and so splitting a field into two never improves optimal therapy time. For an upper bound on the ratio, note that $S1(I) \geq \min\{I(x_{j-1}), I(x_j)\}$ since at least $\min\{I(x_{j-1}), I(x_j)\}$ MUs are required to deliver I. So $S2(I) \leq 2 * S1(I)$. The example of Figure 6 shows that the upper bound is tight. The profile I has 2w sample points, i.e., it has a width $2w\Delta x$. So it has to be split exactly at x_{w+1} . The resulting left and right profiles each have an optimal therapy time equal to that of I.
- (b) $S3(I) = S1(I) + \min\{I(x_{j-1}), I(x_j)\} + \min\{I(x_{k-1}), I(x_k)\}$, where j and k are as in Algorithm S3. Clearly, $S3(I)/S1(I) \ge 1$. Also, $S1(I) \ge \min\{I(x_{j-1}), I(x_j)\}$ and $S1(I) \ge \min\{I(x_{k-1}), I(x_k)\}$. Therefore, $S3(I) \le 3 * S1(I)$. Once again the upper bound is tight as shown in the Figure 7. The profile shown has width $3w\Delta x$ and

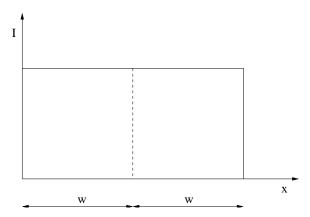


Figure 6. Tight upper bound for Lemma 4a

needs to be split at x_{w+1} and at x_{2w+1} . Each of the resulting profiles has optimal therapy time equal to S1(I).

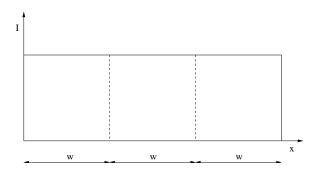


Figure 7. Tight upper bound for Lemma 4b

(c) From (a) and (b), $S3(I) \geq S1(I)$ and $S2(I) \leq 2*S1(I)$. So $S3(I)/S2(I) \geq 0.5$. S3(I)/S2(I) = 0.5 only if S3(I) = S1(I) and S2(I) = 2*S1(I). Suppose that S3(I) = S1(I). Then there exist indices j,k such that $\min\{I(x_{j-1}),I(x_j)\} + \min\{I(x_{k-1}),I(x_k)\} = 0$, i.e., $\min\{I(x_{j-1}),I(x_j)\} = 0$ and $\min\{I(x_{k-1}),I(x_k)\} = 0$. This and the fact that $I(x_1) \neq 0,I(x_g) \neq 0$ implies that the profile has at least two disjoint components separated by a sample point at which the desired intensity is zero. Sample points in the two disjoint components cannot be exposed at the same time and so there does not exist a point x_i such that $I(x_i) = S1(I)$. So $S2(I) = S1(I) + \min_{g-w < i \leq w+1} \min\{I(x_{i-1}), I(x_i)\} < 2*S1(I)$. It follows that S3(I)/S2(I) > 0.5. Figure 8 shows an example where the ratio can be made arbitrarily close to 0.5. In this example, $S1(I) = I_2$. The profile has a width of

 $2w\Delta x$ and therefore needs to be split at x_{w+1} . The resulting profiles each have an optimal therapy time of S1(I) so that S2(I) = 2 * S1(I). $S3(I) = S1(I) + 2I_1$ and so $S3(I) \to S1(I)$ as $I_1 \to 0$.

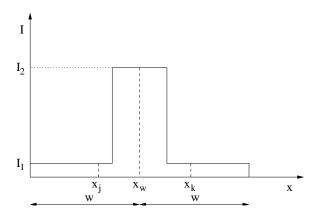


Figure 8. Tight lower bound for Lemma 4c

To obtain an upper bound note that the best split point for S2 (say x_j) is always a permissible split point for S3. By selecting this as one of the two split points for S3, we can construct a split into three profiles such that the total therapy time of profiles resulting from this split is $S2(I) + \min\{I(x_{k-1}), I(x_k)\}$, where k is the second split point defining that split. Since $\min\{I(x_{k-1}), I(x_k)\} \leq S1(I) \leq S2(I)$, the total therapy time of the split $\leq 2 * S2(I)$. So $S3(I)/S2(I) \leq 2$. The ratio can be arbitrarily close to 2 as demonstrated in Figure 9. One can verify that for the profile I in this example, $S3(I)/S2(I) \rightarrow 2$ as $I_1 \rightarrow 0$.

Proof of Lemma 7

Proof: (a) $M2(I) = \max_i \{S1(P_j^i)\} + \max_i \{S1(S_j^i)\}$, where j is as determined by Algorithm M2. $\max_i \{S1(P_j^i)\} + \max_i \{S1(S_j^i)\} \ge \max_i \{S1(P_j^i) + S1(S_j^i)\} \ge \max_i \{S1(I_i)\} = M1(I)$. This implies $M2(I)/M1(I) \ge 1$ and so splitting a field into two never improves optimal therapy time. For an upper bound on the ratio, note that $\max_i \{S1(P_j^i)\} \le \max_i \{S1(I_i)\}$ and $\max_i \{S1(S_j^i)\} \le \max_i \{S1(I_i)\}$. It follows that $M2(I) = \max_i \{S1(P_j^i)\} + \max_i \{S1(S_j^i)\} \le 2 * M1(I)$.

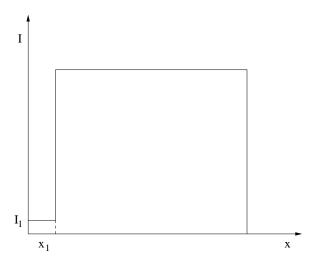


Figure 9. Tight upper bound for Lemma 4c

- (b) $M3(I) = \max_i \{S1(P_j^i)\} + \max_i \{S1(M_{(j,k)}^i)\} + \max_i \{S1(S_k^i)\}$, where j, k are as in Algorithm M3. The proof that $M3(I)/M1(I) \ge 1$ is similar to that of (a). As in (a), $M1(I) \ge$ each of the three terms in M3(I). Therefore, $M3(I) \le 3 * M1(I)$.
- (c) From (a) and (b), $M3(I) \ge M1(I)$ and $M2(I) \le 2*M1(I)$. So $M3(I)/M2(I) \ge 0.5$. To obtain an upper bound note that the best split point for M2 (say x_j) is always a permissible split point for M3. By selecting this as one of the two split points for M3, we can construct a split into three profiles such that the total therapy time of profiles resulting from this split is $\max_i \{S1(P_j^i)\} + \max_i \{S1(M_{(j,k)}^i)\} + \max_i \{S1(S_k^i)\}$, where k is the second split point defining that split. Since $\max_i \{S1(M_{(j,k)}^i)\} + \max_i \{S1(S_k^i)\} \le 2*\max_i \{S1(S_j^i)\}$, it follows that the total therapy time of profiles resulting from this split is $\max_i \{S1(P_j^i)\} + \max_i \{S1(M_{(j,k)}^i)\} + \max_i \{S1(S_k^i)\} \le \max_i \{S1(P_j^i)\} + 2*\max_i \{S1(S_j^i)\} \le 2*M2(I)$. So $M3(I)/M2(I) \le 2$.

Note that the examples used to show tightness of bounds in the proof of Lemma 4 can also be used to show tightness of bounds in this case.