

Purpose

To develop an effective and efficient leaf sequencing algorithm for intensity-modulated arc therapy (IMAT).

Methods

The input to our sequencing algorithm includes: (a) A set of (continuous) intensity patterns optimized by a treatment planning system for a sequence of equally spaced beam angles (10 degrees apart); (b) the IMAT maximum leaf motion constraint; (c) the number of arcs, k , that the user specifies based on the complexity of the problem. The output is a set of k treatment arcs that best approximates the set of input intensity patterns at all beam angles. The MLC shapes for each output arc are interconnected to guarantee a smooth delivery without violating the IMAT maximum leaf motion constraint. Our sequencing algorithm consists of two key steps. First, the intensity profiles aligned with each MLC leaf pair at all beam angles are converted into k MLC leaf openings using a k -link shortest path algorithm, where k is the specified number of arcs for the delivery. The delivered photon flux using these leaf openings best approximates the desired intensity distribution. Second, the leaf openings are connected into k IMAT treatment arcs under the maximum leaf motion constraint using the minimum-cost matching and shortest path algorithms.

Results

The performance of our leaf sequencing software has been tested for four treatment sites (prostate, breast, head-and-neck, and lung). In all cases, our leaf sequencing algorithm provides efficient and highly conformal IMAT plans that rival the counterpart tomotherapy plans and significantly improve the IMRT plans. Execution times of our software that range from a few seconds to 2 minutes are observed on a laptop computer equipped with a Pentium M Processor of 2.0 GHz.

Conclusion

This research provided strong evidence that IMAT equipped with an effective leaf sequencing algorithm can provide a feasible and high quality implementation of IMRT.