

Conventional IMRT inverse planning is done in two steps. Firstly, the intensity maps of the treatment beams are optimized using an optimization algorithm and secondly, each intensity map is decomposed into a number of segments using a leaf-sequencing algorithm. In this work we report a genetic algorithm for segment-based optimization. Our aim is to eliminate the leaf-sequencing step in conventional IMRT planning by optimizing directly the shape and weight of a predefined number of segments/beam. Different from an iterative approach or simulated annealing, the algorithm finds the optimum solution from a population of candidate plans. Each solution is encoded using three chromosomes: one for the position of the left-bank leaves, the second for the position of the right-bank, and the third for the segment weights defined by the first two chromosomes. The convergence towards the optimum is realized by crossover and mutation operators that ensure proper exchange of information between the chromosome triplet of the solutions in the population. The algorithm is applied to a phantom and a prostate treatment. The results are compared with those obtained using beamlet-based optimization. The main conclusion drawn from this study is that the genetic optimization is an effective way to optimize the segment shapes and weights, and capable of producing highly conformal dose distributions. Our study also confirms previous findings that much less segments are needed to generate plans comparable with those obtained using beamlet-based optimization. Given the overall simplicity and efficiency, this approach may find widespread application in radiation therapy.