

AbstractID: 14164 Title: Determining the optimal gating window size by considering the effect of tumor displacement on dose distributions

Purpose:

To develop a population-based multivariate linear regression models for determining the optimal size of the gating window by considering the effect of the distribution of tumor displacements on target dose. This population model can then be used to prospectively guide the selection of gating window size for an individual case, based on tumor displacement distribution.

Method and Materials:

We considered stereotactic body radiation therapy (SBRT) treatment plans for lung tumors planned and calculated using heterogeneity corrections. Fifty tumor trajectories that varied in the distribution of tumor displacement were selected. A set of variables were defined to describe the variability in these trajectories. Four-dimensional dose calculation was performed by sampling the distribution of tumor displacements resulting in the residual tumor displacement influenced target dose. Stepwise elimination was performed to determine only those input variables that were independently predictive of D_{95} and D_{99} . A multivariate regression population-based model was constructed for D_{95} and D_{99} as a function of these independently predictive variables (and as a result the gating window size). This model was then tested on a set of 15 new tumor trajectories and gating window prediction errors were determined.

Results:

Ten different models were generated for D_{95} (5 locations, 2 margins) and ten for D_{99} . Average errors were calculated for all the models in terms of percentage of cases more than 5% off the prediction. For D_{95} the average was 3.8 with and standard deviation of 3.0, whereas for D_{99} it was 4.5 with a standard deviation of 3.4.

Conclusion:

The MLR models built show a great degree of predictability in D_{95} and D_{99} for all the 5 tumor locations and 15 breathing trajectories studied in prospective prediction. The methodology developed can be used to predict the gating window for any patient using only the tumor trajectory as input.