

Purpose: Simplifications and reductions in 4D dose accumulation can be achieved using the motion probability density function (PDF) with properly selected weighting and sampling. One scheme to select phase sampling and weighting scheme is to use k-means clustering from motion PDF. In this study, we investigated the accuracy and feasibility of this method for 4D dose construction.

Method and Materials: Respiration curves from 6 patients and 15 static dose profiles were used in the evaluation. Motion PDFs were constructed from respiration curves for dose convolution and phase sampling. Four sampling schemes were compared: (1) Equal phase sampling; (2) Equal amplitude sampling; (3) K-means clustering based sampling; (4) PDF and dose profile specific optimal sampling. The cumulative 4D dose from different methods were compared to the expected 4D dose. A digital motion phantom was constructed with dose computed at various displacements for 3D dose evaluation on the above methods. Mid phase dose profile through isocenter was used for optimization in method 4.

Results: For dose profiles analysis, the residual errors (normalized to the maximum dose) for the method 1 to 4 are: $1.9 \pm 1.4\%$, $2.2 \pm 0.59\%$, $0.88 \pm 0.70\%$, and $0.55\% \pm 0.48\%$. For phantom study, the maximum residual errors are 7.8%, 3.6%, 2.9%, and 3.5%. The 3D gamma analysis passing rates are (dose difference 2%, distance to agreement 2mm, and dose threshold 30% of maximum dose): 96.1%, 99.6%, 99.7%, and 99.6%.

Conclusion: K-means clustering sampling is effective in 4D dose accumulation. Method 4 will be most accurate sampling method for single dose profile analysis, with all the information included for optimization. K-means sampling has slightly larger residual error in dose profile approximation, but it applies to multiple dose profiles for a given PDF. In 3D dose analysis, k-means sampling is the most effective and accurate among the four methods.

Conflict of Interest (only if applicable):