Journal of Physics: Conference Series **444** (2013) 012097 doi:10.1088/1742-6596/444/1/012097

A novel method for 4D measurement-guided planned dose perturbation to estimate patient dose/DVH changes due to interplay

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Abstract. As IMRT/VMAT technology continues to evolve, so do the dosimetric QA methods. We present the theoretical framework for the novel planned dose perturbation algorithm. It allows not only to reconstruct the 3D volumetric doe on a *patient* from a measurement in a cylindrical *phantom*, but also to incorporate the effects of the interplay between the intrafractional organ motion and dynamic delivery. Unlike in our previous work, this 4D dose reconstruction does not require the knowledge of the TPS dose for each control point of the plan, making the method much more practical. Motion is viewed as just another source of error, accounted for by perturbing (morphing) the planned dose distribution based on the limited empirical dose from the phantom measurement. The strategy for empirical verification of the algorithm is presented as the necessary next step.

1. Introduction

Historically, the most frequently used method for patient-specific end-to-end testing [1] of inverse-planned delivery was limited comparison of the measured and calculated doses in a *phantom*. While this approach was sufficiently rigorous to ensure safe adoption of IMRT techniques in wide clinical practice, it was pointed out that it lacks correlation to the clinically meaningful metrics [2, 3]. It is now recognized that ideally a deliverable dose to the *patient* should be reconstructed volumetrically based on the measurement and compared to the TPS calculations [3, 4]. But even that may not always be sufficient as the interplay between the dynamic delivery and intrafraction organ motion is likely to alter doses accumulated by different structures. Therefore, a 4D approach to patient dose reconstruction is needed for patient-specific end-to-end testing, particularly in the case of hypofractionated/stereotactic delivery.

A prototype method for measurement-guided VMAT 4D patient dose reconstruction was described by Nelms et al [5]. It is based on 3DVH software package (Sun Nuclear Corp., USA). The basic premise of the approach is that the volumetric dose on the *patient* can be estimated by perturbing the patient TPS dose distribution based on the *phantom* measurements. The software was modified to allow this perturbation to occur at the control point (CP) dose level, thus creating a time-resolved volumetric (4D) dose on a *patient*. While proved accurate [5], this method requires the knowledge of planned 3D dose matrices per CP. Not every TPS exports such information and a substantial amount of data needs to be stored and manipulated, rendering this approach less than ideal in practice. Hence

in this paper we set out to demonstrate in theory how measurement-guided 4D dose reconstruction on the patient can be done bypassing the TPS CP doses, by treating the motion as another source of perturbation to the TPS-generated dose that can be quantified from the 3D phantom dose.

2. Method description

2.1. Dose to stationary target in a phantom

A stationary target can be defined by (i.e. discretized into) a collection of small voxel elements in the couch coordinate system (Figure 1). A contoured target volume will contain a finite set of voxel elements in the Cartesian grid, each with a corresponding radius-vector $\mathbf{r}_{ijk} = [x_i, y_j, z_k]$

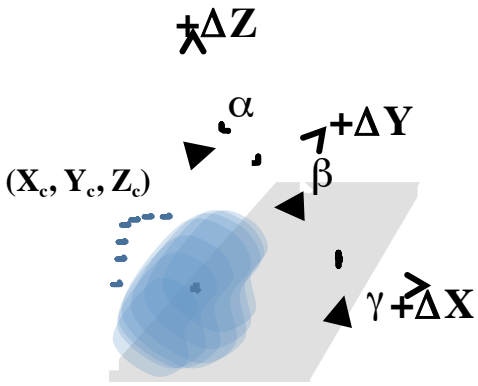

Figure 1: Six degrees of freedom vs. time are used to define the rigid body transformation model for a radiation therapy target in motion. The orthogonal motion axes are parallel to the unified couch coordinate system axes. (ΔX, ΔY, ΔZ) = (0,0,0) represents the centroid of the target volume at t = 0, with that centroid located at point (Xc, Yc, Zc) in the couch coordinate system. Rotations are about this centroid.

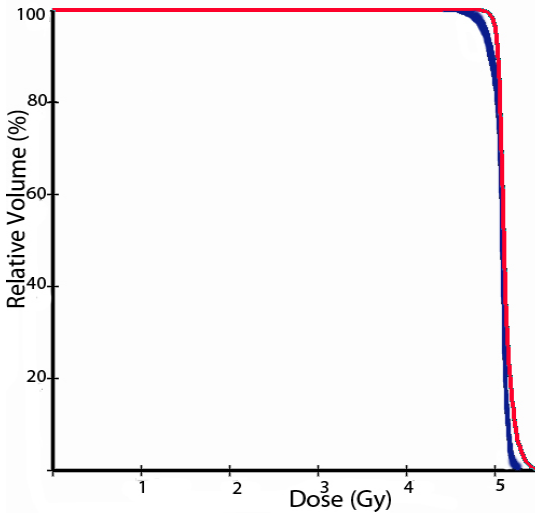

Figure 2: PTV per-fraction DVHs (5 Gy per fraction VMAT plan) simulated for 10 fractions, compared to stationary target DVH. The blue (wider) curves overlap to capture the variation of "Motion DVHs" over 10 fractions, and the red curve is the stationary target DVH.

If continuous, instantaneous dose rate as a function of time in the fixed couch coordinate system is $\bar{d}(x, y, z, t)$, the cumulative dose for a stationary voxel element ***(i,j,k)*** over a single fraction (T_0 to T_f) is given by:

$$D^{\text{Phantom}}_{\text{St, 1 fx}} = \int_{T_0}^{T_f} \bar{d}(x_i, y_j, z_k, t)\, dt$$

And for a course of N fractions, the cumulative dose for a stationary voxel element ***(i,j,k)*** is simply:

$$D^{\text{Phantom}}_{\text{St, N fx}} = N \times \int_{T_0}^{T_f} \bar{d}(x_i, y_j, z_k, t)\, dt$$

2.2. Dose to moving target in a phantom

A target in motion can be approximated by the finite set of voxels that move in time, generally described in the unified couch coordinate system as $r_{ijk}(t) = [x_i(t), y_j(t), z_k(t)]$. For now, target motion is modeled as a rigid body with six degrees of freedom, each of the six a function of time:

$$\{\Delta x(t), \Delta y(t), \Delta z(t), \alpha(t), \beta(t), \gamma(t)\}$$

At any given time ***t*** a moving voxel's location can be mapped to the couch coordinate system (Figure 1):

$$\begin{bmatrix} x_i(t) \\ y_j(t) \\ z_k(t) \\ 1 \end{bmatrix} = \begin{bmatrix} \cos\alpha\cos\beta & \cos\alpha\sin\beta\sin\gamma - \sin\alpha\cos\gamma & \cos\alpha\sin\beta\cos\gamma + \sin\alpha\sin\gamma & \Delta x \\ \sin\alpha\cos\beta & \sin\alpha\sin\beta\sin\gamma + \cos\alpha\cos\gamma & \sin\alpha\sin\beta\cos\gamma - \cos\alpha\sin\gamma & \Delta y \\ -\sin\beta & \cos\beta\sin\gamma & \cos\beta\cos\gamma & \Delta z \\ 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x_i \\ y_j \\ z_k \\ 1 \end{bmatrix}$$

The same continuous, instantaneous dose rate as a function of time in the fixed couch coordinate system is used as the source of 4D dose data for all voxels in a moving target. Potential small perturbations in the dose matrices due to patient shape and internal anatomy changes due to motion are ignored. But for a moving target, each voxel's instantaneous location is also a function of time, so per-voxel motion traces are performed to accumulate dose over a full fraction:

$$\mathrm{D}^{\mathrm{Phantom}}_{\mathrm{Mov,\,1\,fx}} = \int_{T_0}^{T_f} \bar{d}(x_i(t), y_j(t), z_k(t), t)\, dt$$

For a course of N fractions, if the phase of motion is allowed to vary per fraction (with respect to the time frame of the dynamic delivery), the cumulative dose for a stationary voxel element (***i,j,k***) is no longer simply multiplicative with respect to the number of fractions. Instead, per-fraction variation due to motion phase must be modeled as:

$$\mathrm{D}^{\mathrm{Phantom}}_{\mathrm{Mov,\,N\,fx}} = \sum_{fx=1}^{N} \int_{T_0}^{T_f} \bar{d}(x_i(t_{fx}), y_j(t_{fx}), z_k(t_{fx}), t)\, dt$$

where t_{fx} represents an altered phase in the per-voxel motion trace with each fraction "fx". Phases are randomized. If the number of fractions is small (i.e. hypofractionation), many courses of N fractions can be simulated to capture the differences due to small sampling of potential motion phase shifts.

2.3. Accounting for time-discretized 4D dose grids

The six degrees of motion are derived empirically (e.g. from 4D CT) and are entered as values at known relative time points. Assuming there are enough multi-phased, time-resolved data points entered, the motion trajectory can be treated as continuous in time with smooth transitions between the entered data values, each of the six degrees of freedom interpolated linearly with time.

However, the theoretical continuous, instantaneous dose rate as a function of time is not known. Instead, what is known is a time-resolved series of dose grids (i.e. a 4D dose grid set). Each component of the 4D dose series is a 3D grid of dose accumulated over a short period of time ΔT. Those ΔT intervals are determined by the measurement-guided dose reconstruction process and are not all equal. For VMAT plans, ΔT intervals typically range from 0.2-0.4 seconds.

Thus, the theoretical models of dynamic dose must be discretized. For the stationary target, the integral of a full fraction dose to a voxel element becomes a summation:

$$\mathrm{D}^{\mathrm{Phantom}}_{\mathrm{st,\,1\,fx}} = \sum_{Dose=4D_0}^{4D_f} Dose(x_i, y_j, z_k, \Delta T_i)$$

where $4D_0$ through $4D_f$ represent the range of time-discretized 4D dose grids covering the full fraction delivery. For the moving voxels, instantaneous dose rates per (x,y,z) within the 4D dose grids must be considered in order to model the continuous motion, and the full fraction dose to a moving voxel becomes:

$$D^{Phantom}_{Mov,1\,fx} = \sum_{Dose=4D_0}^{4D_f} \int_{\Delta T_i start}^{\Delta T_i end} \left[\frac{Dose(x_i(t), y_j(t), z_k(t), \Delta T_i)}{\Delta T_i} \right] dt$$

This in turn must be discretized in time rather than solved in closed form within each ΔT interval (in order to model motion within each 4D dose time interval). Sub-intervals of ~0.1 seconds are more than sufficient to capture the range of motion.

2.4. Estimating patient dose/DVH changes due to interplay

So far we addressed the dose values in a homogeneous cylindrical *phantom*. The dose perturbation method described previously can equally well estimate *patient* dose for a full fraction or any interval thereof, but for the latter the TPS dose per CP has to be known [5]. This is impractical, but fortunately it can be shown that the same perturbation method used to estimate the patient dose from the phantom measurement and dose reconstruction can be readily employed to estimate the impact of motion.

For motion perturbation, each target voxel is still analyzed, but the static patient dose voxels are now modified for motion errors/differences derived from the phantom doses. For each target dose voxel element (***i,j,k***) the estimated patient dose to the moving voxel is well approximated for 1 fraction and N fractions by:

$$D^{Patient}_{Mov\,ijk,\,1\,fx} = D^{Patient}_{St\,ijk,\,1\,fx} \times \frac{D^{Phantom}_{Mov\,ijk,\,1\,fx}}{Dose^{Phantom}_{St\,ijk,\,1\,fx}}$$

$$D^{Patient}_{Mov\,ijk,\,N\,fx} = D^{Patient}_{St\,ijk,\,N\,fx} \times \frac{D^{Phantom}_{Mov\,ijk,\,N\,fx}}{Dose^{Phantom}_{St\,ijk,\,N\,fx}}$$

With patient per voxel doses now approximated for a moving target, all voxels may be binned to create the estimated DVH to the moving target. This "Motion DVH" can directly compared to the stationary target DVH in order to quantify the impact of interplay, in particular to assess if the target dose coverage is robust (or fragile) with respect to the patient-specific target motion.

2.5. Analysis Example

Figure 2 illustrates how per-fraction, "Motion DVHs" can be readily compared to the stationary target DVH. Likewise, the summation of each fraction's voxel doses re-binned for the cumulative dose over N fractions reduces to a single DVH-to-DVH comparison.

3. Conclusions

So far only the theoretical framework of the 4D dose perturbation algorithm has been presented. The next necessary step is to verify this formalism empirically. In its most obvious form, such verification would involve measuring the cumulative dose per fraction with any integrating dosimeter in a moving phantom representing a patient, and comparing the results with the planned dose perturbation dose grid derived from the measurement in the stationary cylindrical phantom. In addition, dose rate vs. time values can be obtained from the time-resolved ion chamber measurements [5] and compared to the values predicted by the novel 4D reconstruction algorithm.

4. References

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