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Independent Dose Calculation Software Development and Validation for Helical Tomotherapy

Introduction: The TomoTherapy® Hi-Art® unit is able to deliver intensity modulated radiation therapy (IMRT) via a helical trajectory about the patient using a fan beam irradiation geometry [1]. It is common practice to have an independent monitor unit or dose calculation to verify the treatment plan in addition to patient specific quality assurance (QA) measurement. In this study, we report on the development of in-house software called *MU-Tomo* which performs an independent point dose validation of helical TomoTherapy® treatment plans using analytic methods.

Material and methods

***MU-Tomo* software dose calculation:** The software has three elemental components: the archived patient documents, the initial set up coordinates and dose to the QA point, and machine-specific dosimetric functions. Figure 1 illustrates a flowchart of the methodology used for *MU-Tomo*.

The archived patient files provide core plan information such as the initial gantry start angle, treatment time, pitch, initial IEC-Y position of the target, field width size and end of planning (EOP) sinogram. These parameters are retrieved automatically from the archived documents through the Extensible Markup Language (XML) file associated with the patient. The Hi-Art® unit has 32 pairs of multileaf collimator (MLC) leaves. The sinogram contains the relative open time of each individual leaf as a function of leaf number and projection. The leaf opening times along leaves are normally un-symmetric. *MU-Tomo* symmetrically averages the leaf opening time around the central leaf right above the point of calculation, and a new leaf segmentation sequence is determined from the largest open leaf field to the central leaf with evenly distributed time pattern.

The initial coordinates and tomotherapy-calculated point dose must be acquired from the treatment planning system. *MU-Tomo* utilizes these parameters to calculate the point dose independently and compares the value to the tomotherapy-calculated point dose. Additionally, dosimetric functions, such as the off-axis ratio along IEC-X and IEC-Y (OAR_x and OAR_y) directions, tissue phantom ratio (TPR), and output function (S_{cp}), are embedded into the *MU-Tomo* software. These dosimetric functions are acquired from the machine commissioned data.

$$D_p = \dot{D}_0 \times \sum_{i=1}^{N_{proj}} \left(\frac{85}{SPD_i}\right)^2 \times OAR_x(X_i) \times \sum_{j=1}^{N_{seg,t}} \left\{ t_{ij} \times S_{cp,j} \times TPR_j(d_i) \times OAR_{y,j}(Y_i, d_i) \right\} \quad (1)$$

Equation (1) was proposed by [2] and shows how the dose at a point P is calculated based on the information entered into *MU-Tomo*. $\dot{D}_0$ is the dose rate under normalization conditions and is measured at a depth of 10.0cm in water with a field size of $40.0 \times 5.0 cm^2$ and SAD=85.0cm. SPD is the source to point of measurement distance. Both OAR_x and OAR_y values were normalized at the maximum value and interpolation and extrapolation procedures were applied. TPR values are calculated from percent depth dose (PDD). For each segmentation pattern, the $S_{cp,j}$ value is the output factor for the j^{th} segmentation pattern, and t_{ij} is the delivery time in the j^{th} segmentation pattern within the i^{th} projection.

OAR_y optimization: OAR_y is a parameter dependent on three factors: the off-axis distance in the longitudinal direction, the depth of the point of calculation in the patient or phantom, and the segmented field size. OAR_y profiles were fitted by Gaussian functions and an optimization investigation looking at the fluctuation of the tail region of the OAR_y profile was performed. OAR_y profiles from different MLC patterns, for a fixed depth, were mostly equivalent with the exception of the tail region which is defined as the region of the profile with values ≤ 10% of the maximum value. During the segmentation process of the sinogram, leaf openings at different segmentation patterns are proportional to the full width at half maximum (FWHM). Thus, the Gaussian variation between two segmentation patterns can be expressed as:

$$\frac{f_1}{f_2} = e^{\frac{\lambda(LO_1^2 - LO_2^2)}{LO_1^2 LO_2^2} y^2} \quad (2)$$

where λ is the Gaussian variation factor between the two segmentation patterns, LO_1 and LO_2 are the leaf openings, and y is the off-axis distance. Fluctuations of the tail region were separated into two sub-regions: one between the 10% to 5% OAR_y sub-region, and the other from 5% to the end of the OAR_y profile. Two different lambda values were denoted as exponential factors α and β respectively. Optimization was executed by varying α and β at 50 different channels from 0 to 49, separately, and on 50 different patients. For the 50×50 exponential factor channel pairs, the absolute values of dose differences from all patients were summed together to provide a volume map. The minimum volume is used to obtain the optimized parameters.

Results and discussion

Software Validation: The second check software, *MU-Tomo*, has been validated on four different phantom studies: (1) dose calculation using a phantom composed of a 20.0cm thick, rectangular slab of Virtual Water™, (2) step valley dose calculation in the same Virtual Water™ phantom, (3) dose calculation of a monthly output check procedure in a cylindrical cheese

phantom (radius 15 cm and length 18 cm), and (4) dose calculation of seven patient dose validation (DQA) treatment plans in the cheese phantom.

In the first validation phantom study, the ion chamber dose measurement for the irradiation was 211 cGy. *MU-Tomo* calculated a dose of 207 cGy leading to a difference of 1.9%. In the second phantom study, the ion chamber was placed between 6.0cm of build-up and 10.0cm of backscatter material along the IEC-X direction at discrete positions—i.e. 0, ±2.5, ±5, ±7.5, ±10, and ±12.5 cm from the machine center. The dose differences for all eleven-measurement points were within 3.0%, with a mean of -0.94% and standard deviation of 1.6%. The third phantom study validated the helical radiation delivery on the cylindrical cheese phantom proceduing routinely as an our montly QA IMRT dose output verification. The dose difference between the *MU-Tomo* calculated point dose and ion chamber measured point dose was -0.31%.The fourth phantom study was for validation of six patient IMRT DQA plans on the cheese phantom. For all six plans, dose differences between DQA planned point dose and *MU-Tomo* calculated point dose were within 2.0% with a mean of 0.08% and standard deviation of 1.3%.

Algorithm optimization and second check on fifty patient plans: Figure 2 (A) shows the two exponential factors α and β for two different regions. Each channel at the α - β plane in Figure 2 (B) represents an iteration of the absolute dose difference summing for all 50 patients' second check results. Volumes were generated from absolute values of percentage dose differences and multiplied by 100. The minimum volume was used to obtain the optimized parameters by relating the selected channel to the corresponding exponential factors.

For the second check study, 50 patients were selected from a broad range of sites: 15 prostate, 8 lung, 14 head & neck and chest, 7 abdomen/pelvis, 2 liver, and 4 brain cancers. They were all planned using a 2.5cm field width. The result is shown in Figure 3 and point dose differences between TomoTherapy® TPS and *MU-Tomo* were within 5.0% for all cases evaluated, where 49 of 50 were within 3.3%. For all the cases, the mean dose difference was 0.22% with a standard deviation of 1.77%.

Discussion and Conclusion: *MU-Tomo* utilizes a correction-based analytical dose calculation method requiring dosimetric functions, archived patient documents, and the point dose measurement. The aim of the software development was to perform a fast and independent dose calculation within one minute. Most of the second check procedures performed for this study finished within twenty seconds using a computer with an Intel dual-core CPU@3 GHz processor and 3.0GB RAM. Because of this rapid calculation time, *MU-Tomo* can serve as a quick and accurate secondary check method as compared to a full Monte Carlo-based calculation.

Optimization of the OAR_y using a Gaussian variation method benefits *MU-Tomo* in two aspects: (1) the calculation accuracy improves and (2) only the OAR_y from the fully open field size is required for the software and the reduction of OAR_y from all other leaf openings improves the calculation efficiency by a magnitude of ten. The optimization applied in this study may not be the best overall method, but it yielded good results with fast calculation time.

Results show that the *MU-Tomo* software is able to perform independent dose calculations accurately and may be used to satisfy the clinical need for a secondary dose calculation of TomoTherapy® treatment plans.

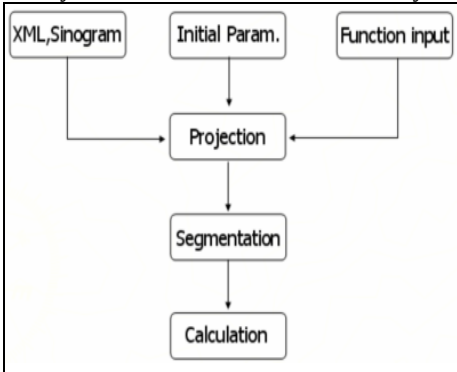

Figure 1. Methodology flowchart utilized by MU-Tomo for independent dose calculations

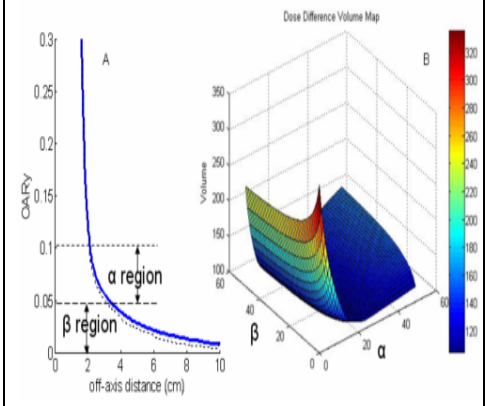

Figure 2. The dose difference volume map of 50 patients plans over 2500 channels.

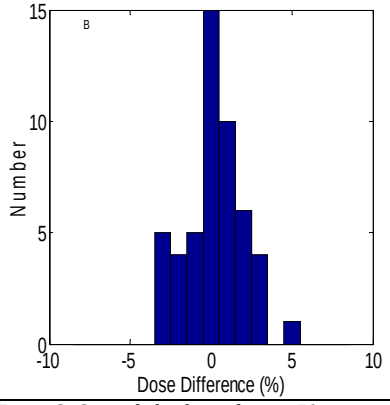

Figure 3. Second check result over 50 patient plans.

References:

[1] Mackie T R, Holmes T, Swerdloff S, Reckwerdt P, Deasy J O, Yang J, Paliwal B, and Kinsella T 1993 TOMOTHERAPY - A NEW CONCEPT FOR THE DELIVERY OF DYNAMIC CONFORMAL RADIOTHERAPY *Med Phys* **20** 1709-1719.

[2] Gibbons J P, Smith K, Cheek D, and Rosen I 2009 Independent calculation of dose from a helical TomoTherapy unit *J Appl Clinl Med Phys* **10** 103-119.