A Simple DVH Generation Technique for Various Radiotherapy Treatment Planning Systems for an Independent Information System

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(Received 8 December 2014, in final form 7 March 2015)

In recent years, the use of a picture archiving and communication system (PACS) for radiation therapy has become the norm in hospital environments and has been suggested for collecting and managing data using Digital Imaging and Communication in Medicine (DICOM) objects from different treatment planning systems (TPSs). However, some TPSs do not provide the ability to export the dose-volume histogram (DVH) in text or other format. In addition, plan review systems for various TPSs often allow DVH recalculations with different algorithms. These algorithms result in inevitable discrepancies between the values obtained with the recalculation and those obtained with TPS itself. The purpose of this study was to develop a simple method for generating reproducible DVH values by using the TPSs. Treatment planning information, including structures and delivered dose, was exported in the DICOM format from the Eclipse v8.9 or the Pinnacle v9.6 planning systems. The supersampling and trilinear interpolation methods were employed to calculate the DVH data from 35 treatment plans. The discrepancies between the DVHs extracted from each TPS and those extracted by using the proposed calculation method were evaluated with respect to the supersampling ratio. The volume, minimum dose, maximum dose, and mean dose were compared. The variations in DVHs from multiple TPSs were compared by using the MIM software v6.1, which is a commercially available treatment planning comparison tool. The overall comparisons of the volume, minimum dose, maximum dose, and mean dose showed that the proposed method generated relatively smaller discrepancies compared with TPS than the MIM software did compare with the TPS. As the structure volume decreased, the overall percent difference increased. The largest difference was observed in small organs such as the eye ball, eye lens, and optic nerve which had volume below 10 cc. A simple and useful technique was developed to generate a DVH with an acceptable error from a proprietary TPS. This study provides a convenient and common framework that will allow the use of a single well-managed storage solution for an independent information system.

PACS numbers: 87.53.Tf, 87.57.Ce
Keywords: DVH, Supersampling, RTPACS
DOI: 10.3938/jkps.67.254

I. INTRODUCTION

Dose-volume histograms (DVHs) are currently used in radiotherapy departments and play a significant role in treatment plan evaluation and treatment approval with three-dimensional (3D) dose distributions [1, 2]. Their main benefit for complex treatment plans is that they provide summarized data for the 3D dose distribution as a graph and statistical format for structures. They are a useful tool for comparing various treatment plans from different planning techniques or multiple treatment planning systems (TPSs) [3–7]. Moreover, they provide criteria for overviewing multi-institutional clinical trials involving advanced delivery technologies [8]. The use of the Digital Imaging and Communications in Medicine (DICOM) and Picture Archiving and Communication System (PACS) has become the norm in radiotherapy [9–11]. Digitally-saved dose data, such as the dose distribution, the DVH, and dose points, are widely used for transferring or sharing datasets. However, some treatment systems do not provide DVH export with DICOM or another format; therefore an independent DVH calculation algorithm is necessary for comparisons of multiple treatment plans obtained by using different TPS data.

Several studies have generated DVHs based on dose and structure data [2,12–14]. Typically, the DVH is calculated by using a 3D dose distribution and a shape-based interpolation model for individual structures. The calculation points are chosen by using a dose grid and 3D structure delineation through a sampling technique [15].

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Table 1. Comparison of selected planning data from treatment planning systems (TPSs).

| Manufacturer | Philips | Varian |
|--------------|---------|--------|
| Version      | Pinnacle v9.6 | Eclipse v8.9 |
| CT slice thickness (mm) | 2.5 − 5.0 | 2.5 |
| CT pixel widths (mm) | 0.78 − 1.21 | 0.78 − 1.21 |
| Dose grid voxel width (mm) | 2.5 − 4 | 2.5 |
| DVH dose resolution (cGy) | 5 − 15 | 1 − 15 |
| Number of treatment plans | 18 | 7 |

These interpolation and sampling methods from multiple sources could lead to differences in the DVH calculation. The structure matching via an independent methodology could differ from that of an individual TPS. Discrete digital image data and different calculation algorithms in various TPSs could also contribute to variations in the dose calculation and the DVH statistics. Thus, the results of DVH calculations are affected by the structure delineation, the sampling resolution, and the interpolation algorithm.

In this study, a simple DVH generation method using a dose map from various TPSs was developed to reproduce the value obtained with the TPS itself. DICOM radiotherapy (RT) structures and dose files were exported from each TPS and utilized for the DVH calculations. The statistic data extracted from each TPS and the data calculated by using the proposed method were evaluated with respect to the influence of the CT slice thickness, the CT pixel widths, and the dose grid widths. The percent discrepancies of the minimum, maximum, and mean doses were evaluated by varying the sampling rate of the dose grid. All planning data were transferred to a commercial radiation therapy picture archiving and communication system (RTPACS) as a reference system.

II. MATERIALS AND METHODS

1. Data Collection

Thirty-five patients treated for brain tumors, head and neck cancer, upper abdominal cancer or prostate cancer were selected so that we could evaluate DVH data from different treatment planning systems for 3D conformal radiation therapy (3D-CRT), intensity-modulated radiation therapy (IMRT), and volumetric-modulated arc therapy (VMAT). DICOM RT objects, including RT structure, RT dose, and RT image, were exported from the Pinnacle v9.6 (Philips, Guildford, Surrey, UK) or the Eclipse v8.9 (Varian, Palo Alto, CA) treatment planning system and we summarized in Table 1. All 3D CT images were acquired using a 16-slice multi-detector CT simulation scanner (LightSpeed RT16, General Electric Healthcare, Milwaukee, WI). The CT slice thickness and the CT pixel width were varied from 2.5 to 5.0 mm and from 0.78 to 1.21 mm, respectively. Among the patients, 19 patients underwent CT scanning using a 2.5-mm slice thickness, and the others underwent CT scanning using a 5-mm slice thickness according to our clinical scanning protocol. All CT datasets were transferred to the Pinnacle treatment planning system for structure contouring.

2. DVH Calculation Algorithm

The DICOM RT structure and the DICOM RT dose datasets exported from the treatment planning systems were utilized to calculate the DVH data. The 3D image and the dose volumes consisted of a set of voxels with a resolution predefined by the user [16]. Because the grid size and its cross section affect the DVH calculation, a supersampling method, which is a spatial anti-aliasing method, was proposed to improve the sampling rate for the calculation [17,18]. The voxels of the dose dataset were divided into sub-pixels by $2 \times 2$, $4 \times 4$, $6 \times 6$, and $8 \times 8$ in the transverse direction.
Fig. 1. (Color online) Comparisons of the minimum, maximum, and mean doses as functions of the structure volume between the developed algorithm and a TPS with a 2.5-mm CT slice thickness.

The proposed DVH generation algorithm was used according to the Advanced Technology Consortium (ATC) for Clinical Trials Quality Assurance recommendations. The structures were assumed to be in transverse imaging plane in a set of stacked right prisms. The region of interests (ROIs) consisting of a series of closed coplanar axial loops were defined in DICOM RT structures at the center position of the CT image. Trilinear interpolation for the x, y, and z directions was employed to represent a continuous structure. If the center of each voxel was within a structure, it was examined and included in the volume.

The statistical values of the doses obtained from the TPSs were compared to the values recalculated by using the proposed supersampling method. The percent differences of minimum dose, maximum dose, and mean dose were evaluated in terms of supersampling ratio. All planning data were transferred to the MIM Maestro v6.1 (MIM Software Inc., Cleveland, OH), which was used as a reference system for multiple-plan comparison. The statistical values were evaluated by comparing results from each TPS and with those from the MIM software.

3. Computation Time Measurement

Supersampling is computationally expensive because it requires many more computations and much more memory. Therefore, the large structure volumes with fine spatial sampling lead to a heavy computation burden. The calculation time for a relative supersampling rate was measured to evaluate the performance. The measurements of the computation time were performed on a general purpose computer with an Intel Core2 Duo CPU (3 GHz) and 4 GB of system memory. The information on the structure and the dose maps was register in the system memory to enhance the performance and
to reduce the memory access time.

III. RESULTS

1. DVH Calculation Algorithm

A total of 407 structures from 35 treatment plans were analyzed to evaluate the proposed DVH calculation algorithm. Computed structure volumes for various organs are summarized in Table 2. The minimum and the maximum values of the median volumes for the anatomic structures were 0.2 cc (eye lens) and 1698.7 cc (lung). The brain, lung, liver, and bowel showed large standard deviations. Most structures had volumes under 100 cc.

Figures 1 and 2 demonstrate the percent difference between the values from the proposed algorithm and those from the TPS as functions of the structures’ volumes. The values of the minimum, maximum, and mean doses from the TPS were compared with those from the proposed calculation method for different supersampling ratios and with those from the MIM software as a reference. As the structure’s volume decreased, the overall percent difference for the minimum, maximum, and median doses increased. These results were similar to those from the MIM software. A comparison between the values from the TPS and those from the proposed method showed good agreement, but significant differences in the minimum doses were noted. The largest difference was observed in the small organs such as the eye ball, eye lens, and optic nerve, which had volume below 10 cc. The small absolute values of the minimum dose cause big percent discrepancies; some minimum doses from the TPS were below 1.0 cGy. Even though percent difference was larger than 3%, the absolute value was below 5 cGy.
Table 3. Percentage of the percent discrepancies against TPS, where min, max, and mean are the minimum, maximum, and mean doses, respectively.

| % discrepancy | Supersampling ratio = 0 | Supersampling ratio = 2 | Supersampling ratio = 4 |
|---------------|-------------------------|-------------------------|-------------------------|
|               | Min  | Max  | Mean | Min  | Max  | Mean | Min  | Max  | Mean |
| ~ 0.5         | 55.0%| 77.4%| 55.5%| 58.6%| 81.5%| 70.2%| 60.4%| 82.8%| 83.5%|
| 0.5 ~ 1       | 13.6%| 8.0% | 18.5%| 13.1%| 6.7% | 18.3%| 10.3%| 8.5% | 6.9% |
| 1 ~ 2         | 9.5% | 6.7% | 17.5%| 7.5% | 7.2% | 6.4% | 9.0% | 4.6% | 5.4% |
| 2 ~ 4         | 8.2% | 5.4% | 5.1% | 8.0% | 3.6% | 2.8% | 7.2% | 3.1% | 2.8% |
| 4 ~           | 13.6%| 2.6% | 3.3% | 12.9%| 1.0% | 2.3% | 13.1%| 1.0% | 1.3% |

Table 4. Speed measurement results for various values of the supersampling ratio.

| Supersampling ratio | 0 | 2 | 4 | 6 | 8 |
|---------------------|---|---|---|---|---|
| Average computation time (s) | 0.8 | 1.7 | 2.9 | 5.9 | 10.3 |

However, discrepancies in excess of 10% were observed for structures with volumes of less than 50 cc.

Table 3 shows a summary of the percentages of the overall discrepancy compared to TPS. As the supersampling ratio was increased, the discrepancy between the recalculated and the TPS values decreased. The DVH-based statistics generally become more similar up to a point as the sampling resolution increased. The percent discrepancies of the dose values obtained by using the custom-made method were better than those obtained from the MIM software.

## 2. Computation Time

The measured calculation times for various supersampling ratios are presented in Table 4. As supersampling required more memory and buffer, adaptive supersampling implemented in certain structure areas within the entire dose grid was used to increase the calculation speed. The average of three measurements for each structure was presented. The calculation time was increased by a factor of the supersampling ratio.

### IV. DISCUSSION

In the present study, a simple interpolation method for DVH calculation was developed to improve the reproducibility and data consistency from various TPSs. Because the issue of dose uncertainty from multiple treatment planning systems was not addressed in this study, the main goal was to restore the original DVH data from each TPS. The statistical values obtained with the developed DVH calculation by using the supersampling method were generally similar to the original values from each TPS. The results demonstrated relatively decreased percent differences with increasing structure volume for the minimum, maximum, and median doses. These trends were also similar to the result obtained by comparing DVH from the TPS with that from the MIM software. The increased spatial resolution obtained by using supersampling was attributed to the reduced uncertainty caused by interpolation for matching structure’s coordinates to the dose grid. However, no significant reduction in the discrepancy was observed, when the supersampling ratio was continually increased. Because more sampling required more calculation time, $4 \times 4$ sampling showed a reasonable supersampling ratio. Although the different interpolation algorithms resulted in variations [2], the results obtained by using our custom-made DVH generation algorithm demonstrated good agreement with those obtained from the TPSs. The largest difference was observed in the minimum dose, which was below 10 cGy.

DVHs are generally calculated by using a combination of a discreet uniform dose grid and a structure dataset. Thus, sampling and interpolations are needed to represent a continuous structure matching with the dose and
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image matrices. Although the structures are sampled and interpolated from the 3D image matrix, they do not exactly match the dose grid. Regular or random samplings are used to compute dose points inside regions of interest. This process results in uncertainties in the dose statistics obtained from various treatment planning systems with different algorithms. In this study, a simple DVH calculation method was proposed to improve the sampling resolution when a dose grid matches with the structure set. The supersampling method was used for finer resolution near the structure edges because most of the uncertainty was due to different interpolations and dose modeling at the boundaries of the structure. As a result, most discrepancies were observed in small structures that had many voxels penetrated by contour edges. Because the trilinear interpolation for the x, y, z directions was utilized for the calculation, no dependency, based on CT slice thickness, in matching the dose grid was noted that the results using 2.5-mm and 5-mm CT slice thicknesses were similar.

Typically, the radiation oncology department operates a different TPS for different modalities. Each system has an independent database in a different place to archive treatment plan data, and the systems have limited interfaces with one another. Collecting multiple data sources in a data warehouse combined with an information technology solutions is beneficial for clinical research because it reduces the time needed to collect necessary data [10]. Proper use of a standard protocol is required to effectively communicate between information systems and TPSs from various vendors. The DICOM RT standard, which deals with imaging equipment and PACS, is especially meaningful when specifying data for imaging systems. However, some TPSs do provide the DVH information in a DICOM file; therefore, an independent DVH generation method is necessary for any analysis of the data [2,13,14].

Although the drawback of this study was the computation time due to the larger amount sampling, this disadvantage can overcome by using dazzling new IT technology. Improved computing speed and larger multiprocessing capacity remove these handicaps.

V. CONCLUSION

In conclusion, a simple DVH calculation method was developed and evaluated for data consistency to evaluate multiple treatment plans and for integration with an independent information system. The results demonstrated that an additional spatial sampling of dose grid is useful for restoring the original DVH statistics from various TPSs. This algorithm could be applied to develop a single well-managed database solution, such as RTPACS, for an independent information system.

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