Results of 1 year of clinical experience with independent dose calculation software for VMAT fields

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ABSTRACT

It is widely accepted that a redundant independent dose calculation (RIDC) must be included in any treatment planning verification procedure. Specifically, volumetric modulated arc therapy (VMAT) technique implies a comprehensive quality assurance (QA) program in which RIDC should be included. In this paper, the results obtained in 1 year of clinical experience are presented. Eclipse from Varian is the treatment planning system (TPS), here in use. RIDC were performed with the commercial software; Diamond® (PTW) which is capable of calculating VMAT fields. Once the plan is clinically accepted, it is exported via Digital Imaging and Communications in Medicine (DICOM) to RIDC, together with the body contour, and then a point dose calculation is performed, usually at the isocenter. A total of 459 plans were evaluated. The total average deviation was -0.3 ± 1.8% (one standard deviation (1SD)). For higher clearance the plans were grouped by location in: Prostate, pelvis, abdomen, chest, head and neck, brain, stereotactic radiosurgery, lung stereotactic body radiation therapy, and miscellaneous. The highest absolute deviation was -0.8 ± 1.5% corresponding to the prostate. A linear fit between doses calculated by RIDC and by TPS produced a correlation coefficient of 0.9991 and a slope of 1.0023. These results are very close to those obtained in the validation process. This agreement led us to consider this RIDC software as a valuable tool for QA in VMAT plans.

Key words: Clinical experience; diamond; redundant independent calculation; VMAT

Introduction

Uncertainties in dose delivery can originate by means of errors in daily treatment, which includes human errors, or errors in the process of calculating monitor units (treatment planning). The former class of errors will probably affect only one treatment session, but the latter can affect the whole course of treatment and more than likely many patients. A significant number of reported incidents could have been prevented by performing a redundant independent dose calculation (RIDC) prior to treatment, even more so, the International Commission on Radiological Protection (ICRP) has indexed the task “monitor unit calculation” with a risk level of 3 being the maximum.

It is widely accepted that RIDC must be included in three-dimensional conformed radiotherapy (3D-CRT) as part of the treatment planning verification. This has been recommended in the report of AAPM Task Group 40. Intensity-modulated radiation therapy (IMRT) and specifically volumetric modulated arc therapy (VMAT) requires an individualized quality assurance (QA) procedure, and RIDC should also be included in a comprehensive QA protocol. Diamond® (PTW) is a commercial software which is capable of calculating VMAT fields. In the revised literature this software is cited for dynamic IMRT, for VMAT there is only one reference, proposing a validation procedure. In the present work, the results obtained in 1 year of clinical experience are analyzed.

Materials and Methods

The treatment planning system (TPS) used is Eclipse v10.0 from Varian Medical Systems. All calculations were performed using the analytical anisotropic...
algorithm (AAA), which is a convolution-superposition based algorithm. A detailed description can be found in the literature.\cite{10,11} Linacs and TPS are integrated into the ARIA R&V network (Varian Medical Systems), version 10.0. Before using the TPS in clinical practice, it was commissioned based on various international recommendations.\cite{10,11} The testing procedure and results obtained are detailed in the literature.\cite{12} RIDC were made with Diamond® version 5.01.02.131 (PTW) and all of them were point dose calculations. For VMAT fields, Diamond provides a “Clarkson modified” type algorithm.\cite{7,13} Two features related to this algorithm should be explained in detail:

- **Body contour importation**: Diamond includes an option to import the body contour for VMAT plans. This feature makes it possible to assign a source to surface distance (SSD) and depth of calculation, to each control point (a VMAT field is composed of 177 control point), otherwise averaged values of SSD and depth must be assigned to all control points.

- **Heterogeneity correction**: This correction is made by setting an effective depth different from the geometric one. For IMRT and 3D plans, this can be done easily by using values obtained from TPS and setting them manually in Diamond. For VMAT this is not possible as TPS only gives an averaged effective depth for the 177 control point, and if this value is set for all control points, an averaged SSD is used thereby losing all information relating to the body contour. Based on the above, calculations were made without heterogeneity correction. Similar papers for 3D and IMRT plans use the same approximation.\cite{14,15}

As said in introduction, prior to its clinical use, a software validation procedure was performed, this procedure included a separate validation for 3D fields and for VMAT fields, for better clearance a brief description of the procedure is included (a more detailed description can be found in reference 7).

**Conventional fields**

First, a validation for conventional (3D) fields was carried out. For this purpose, a set of fields was selected following the guidelines recommended in ESTRO documentation.\cite{16} For dose measurements a PTW T-31016 Pin-Point (0.016 cm3) ionization chamber, a PTW UNIDOS E electrometer, and a PTW RW3 slab phantom were used. The phantom was CT scanned with a slice spacing of 2 mm, and introduced in TPS. Fields were generated with the isocenter (corresponding to the calculation point) placed at the center of the sensitive volume of the chamber, at a depth of 5, 10 and 20 cm. The results obtained in Diamond were compared with TPS and with experimental measurements. All calculations were done including the heterogeneity correction in Eclipse. As said above, this correction can be included in Diamond by manually entering an “equivalent depth” obtained from Eclipse.

**VMAT fields**

This validation procedure included two different comparisons: Diamond versus TPS and versus measurements. The validation was carried out using a cylindrical phantom made of homogeneous plastic, QUASAR (Modus Medical Devices), with the pin-point ionization chamber (PTW T-31016) located at its center. This phantom was CT scanned with a slice spacing of 2 mm. CT data were exported to TPS. A total of 59 VMAT plans clinically accepted were recalculated in the phantom and then were exported to Diamond where a point dose calculation at isocenter was carried out. Results were analyzed obtaining average deviations and standard deviation values from the comparisons Diamond versus measurements and versus TPS.

A total of 459 clinically accepted plans were evaluated. VMAT plans can include one or more arcs, but in this paper only completed plans are analyzed. The plans were grouped by location in: Prostate (119), pelvis (82), abdomen (26), chest (54), head and neck (H&N) (87), brain (31), and miscellaneous (8). Due to particular features, two categories have been included separately: Stereotactic radiosurgery (SRS) (8) and lung stereotactic body radiation therapy (SBRT) (14). The number of plans for each category is in brackets. All treatments consist of a unique course, using a simultaneous integrated boost technique when required. The prescribed dose per session ranged between 180 and 1,800 cGy (SRS). Nevertheless, point dose values calculated by TPS and Diamond can be different from the prescribed dose due to factors such as point dose selection, calculation without heterogeneity correction, and plan recalculation in a phantom.

In our center, VMAT pretreatment QA includes three independent verifications: Portal Dosimetry (Varian Medical Systems), two-dimensional (2D) absorbed dose distribution with 2D array-729 plus OCTAVIUS phantom (PTW), both analyzed in absolute mode, and a RIDC with Diamond.

The procedure for RDIC consists of the following steps:

- a) The plan is calculated without heterogeneity correction in the TPS and the isocenter is selected as the reference dose point.
- b) The plan and body contour are exported via Digital Imaging and Communications in Medicine (DICOM) to Diamond.
- c) Once the plan and body structure are imported into Diamond, a calculation is performed for each control.
point using SSD, and geometric depths derived from the body contour and the calculation point position.

d) A comparison between TPS and RIDC dose values is made. If the percent difference between TPS and Diamond is below ± 4%, the verification is correct and the procedure is finished. This value has been chosen by taking into account the mean and standard deviations obtained in the validation procedure.\([7]\)

If that difference was ±4% or higher:

e) A review of the previous procedure must be carried out, looking for errors such as inappropriate point dose selection and problems with body contour importation.

When an error is detected it must be corrected, and the procedure repeated again. This procedure is schematized in Figure 1. However, if the difference remains equal or higher than ± 4%, the other experimental verifications must be evaluated in order to accept or reject the plan.

Averaged percent deviations, maximum and minimum values, and standard deviations were analyzed for overall and by location. Dose deviations were calculated using the expression:

\[
\text{Dev}(\%) = \left(1 - \frac{d_D}{d_E}\right) \times 100
\]

Being \(d_D\) and \(d_E\) the dose values in cGy obtained in Diamond and Eclipse, respectively.

**Results and Discussion**

**Conventional fields**

For conventional fields, the average deviation between doses calculated using Diamond and Eclipse was -0.1 ± 0.7% (one standard deviation (ISD)). Similarly, a comparison with Diamond and the ionization chamber obtained a result of 0.4 ± 0.8% (ISD). Deviations ranged between ±1.4 and ±1.9% for comparisons with Eclipse and
measurements, respectively. In 1 year of clinical practice, a total of 221 fields were verified, obtaining an average dose deviation of 0.2 ± 1.4% (1SD).

**VMAT fields**

For the total number of plans, an average deviation of –0.3 ± 1.8% (1SD) was obtained by comparing Diamond and Eclipse. Figure 2 shows a histogram for all deviations found. Four plans showed deviations higher than 4%, 4.5% being the maximum value obtained, and two plans had deviations below -4% with a minimum value of -5.0%. These results are very close to those obtained in the validation process (-0.2 ± 1.7% comparing Diamond versus TPS),\footnote{[7]} and are also very similar to those reported, by Al Amri \textit{et al.},\footnote{[6]} for sliding windows IMRT.

The standard deviation obtained was slightly higher than in validation. This may be explained by the increase of variability inherent in the use of body contours instead of a fixed circular phantom contour, used in validation. Figure 3 shows dose values (in cGy) calculated by Diamond versus those calculated using Eclipse. A linear fit produced a slope of 1.0023, and a correlation coefficient of 0.9991, demonstrating a good match between both data sets, Figure 3.

A composite distribution of deviations separated by location is shown in Figure 4, excluding the miscellaneous group. In Table 1, a summary of data and results is shown. The groups with higher absolute deviations were prostate and abdomen (with -0.6% and + 0.8%, respectively. The group with the highest standard deviation was miscellaneous (2.4%) followed by SBRT (2.2%). The lowest standard deviation was obtained in SRS (1.2%) followed by prostate (1.5%). SRS and SBRT groups consist of very few cases but, despite low statistical significance, they have been intentionally included in order to comment on some peculiarities: SRS and SBRT plans are similar in respect of PTV volume and shape; and because dose prescriptions are not relevant for Diamond calculations, therefore, in principle, standard deviations should be very similar in both groups. However, as previously stated this is not the case. The origin of this apparent incongruence may originate from one aspect of the calculation procedure: RIDC are made using the clinically accepted plan, but recalculated without heterogeneity correction. In the case of SRS, due to the reasonable homogeneity and almost water equivalence of brain tissue, this recalculation does not modify the dose distribution, remaining uniform inside the PTV. On the contrary, in SBRT plans the dose distribution undergoes immense change when recalculated without heterogeneity correction. Here the PTV is located inside or adjacent to lung tissue which is far from water equivalent resulting in dose gradients inside PTV being nonexistent in the original plan. Therefore, in SRS plans a suitable calculation point can easily be located, unlike in SBRT. The dose homogeneity inside the PTV can be characterized by different indexes, Yoon \textit{et al.}\footnote{[17]} introduced the sigma index (s-index), defined as the standard deviation of the normalized differential dose–volume histogram curve. For the SRS group, the averaged values of the s-index were 0.9 ± 0.4% (with heterogeneity correction) and 1.0 ± 0.4% (without heterogeneity correction); whilst for the SBRT group, the values were 0.9 ± 0.2 and 4.3 ± 1.3%, respectively. Thus, s-index variations, between plans with and without heterogeneity correction, were higher for the SBRT group. This result was expected because significant heterogeneities are present on this anatomical
location (lung). This may explain the higher standard deviation for the SBRT group.

As stated above, some plans showed deviations equal to or higher than ±4% between point dose calculated by TPS and by Diamond in these cases the revision corrects one or both of the following aspects:

- Isocenter located outside the PTV or in a dose gradient region: In such situations, an alternative calculation point was selected in a dose homogeneous region inside the PTV. This was carried out in seven plans.
- Phantom recalculation: It was necessary to make a recalculation in a Phantom and carry out a check in Diamond due to uncertainties arising from the different scattering conditions in TPS and Diamond. Furthermore, recalculations were made for a few of these eight plans in which errors had occurred in the body contour import process.

Once revised, the deviations of 6 of these 15 plans remained out of the interval (-4%, +4%), but within the interval (-5%, +4.5%). Nevertheless, these plans were accepted for clinical use due to the results obtained in the other two verifications included in our QA protocol. During the validation procedure, two out of 59 plans showed a deviation outside the interval (-3.5%, +3.5%), representing 3.4% of the total plans. In clinical practice 7 of 459 plans were out of that interval, being 1.5% of the total cases studied.

Software limitations

Summarizing, different limitations of this software have been found in validation and clinical practice. From our point of view the most significant are:

a. Body contour importation errors:

   This problem forces us to recalculate in a homogeneous phantom and this new geometry can deteriorate the dose distributions and makes it difficult to choose an appropriate point dose calculation.

b. Dose calculation point selection:

   The default point dose is the isocenter. This criteria is appropriate for 3D plans because the dose distribution is, usually, quite homogeneous around this point. But for VMAT plans, high dose gradients can be present. In such cases, a new point dose must be selected in a more homogeneous dose region.

c. Heterogeneity correction:

   This correction cannot be included in our version of Diamond software for VMAT fields. This forces us to recalculate the plan in TPS without correction, for comparisons with Diamond.

These limitations and sources of error must be taken into account when establishing the treatment QA workflow.

Conclusion

Our 1 year experience results are very similar to those obtained in the validation procedure. This led us to consider Diamond a valuable tool for QA in VMAT plan and to stress the need to perform a comprehensive and detailed validation procedure before its clinical use.

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