

A Monte Carlo model for independent dose verification in IMRT and VMAT for the Varian Novalis TX with high definition MLC

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Original Article

Abstract

Purpose: With intensity modulated radiation therapy (IMRT), the physician can prescribe, design and deliver optimized treatment plans that target the tumor and spare adjacent critical structures. The increased conformity of such plans often comes at the expenses of adding significant complexity to the delivery of the treatment. With volumetrically modulated arc therapy (VMAT), in addition to the modulation of the intensity of the radiation beam, other mechanical parameters such as gantry speed and dose rate are varied during treatment delivery. It is therefore imperative that we develop comprehensive and accurate methods to validate such complex delivery techniques prior to the commencement of the patient's treatment. **Methods:** In this study, a Monte Carlo simulation was performed for the high definition multileaf collimator (HD-MLC) of a Varian Novalis TX linac. Our simulation is based on the MCSIM code and provides a comprehensive model of the linac head. After validating the model in reference geometries, treatment plans for different anatomical sites were simulated and compared against the treatment planning system (TPS) dose calculations. All simulations were performed in a cylindrical water phantom as opposed to the patient anatomy, to remove any complexities associated with density effects. Finally, a comparison through gamma analysis of dose plane between the simulation, the TPS and the measurements from the Matrixx array (IBA) was conducted to verify the accuracy of our model against both the measurements and the TPS. **Results:** Gamma analysis of ten IMRT and ten VMAT cases for different anatomical sites was performed, using a 3%/3 mm passing criterion. The average passing rates were 97.5% and 94.3% for the IMRT and the VMAT plans respectively when comparing the MCSIM and TPS dose calculations. **Conclusion:** In the present work a Monte Carlo model of a Novalis TX linac which has been tested and benchmarked to produce phase-space files for the treatment head of the linac was used to produce a input phase-space to calculated dose deposition phenomena in different geometries for IMRT and VMAT treatment modalities. The control points defined for the MLC were replaced by blocks with the same characteristics and materials of the linac MLC to speed up the simulation time. With this technique a simulation of a typical IMRT case can be performed with a 10 computer cluster in about 1.02 hours in average. If the number of computer used is increased the computing time can be reduced even more which make our model suitable for clinical use as a second check method to compare the TPS dose calculated. Our results showed that for IMRT and VMAT deliveries with a HD-MLC, there is an average of 95.9% of the points have a gamma index less than 1 with our chosen criterion between our Monte Carlo simulations and the corresponding measurements and TPS calculations in a cylindrical water equivalent phantom. This Monte Carlo code can be used as pre-treatment, independent dose calculation verification for IMRT and VMAT deliveries.

Keywords: Monte Carlo simulations; BEAMnrc; MCSIM; Novalis TX; HD-MLC

Introduction

Monte Carlo based radiation transport techniques have been used for several years as the most accurate method for dose calculation in radiotherapy ¹, including plans for intensity modulated radiation therapy (IMRT) ²⁻²³. With the introduction of IMRT, the treatment planning team can generate very conformal plans with high complexity that can be delivered either as multi-gantry step-and-shoot or sliding window

beams (classic IMRT delivery) or as volumetrically modulated arc therapy (VMAT). With the VMAT delivery, in addition to the modulation of the radiation beam intensity, the gantry speed and the dose rate can also vary during treatment. Such complexity of treatment delivery requires accurate methods to validate the dose prior to treatment delivery.

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The planning aspects of MLC-based IMRT represent a challenge, primarily because the IMRT beams consist of a large number of control points (also known as segments) which could, depending on their area, introduce conditions of electronic disequilibrium.²³⁻²⁴ For a complex intensity pattern, the resulting dose distributions can be very sensitive to the detailed structure of the MLC.²³⁻²⁵

The high definition multi-leaf collimator (HD-MLC) on the Novalis^{TX} Varian system has 60 leaf pairs (Varian Medical System, Inc., Palo Alto, CA). The inner 32 leaf pairs have a 2.5 mm width projection at isocenter while the outer 28 leaf pairs have a projection of 5 mm at isocenter. The purpose of this study is to investigate the use of our previously presented Monte Carlo model of the Novalis TX machine²³ for IMRT and VMAT independent dose verification.

Methods and Materials

According to the American Association of Physicists in Medicine (AAPM) task group report TG-105, Monte Carlo simulations need to be performed under the same conditions as the measurements. The authors have reported the Monte Carlo modeling and benchmarking of a Novalis TX Varian 6 MV with HD-120 multileaf collimator (MLC).²³ The resulting model of the Novalis TX linac from the precedent investigation was tested for regular and irregular fields defined by jaws and by the MLC as well for leakage. A number of regular fields ranging from 1×1 to 20×20 cm² and irregular fields were simulated and compared to the commissioning data from the linac.²³ The Monte Carlo model of the Novalis TX linac mentioned above was performed in two steps. First, a phase-space file was obtained from the simulation of the treatment head at a location immediately after the HD-MLC. The phase-space files were then used as input for the dose calculations in the phantom.

In the present investigation the Monte Carlo simulation of dose deposition were implemented in two steps again. First, a phase-space file was obtained from the simulation of the treatment head at a location immediately after the Jaws for a 20×20 cm² field using BEAMnrc code. Secondly, this phase-space file was used as input for the dose calculation in the phantom and patient CT using MCSIM code. The use in this study of the MCSIM code was to speed up the computation time for the simulations by replacing the MLC by blocks with the same characteristics of the MLC but with this feature the entire simulation can be done in a single simulation and calculate the dose for each control point for IMRT and VMAT cases.

BEAMnrc simulations

Phase-space files for the different field size of the Novalis TX 6 MV photon beams were created using the EGSnrc\BEAMnrc system.^{2, 5, 12} The cutoff energies used in

the simulations were ECUT = 700 keV for electrons and PCUT = 10 keV for photons. A monoenergetic source of kinetic energy of the beam of 6 MeV was used with full width at half maximum (FWHM) for the X and Y directions of 0.125 cm. Geometry and materials used to build the Monte Carlo model of the linear accelerator were based on machine specifications as provided by the manufacturer. The linac was structured in the following order: a target slab of tungsten and copper, primary collimator of tungsten, flattening filter, ion chamber, and jaws (tungsten), as in **Figure 1**. All materials used in the MC simulation were extracted from the 700 ICRU PEGS4 (preprocessor for Electron Gamma Shower) cross section data available in BEAMnrc, and met the specifications for the linac as provided by the manufacturer.²³ Simulations had a minimum requirement of 100,000 particles per cm², this was done to ensure reliable statistics in the phase-space file generated by BEAMnrc simulations.

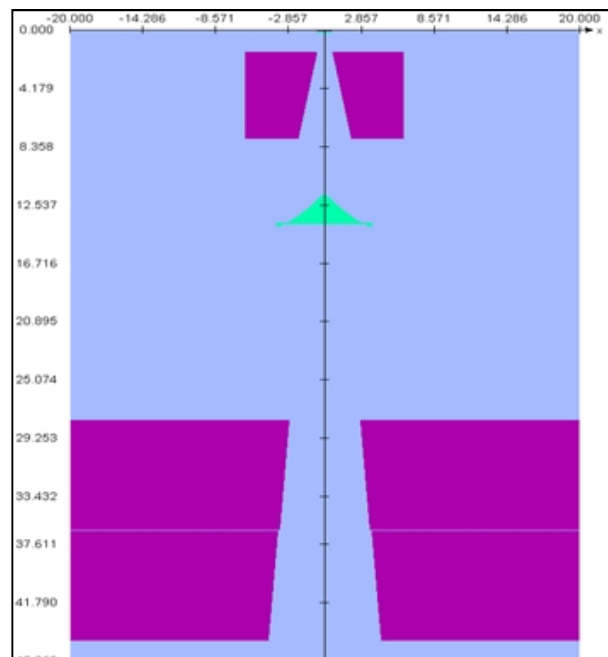


FIG. 1: Novalis TX linac head geometry in BEAMnrc.

Monte Carlo phantom for simulations

Using the stand-alone code ct-create which is included in the HEN-HOUSE/EGSnrc package of the BEAMnrc code CT data sets can be converted to a phantom which relevant information is written into the file (*.egsphnt). This file contains all the information needed in the MCSIM to perform the simulations in this geometry which corresponds to the original CT data from which it was extracted. Basically, ct-create reads the original CT data (Pinnacle, CADPLAN, or DICOM format), in our case DICOM format exported from the treatment planning system (TPS). Then select a subvolume of CT data, after that it resamples the CT resolution and finally it convert the data to material and density. At the end a file is written which contains the material and density data (*.egsphnt) which can be used in MCSIM (by changing the

*.egsphnt to *.egs4phant). In **Figure 2**, an example of how the egs4phant created in ct-create can be visualized in the mcshow software which is included in the MCSIM package. For the present study a cylindrical phantom based on the Tomotherapy (cheese) phantom (TomoTherapy, Inc., Madison, WI) was created to calculate the dose and compare versus

TPS dose calculation. In order to contrast our results with measurements a phantom of the Matrixx array (IBA Dosimetry GmbH, Schwarzenbruck, Germany) was used to create a phantom for this device and compare TPS, Monte Carlo simulations, and Matrixx measurements.

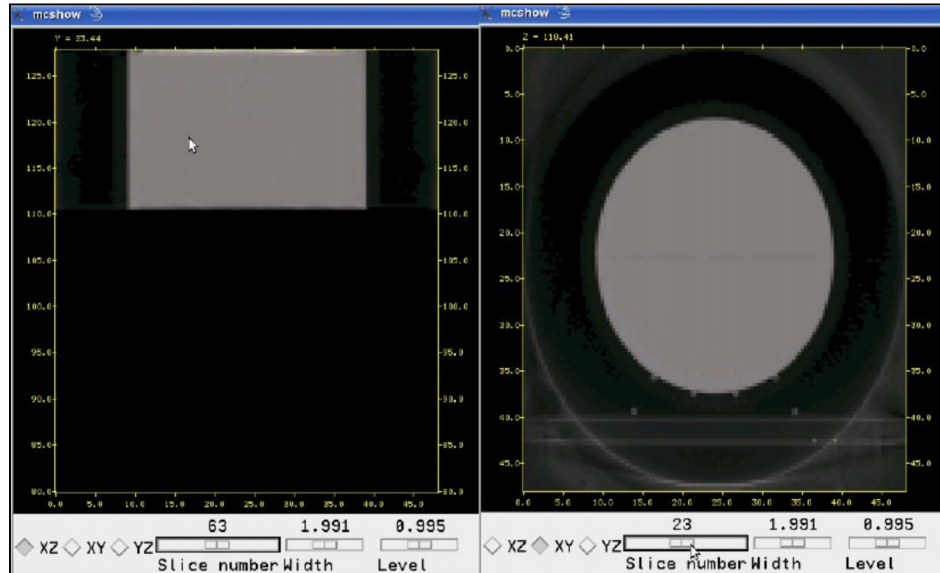


FIG. 2: Use of ct-create routine to convert CT data to *.egs4phant for Monte Carlo simulations.

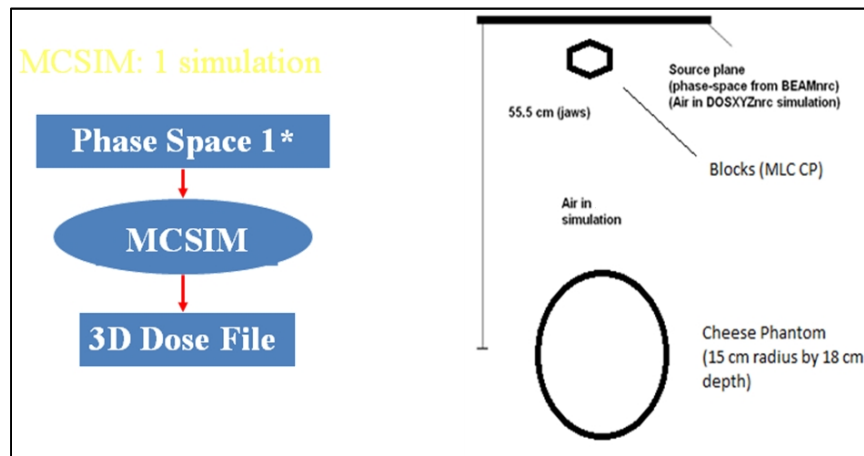


FIG. 3: MCSIM simulation geometry and flow chart.

MCSIM simulations

Monte Carlo dose calculations were performed using the phase space files described above (BEAMnrc) as source input. The energy cutoffs in all simulations were ECUT = 700 keV (rest mass + kinetic energy) for electrons and PCUT = 10 keV for photons. First a Monte Carlo simulation for a 10×10 cm² field defined with the 20×20 cm² phase-space file as input in a cube water phantom of dimensions 30×30×30 cm³ was conducted, this simulation determined the defined dref (dose reference) by which the simulation result is multiplied and convert the results of the simulations to centigray (cGy). The calibration of our model was defined using the cube phantom

described above with a source to surface distance (SSD) of 100 cm and obtained 1 cGy per monitor unit (MU) at d_{max}. The error in the calibration simulation was less than 1% to the 10 maximum doses at the end of the simulation.

For the IMRT and VMAT simulations a cylindrical phantom was used the so called cheese phantom with dimensions described above. The Monte Carlo phantom of this geometry (*.egs4phant) was created with the same CT data that was used to create the TPS (Pinnacle) phantom. The simulation parameters used were the same as before ECUT = 700 keV and PCUT = 10 keV. The phase-space file for the 20×20 cm² field

from BEAMnrc simulations of the linac head was used as input to the MCSIM simulation.

For each of the IMRT and VMAT plans the corresponding Dicom-RT file was exported. In-house Matlab (Matlab 7.8.0 R2009a, The MathWorks Inc., Natick, Massachusetts) routine was used to extract all the information needed to build a script that later is used in MCSIM to simulate each case. The matlab routine extract from the dicom-rt file the following parameters in order to create the script file (*.egs4inp) used as input in MCSIM: gantry angle, collimator angle, couch angle, MU per control point, jaws position, and MLC position for each control point. With the MLC position information a block is built for each control point of each beam of the plan. This block is saved as a text file and called later by the egs4inp file during the simulation to act as the MLC geometry for the control points. For the IMRT cases a block is built for each control point of each beam of the original treatment. So each beam has the same number of block as the number of control points as it was defined by the TPS during optimization. For the VMAT case each arc contains a number of control points and the code create each control point as a corresponding block. **Figure 3** shows the flow chart of the MCSIM simulation and the geometry of these simulations. For IMRT and VMAT cases an error of less than 2% in the maximum 10 doses of the simulations was achieved.

Finally after the simulation MCSIM results are registered in a matrix file dose (*.3ddose) which contains the dose in the geometry used for the simulation. Again in-house matlab code was used to convert this file to a Tomotherapy dose file which can be read in the commercial RIT113 version 5.3 (Radiological Imaging Technology, Inc.) software to be compared with TPS dose calculation and with Matrixx dose

measurements. As inherited to the final Tomotherapy dose file is a 3D matrix the user once in RIT software need to select the correct plane to be compared. For our simulations in the cheese phantom a transverse central plane where the isocenter was set was the plane used for comparison. For our Matrixx comparison the coronal plane of the isocenter was used for comparison since this is the plane where the ion chamber array of the Matrixx device is located. An IMRT plan was measured for this purpose with the Matrixx with all beams delivered with the gantry at 180 degrees for simplicity. Finally the dose measured with the Matrixx was exported as a Dicom image to be compared to TPS and MCSIM dose calculation in the RIT software.

Results

IMRT cases for different treatment sites were simulated and compared against the dose calculated by the TPS. In this case the simulations were performed over the cheese phantom and the resulting dose from the simulation was converted to a Tomotherapy dose matrix as explained before. In the RIT software TPS and MCSIM simulation doses were compared against each other and a dose difference of 3% and a distance to agreement (DTA) of 3 mm were selected for the gamma pass-fail criterion. **Figure 4** shows the result for an IMRT case with a resulting gamma analysis of 98.47% of the points with a gamma less than 1 for the criterion mentioned. Profiles comparison shows an agreement within 3% dose difference in the comparison of TPS versus MCSIM results. Deviation in the order of less than 3% of the calculated dose is observed specially in the low dose region of the comparison. Similar results were observed for all IMRT cases simulated.

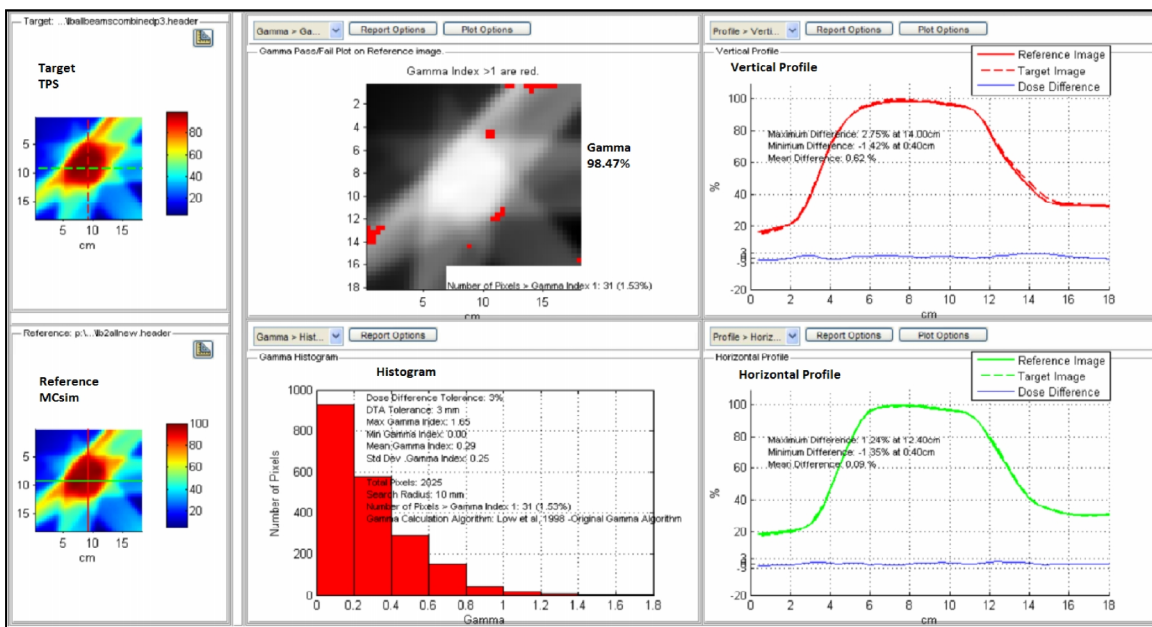


FIG. 4: Comparison between TPS and MCSIM simulation for an IMRT delivery.

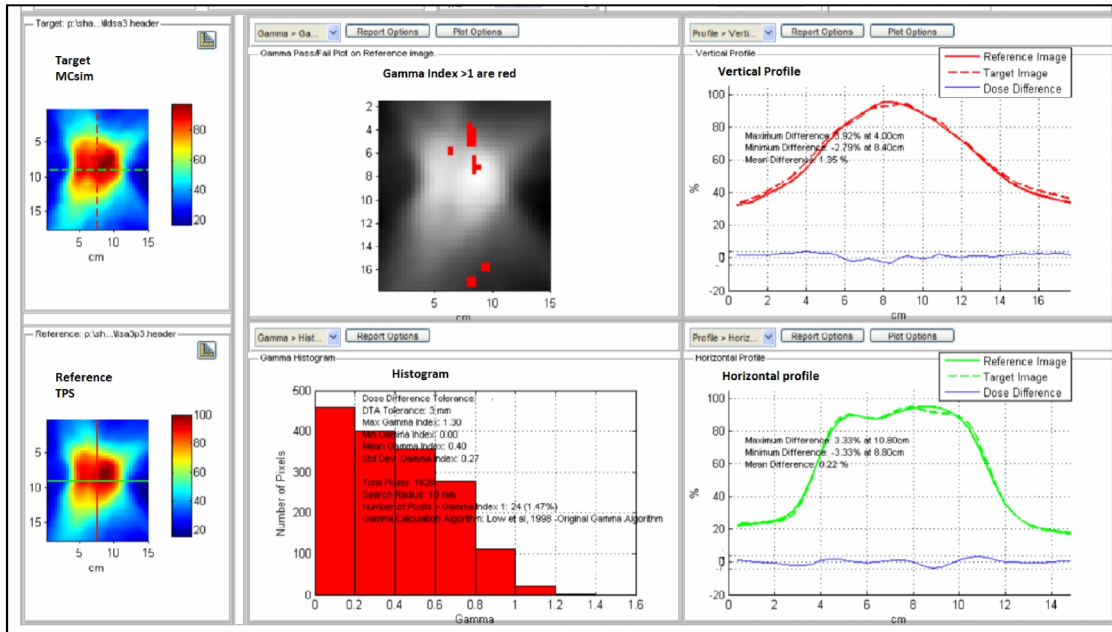


FIG. 5: Comparison between TPS and MCSIM simulation for a VMAT delivery.

VMAT cases were simulated in the same cheese phantom geometry and the resulting dose calculations from MCSIM were converted to a Tomotherapy dose matrix file and compared against TPS dose calculations in the RIT software. **Figure 5** shows the comparison for a VMAT case between TPS versus MCSIM simulation doses. For the gamma analysis a criterion of 3% dose difference and 3 mm DTA were used. The gamma result for this case was 98.53% of the points with a gamma index less than 1. Small deviations of the dose were observed in the low dose region. Profiles comparisons have an agreement within 3% dose difference.

TABLE 1: Gamma analysis results for IMRT and VMAT cases for TPS versus MCSIM simulations comparison in cheese phantom.

Modality	Cases	Gamma <1 (3%, 3 mm)
IMRT	10 (5 Pelvis, 3 brains, 2 HN)	97.5
VMAT	10 (5 Pelvis, 3 brains, 2 Lungs)	94.3

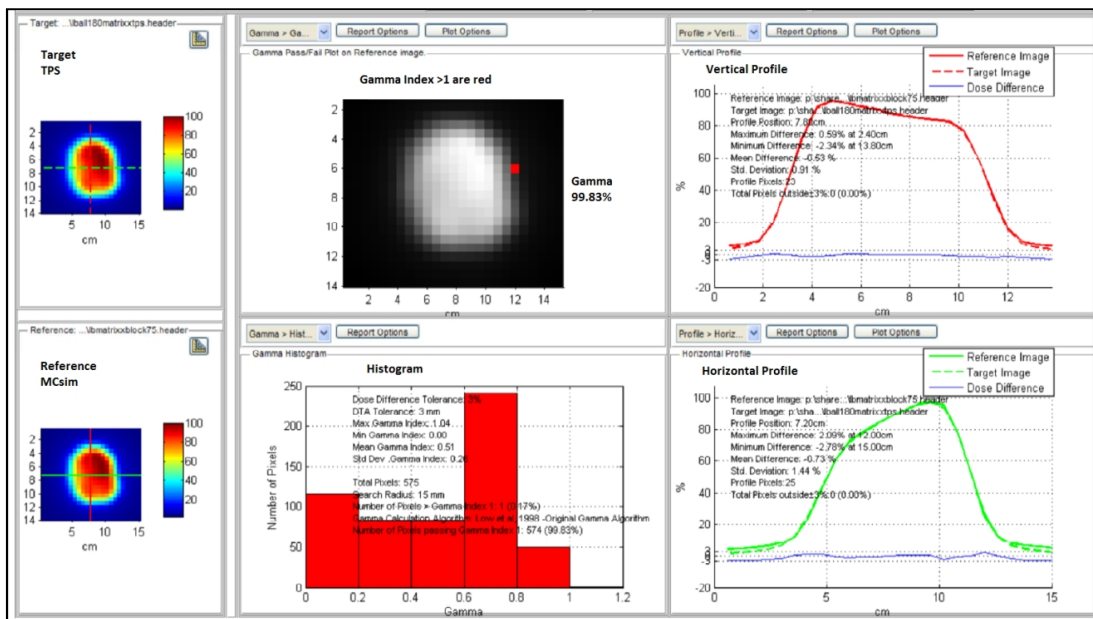


FIG. 6: IMRT result comparison between TPS and MCSIM simulation dose calculation (gamma 3%, 3 mm criterion) in Matrixx phantom geometry.

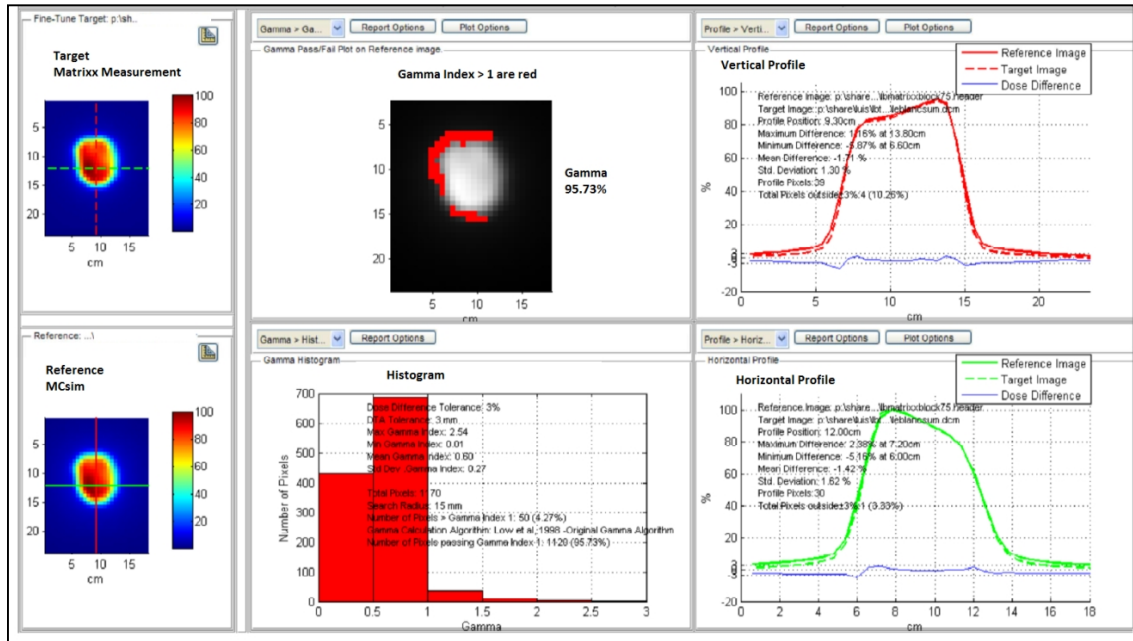


FIG. 7: IMRT result comparison between Matrixx measurements and MCSIM simulation dose calculation (gamma 3%, 3 mm criterion).

Table 1 show the gamma analysis results for 10 IMRT and 10 VMAT cases studied in the present investigation. And average of 97.1% passing gamma were obtained for the IMRT cases and an average of 94.3% passing gamma for the VMAT cases. Agreement within 3% of the dose between the profiles was observed for the cases studied for IMRT and VMAT modalities.

In order to benchmark the MCSIM dose simulations, these were compared against actual measurements performed with a Matrixx ion chamber array device for an IMRT case. Actual measurements with the gantry angle at 180 degrees were performed with the Matrixx phantom. A TPS dose calculation for this plan was exported. And finally a MCSIM simulation over the Matrixx geometry was performed for the same plan. The TPS dose calculation was compared first versus the MCSIM simulation dose results and comparison with a gamma criterion (3%, 3 mm) was performed and illustrated in Figure 6. The result shows that 99.83% of the points have a gamma index less than 1. And Figure 7 shows the comparison in RIT of the Matrixx measurements versus MCSIM simulation for this IMRT case. A gamma criterion of 3%, 3 mm were used and the result shows 95.73% of the points have a gamma index less than 1. Profiles comparison demonstrates agreement within a 3% and deviations as high of 3% in the low dose region but same differences were observed in the TPS versus Matrixx comparison.

Conclusion

In the present work a Monte Carlo model of a Novalis TX linac which has been tested and benchmarked to produce phase-space files for the treatment head of the linac was used

to produce a input phase-space to calculated dose deposition phenomena in different geometries for IMRT and VMAT treatment modalities. The control points defined for the MLC were replaced by blocks with the same characteristics and materials of the linac MLC to speed up the simulation time. With this technique a simulation of a typical IMRT case can be performed with a 10 computer cluster in about 1.02 hours in average. If the number of computer used is increased the computing time can be reduced even more which make our model suitable for clinical use as a second check method to compare the TPS dose calculated.

Our results showed that for IMRT and VMAT deliveries with a HD-MLC, there is an average of 95.9% of the points have a gamma index less than 1 with our chosen criterion between our Monte Carlo simulations and the corresponding measurements and TPS calculations in a cylindrical water equivalent phantom. This Monte Carlo code can be used as a pre-treatment, independent dose calculation verification for IMRT and VMAT deliveries.

Conflict of interest

The authors declare that they have no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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