Total Voxel-wise BED and EQD2 Calculation for combined External Radiotherapy and Brachytherapy treatments.

Maximiliano Musso, Msc[1]; Alberto Adrada, Msc[2]; Rogelio Diaz Msc[1], Daniel Venencia, PhD[1]
[1]Instituto Zunino de Radioterapia, Cordoba, Argentina, [2]Clinica de Occidente, Cali, Colombia

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ABSTRACT

The primary objective of this study is to develop a tool capable of converting physical dose into BED and EQD2 matrices, improving upon traditional summation methods that systematically overestimate the radiobiological effect in combined external beam radiotherapy and brachytherapy.

A Python-based platform was developed to perform voxel-by-voxel EQD2 accumulation using deformable image registration (DIR). By reimporting the mapped matrices back into the TPS, we verified that the traditional parameter-based method significantly overestimates the biological effect on the rectum and bladder.

The tool developed has the potential for clinical implementation, allowing for a spatial evaluation of the effective biological effect produced by radiation on target organs and volumes.

CONTACT

[Maximiliano Musso]
[Instituto Zunino de Radioterapia]
[Obispo Oro 423]
[mmusso@institutozunino.org]
[+549-351326-5806]

INTRODUCTION

In combined treatments involving external beam radiotherapy (EBRT) and brachytherapy (BT), ICRU 89 and GEC-ESTRO guidelines recommend using EQD2 for radiobiological evaluation. However, standard clinical assessment relies on simple DVH parameter addition (e.g., D2cc or D90%), neglecting 3D spatial dose distributions and leading to systematic dose overestimations. To address this specific limitation, the aim of this work was to develop an independent software tool capable of computing voxel-by-voxel BED and EQD2 matrices, incorporating a dual deformable image registration (DIR) engine that enables cross-validation between the generalized deformation field exported from Eclipse and the deformation field generated by our in-house structure-guided deformation algorithm.

METHODS AND MATERIALS

EBRT and brachytherapy plans were generated in the Eclipse (v18.1) TPS using a pelvic phantom, with precise segmentation of the rectum, bladder, and PTV Figure 1. To execute the radiobiological evaluation, an offline processing pipeline was established: complete DICOM datasets (CT images, structures, and physical dose matrices) were exported from the TPS. An independent Python-based software application was developed to import these datasets and apply the linear-quadratic (LQ) model voxel-by-voxel, computing three-dimensional BED and EQD2 matrices (α/β =10 Gy for tumor tissue; 3 Gy for OARs).
To perform spatial dose accumulation, the platform executes a dual-DIR mapping workflow:

1. Importation and application of the generalized deformable vector field (DVF) exported directly from Eclipse.
2. Computing a localized, in-house structure-guided DIR utilizing the SimpleITK framework. To ensure computational efficiency and independence from Hounsfield unit (HU) variations, binary masks of the rectum and bladder were first constrained to their bounding boxes and converted into signed distance maps. The registration was driven by a multi-resolution Diffeomorphic Demons transformation, optimizing a mean squares similarity metric through sparse random spatial sampling.

The generalized Eclipse DVF served as a baseline to cross-validate the geometric and dosimetric consistency of our localized structure deformation. Following the standalone calculation, the cumulative biological dose matrices from both engines were converted back into standard DICOM formats and reimported into the TPS for final clinical evaluation and DVH verification. A graphical user interface (GUI) was integrated to streamline this external data workflow in Figure 2 and Figure 3.

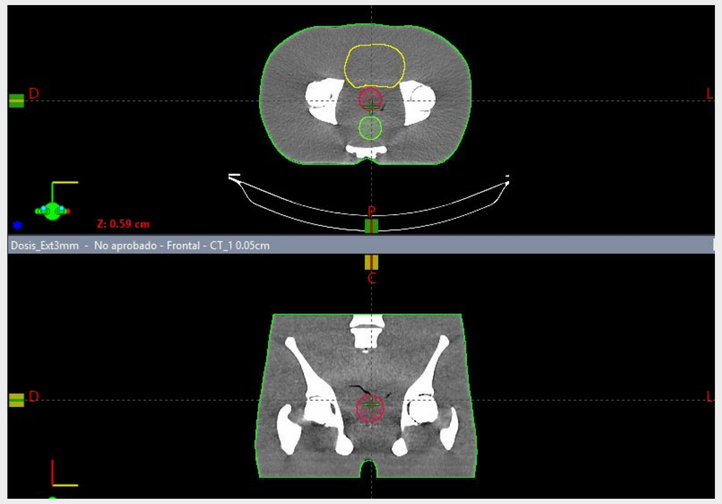

Figure 1. Delineation of the bladder, rectum, and PTV on the pelvic phantom.

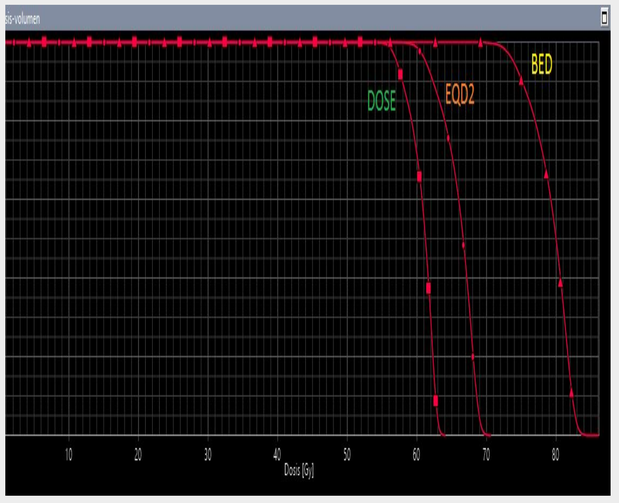

Figure 2. Dose, BED, and EQD2 DVHs for the PTV.

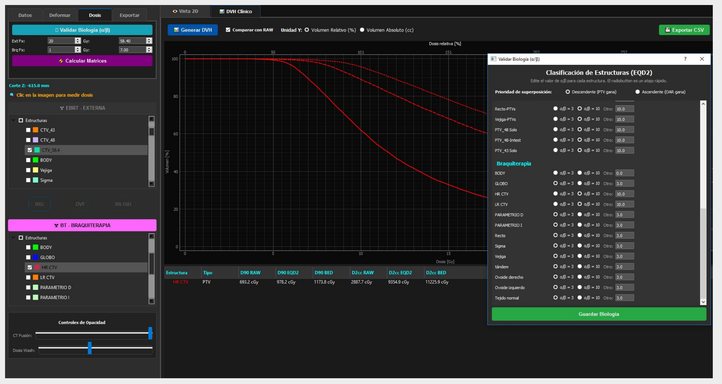

Figure 2. DVHs generated by the GUI.

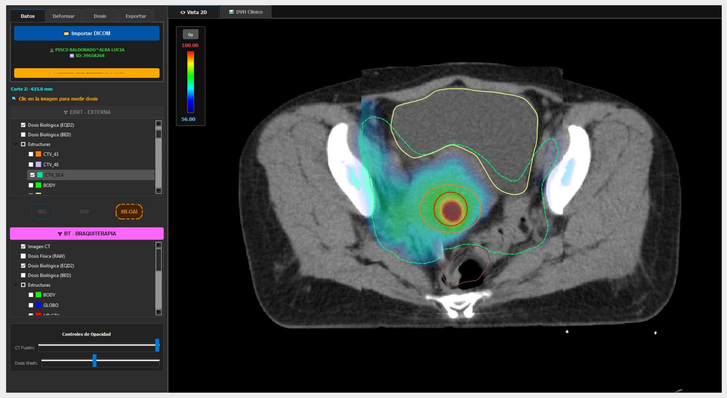

Figure 3. Three-dimensional EQD2 distribution generated by the GUI

RESULTS

Following the import of the BED and EQD2 matrices into Eclipse, the calculations performed by the independently developed software were successfully verified. This verification was achieved through the evaluation of the dose–volume histograms (DVHs) of the organs at risk (OARs), the rectum and bladder, as well as the planning target volume (PTV), whose physical dose, BED, and EQD2 DVHs are shown in Figure 4. Dosimetric comparison demonstrated the clinical superiority of the structure-guided approach. Traditional rigid parameter addition systematically overestimated OAR toxicity; in contrast, the in-house DIR-OAR algorithm reduced the cumulative D2cc for the rectum by approximately 15% across biological models compared to rigid summation. Furthermore, while the commercial intensity-based DVF managed to reduce OAR doses, it artificially compromised target tracking, underreporting the HR-CTV D90 biological coverage by ~3.4%. The in-house DIR-OAR successfully resolved this limitation, maximizing OAR sparing while maintaining >99% geometric fidelity and dose coverage for the HR-CTV .

DISCUSSION

Traditional parameter-based summation systematically overestimates OAR doses assuming that spatial hot spots from EBRT and brachytherapy perfectly coincide. While voxel-wise EQD2 and BED accumulation mitigates this, commercial intensity-based DIR often introduces applicator artifacts that artificially compromise target coverage.
In contrast, our structure-guided DIR-OAR successfully bypasses these distortions. By preserving HR-CTV geometric fidelity while accurately mapping rectal and bladder variations, this tool offers a robust and viable framework for accurate biological dose tracking.

CONCLUSIONS

An independent software tool was successfully developed for voxel-by-voxel BED and EQD2 accumulation in combined EBRT and brachytherapy. By integrating a structure-guided DIR-OAR workflow, the platform overcomes the systematic dose overestimations of traditional rigid addition and the geometric artifacts of commercial TPS registrations. This provides a highly accurate, 3D spatial representation of cumulative biological doses for both OARs and targets, establishing a robust and clinically viable framework for advanced dosimetric evaluation.

REFERENCES

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