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A Clinical Validation of the egs_mird Monte Carlo Code for ^{177}Lu PSMA Patient-Specific Dose Calculations

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ABSTRACT

Purpose: To test EGSnrc user code egs_mird as an independent verification for patient-specific dosimetry calculations in a clinical workflow alongside two commercially available software packages (MIM SurePlan™ MRT and Voximetry TorchMC™).

Methods/Materials: TRT patients were scanned using a Siemens Symbia Intevo Excel approximately 72 hours post-injection. CT and quantitative SPECT image data for 22 injections from 17 patients were imported into both TorchMC and MIM SurePlan MRT, which utilize voxel S-value (VSV) and GPU-based Monte Carlo methods, respectively, to calculate the absorbed dose. All software solutions employed the Hänscheid method to approximate cumulative biological decay. The SPECT/CT images were converted into an EGSnrc-compatible format using a combination of tools available online and in-house MATLAB code. Organ-average and hottest 2cc doses were compared for the kidneys and parotids.

Results: The average percent difference between patient-specific organ average doses calculated by MIM and egs_mird was 4.63% ± 3.05% (0.09 Gy ± 0.06 Gy) for the kidneys and 6.91% ± 8.29% (0.11 Gy ± 0.13 Gy) for the parotids. The corresponding results between Torch and egs_mird were 8.35% ± 3.37% (0.17 Gy ± 0.07 Gy) for the kidneys and 8.26% ± 3.87% (0.16 Gy ± 0.15 Gy) for the parotids.

Conclusions: Doses calculated using egs_mird can be used as part of a clinical workflow to independently verify doses calculated using commercial software. Underlying differences in heterogeneity modeling, radiation transport, variance reduction, and other simplifications to increase efficiency likely led to differences in calculated doses between the software. Patient-specific organ doses varied despite each being given the same injected activity.

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INTRODUCTION

- Targeted radioligand therapies (TRT) such as ^{177}Lu-PSMA-617 are currently administered using fixed activities across all patients, resulting in heterogeneous patient-specific doses for both cancerous targets and healthy organs at risk. Determining patient-specific doses is complicated by complex biokinetics, limited imaging capacity, and the computational expense of accurately calculating the absorbed dose.
- The difficulties in dose determination necessitate multiple independent approaches to address these limitations. This work aims to validate a clinical workflow utilizing egs_mird, an open-source EGSnrc user code, as an independent verification of two commercially available software packages (MIM SurePlan™ MRT and Voximetry TorchMC™) using quantitative SPECT/CT scans of patients who received ^{177}Lu-PSMA-617 treatments.

Figure 1: EGSnrc rendering of a patient-specific dose simulation with electron and photon tracks shown in red and yellow, respectively.

METHODS AND MATERIALS

- The EGSnrc user code egs_mird was used for all Monte Carlo simulations.
- TRT patients were scanned using a Siemens Symbia Intevo Excel approximately 72 hours post-injection.
- CT and quantitative SPECT image data for 22 injections of 17 unique patients were imported into both TorchMC and MIM SurePlan MRT, which utilize voxel S-value (VSV) and GPU-based Monte Carlo methods, respectively, to calculate the absorbed dose.
- All software solutions employed the Hänscheid method to approximate cumulative biological decay.
- The SPECT/CT images were converted into an EGSnrc-compatible format using a combination of tools available online and in-house MATLAB code.
- Organ-average dose values were compared for the kidneys (Figure 2) and the parotids (Figure 3) across all three software solutions.
- Additionally, D2cc values were compared for the kidneys (Figure 3) and the parotids (Figure 4) as they are generally more sensitive to differences in shapes of DVH curves.

RESULTS

- The average kidney dose in the cohort was 2.24 ± 0.72 Gy, ranging from 0.34 Gy to 3.48 Gy. For the parotids, the average dose was 1.84 ± 1.23 Gy, ranging from 0.20 Gy to 5.15 Gy. This high variability in organ absorbed dose occurred despite all patients receiving the same initial injected activity of Pluvicto.
- There were minor differences in average doses calculated by each software, but the magnitudes of these differences were typically on the order of tens of cGy, indicating general agreement among the three approaches. The similarities between the D2cc values also indicate that the DVH curve shapes are likely consistent across all three calculation methods. Overall dose discrepancies were most prominent in localized regions near heterogeneities but did not noticeably impact dose calculations specific to the kidneys and parotids.
- Calculated dose discrepancies between egs_mird and Voximetry TorchMC are likely due to slightly different material and density assignments, differences in variance reduction, and different sampling techniques.
- Similarly, calculated dose discrepancies between egs_mird and MIM SurePlan are likely due to material and density assignment differences.
- The egs_mird uncertainty per voxel was on the order of 1% while running 50 billion histories and each patient- and cycle-specific simulation required approximately 675 CPU hours, or about 12 wall-clock hours across 56 threads on an AMD EPYC 7763 processor. The egs_mird simulations were also run at CT resolution rather than SPECT resolution, which considerably increased computation time.

CONCLUSIONS

- Our results show that egs_mird can be used in a clinical workflow as an independent verification of dose calculations.
- The magnitudes of the dose calculation discrepancies were small relative to the quantities of interest indicating compatible results between the software.
- Future work will analyze tumor doses and include a larger patient cohort.

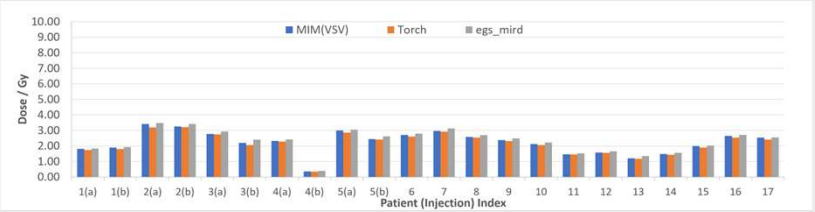

Figure 2: Average kidney doses calculated from each cycle and time integrated using the Hänscheid method for each of the dose calculation solutions

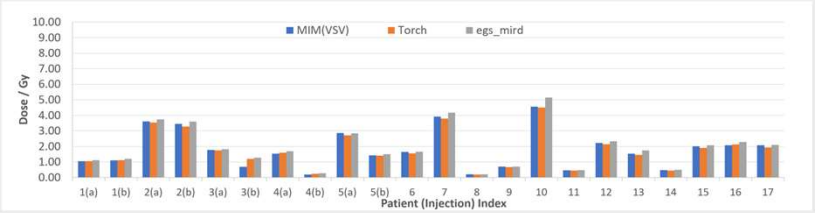

Figure 3: Average parotid doses calculated from each cycle and time integrated using the Hänscheid method for each of the dose calculation solutions

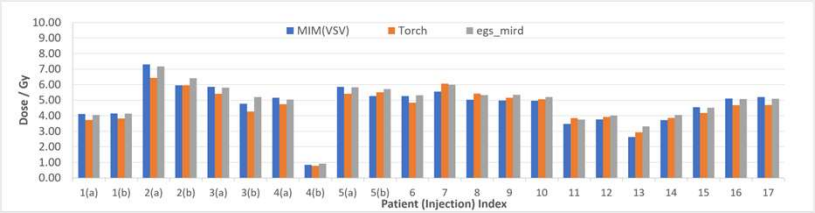

Figure 4: Average kidneys D2cc values [Gy] calculated from each cycle and time integrated using the Hänscheid method for each of the dose calculation solutions

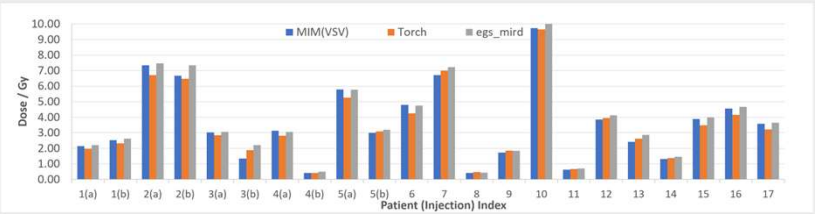

Figure 5: Average parotids D2cc values [Gy] calculated from each cycle and time integrated using the Hänscheid method for each of the dose calculation solutions