verification. However, for dosimetry-guided treatment planning it is essential to obtain reliable absorbed dose estimates independent of dosimetry method or software. In this work, we aim at comparing five different dosimetry approaches for organs and tumors in ^{177}Lu-DOTATATE therapy. ***Materials and Methods:*** This work is based on the SNMMI Dosimetry Challenge ^{177}Lu-DOTATATE patient data sets. The published patient CT, time-integrated activity (TIA) map and volumes of interest (VOIs) for kidneys, liver, spleen and tumors as in Task 5 of the challenge were used. Five different dosimetry (or software) approaches were compared: 1) Full patient-specific Monte Carlo (MC) dose simulation was performed with the CT and TIA map as inputs using GATE. 2) Convolution of the TIA map with a Lutetium-177 soft tissue dose kernel (GATE MC) in an in-house MATLAB code followed by voxel-wise density weighting using the patient's CT (3DVoxDos). For organ-level dosimetry, the total TIA per given VOI was extracted from the TIA map and mass-scaled S-value based dosimetry was performed in 3) OLINDA_v2.2.0(ORNL Legacy Phantom), 4) IDACDose_v2.1, and 5) MIRDcalc_v1.1. Percentage differences (PD) in mean organ and tumor doses against full MC simulation were assessed. ***Results:*** Average PDs against MC were -4.2% [min:-6.3%, max:2.7%] for 3DVoxDos, -6.3% [min:-11.0%, max:0.6%] for OLINDA, -6.5% [min:-11.4%, max:2.7%] for IDAC and -7.1% [min:-11.0, max:-3.3%] for MIRDcalc, taking all healthy organs together (kidneys, liver, spleen). For the 6 tumors, average PDs against MC were -5.5% [min:-6.4%, max:-4.5%] for 3DVoxDos, -12.6% [min:-15.4%, max:-7.0%] for OLINDA, -6.1% [min:-9.8%, max:-0.1%] for IDAC, and -9.5% [min:-12.0, max:-3.9%] for MIRDcalc. ***Conclusion:*** In this work, we found differences between full MC simulation and organ or voxel-level dosimetry approaches. Largest discrepancies in absorbed doses of -11% against MC were found for the liver for all organ-level dosimetry methods. MIRDcalc, IDAC, OLINDA, and 3DVoxDos showed overall comparability between each other with less than 3% difference for healthy organs. The smallest PDs for tumors were found for 3DVoxDos. This work showed little differences between dosimetry approaches and software, which suggests that the main variability in absorbed dose estimates originates from other steps of the dosimetry workflow.

EPS-212

Accuracy assessment of absorbed dose rate calculation: evaluation of two treatment planning systems for molecular radiotherapy

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Aim/Introduction: Assessing the accuracy of clinical dosimetry in molecular radiotherapy is a challenging task, since the different steps that contribute to the determination of the absorbed doses (clinical dosimetry workflow - CDW) have to be considered. We initiated a study of the variability of each CDW step on two software, by analyzing the impact of different approaches/methodologies. In this work, we first present results obtained for the absorbed dose computation step, by comparing local energy deposition (LED) and dose voxels kernel (DVK) convolution, with or without media density correction. Monte Carlo radiation transport modelling was set as the reference. ***Materials and Methods:*** Clinical dosimetry was performed on a group of patients who received Lutathera® treatment at the Institut Régional du Cancer de Montpellier (ICM). The CDW was implemented using PLANET® Dose (DOSIsoft SA) software. It included image registration, segmentation, absorbed dose rates (ADR) computation, and integration over time to obtain the absorbed doses. The overall variability of the CDW was compared with OpenDose3D software. Monte Carlo simulations were conducted using GATE version 9.1. ***Results:*** By looking first at the absorbed dose computation step, the initial differences on ADR between software were in the range of 4% to 11% (for kidneys and liver) depending on the algorithm used and media density management. Further studies and software comparison put in evidence differences in density correction implementation. By using a similar Hounsfield Unit-densities calibration function, the observed differences were reduced. For example, the difference for LED with media density correction decreased from 4% to 1%. The final comparison of convolution vs. direct Monte Carlo simulations shown a very good agreement (around 2% of difference at maximum). We are now studying the impact of registration and VOI definition across time. For lesions, a 20% difference in volumes was obtained, inducing discrepancies up to 30% on the final absorbed dose between both software. This is being further studied, as well as integration over time. ***Conclusion:*** This work assesses the accuracy and validates the absorbed dose computation approaches implemented in the 2 software for ^{177}Lu-based radiopharmaceutical therapies. It is gradually extended: first, to other steps of the CDW, then on other isotopes (e.g. ^{131}I). In perspective, the study of the impact of registration and VOI definition across time, is currently ongoing. In that context, the availability of an open-source software, freely available, is an invaluable asset when benchmarking clinical dosimetry software.

EPS-213

Assessing the Impact of Dosimetry Method on Healthy organ and Lesion Absorbed Dose Estimates for 177Lu-PSMA-617 Therapy of Prostate Cancer: Early Experience from the Canadian Cancer Trials Group PR21 trial (NCT 04663997)

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Aim/Introduction: Radiopharmaceutical therapies with PSMA-ligands have recently shown promising treatment outcomes for prostate cancer. Since dosimetry plays an essential role for personalized therapy planning and verification, its reproducibility and comparability gains increasing importance. Consequently, we aimed at comparing image-based dosimetry methods for ^{177}Lu-PSMA-617 therapy. ***Materials and Methods:*** 15 therapy cycles of 8 patients with a simplified protocol of quantitative 177Lu-SPECT/CT imaging at 24h and 48h post-injection of 177Lu-PSMA-617 for the 1st cycle, and at 48h for the subsequent cycles were analyzed. Semi-automatic segmentation was performed on the 1st 177Lu SPECT/CT per cycle using MIM v.7.2.1, utilizing threshold-based methods (kidneys, liver, spleen, salivary glands and whole-body) and the