

kcps/MBq at the center of the field-of-view and at 10 cm radial offset, respectively. The NECR peak was 178 kcps @ 23.8 kBq/ml (184 kcps @ 23.0 kBq/ml) and the scatter fraction at the NECR peak was 38.5 (37.9) %. For the TPTV, the sensitivity was 8.0 (8.1) kcps/MBq and 7.9 (8.2) kcps/MBq at the centre of FOV and at 10 cm radial offset, respectively. The NECR peak was 151 kcps @ 27 kBq/ml (161 kcps @ 31 kBq/ml) and the scatter fraction at the NECR peak was 24.8 (32.5) %. **Conclusion:** Both PET/CT and PET/MRI models showed a good accordance (< 10 %) with the measured reference values. The application of these models for the evaluation of different image reconstruction algorithms in simulated numerical phantoms is work in progress. **Acknowledgments:** The financial support of the Austrian FWF Project I3451-N32 is gratefully acknowledged.

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Automating de-identification and sharing DICOMs with a free and open-source software

A. Vongsalat¹, S. Kanoun², A. Berriolo-Riedinger³, O. Humbert⁴, S. Jodogne⁵, F. Lambrechts⁶, D. Vallot², P. Pascal⁷, I. Tal⁸, I. Berry⁷, F. Courbon²; ¹IUT Informatique, Toulouse, FRANCE, ²Institut Claudius Regaud - IUCT Oncopole, Toulouse, FRANCE, ³Centre Georges Francois Leclerc, Dijon, FRANCE, ⁴Centre Antoine Lacassagne, Nice, FRANCE, ⁵University Hospital (CHU) of Liege, Liege, BELGIUM, ⁶Osimis, Liege, BELGIUM, ⁷Centre Hospitalo-Universitaire de Toulouse, Toulouse, FRANCE, ⁸None, Haifa, ISRAEL.

Aim: To build a free and open-source software to automate the mass de-identification of datasets of patients, taking into account the specificities of PET/CT. **Material and Methods:** The free and open-source Orthanc PACS software was used to handle DICOM network communications and to de-identify patients/studies and series following the NEMA 2017c guideline with fine-tunable options through the RESTful API of Orthanc. A standalone application was developed in the JAVA language to drive the Orthanc server using its RESTful API to de-identify DICOM files respecting constraints of PET images, as part of project <http://petctviewer.org/>. The developed software handles: Single or batch de-identification of studies. Manual or automatic definition of de-identified names and/or IDs. De-identification profile adapted to PET series (retaining patient's weight, height, acquisition time, injection time, injected dose) or following the full NEMA guideline (for CT, MRI...). Recognition and automatic removal of secondary capture images (to avoid patient identification hardprinted in the pixels of some image). Local download of de-identified studies (ZIP) and remote sharing service with FTP, SFTP or WebDAV protocol. Report generation about the de-identification process (retracing original identity and de-identified key). **Results:** The Orthanc server was installed and declared in the PACS by a physician with the help of the network manager of the hospital in Dijon (France), in just one afternoon, using the provided user manual. The de-identification software is provided as a standalone executable tool with no installation requirement. The anonymization feature was successfully tested with up to 80 PET/CT studies in a single anonymization procedure. De-identified patients were sent to a third center (located in Nice) using a private ownCloud server (WebDAV protocol)

from the same anonymization software. All de-identified studies were successfully read (preserving SUV values), both on commercial and on open-source workstations. **Conclusion:** A free and open-source software is available for mass DICOM de-identification and sharing of PET/CT images. This package is provided as part of the free and open source PET/CT viewer project (<http://petctviewer.org/>)

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41% of SUVmax threshold is highly reproducible even if obtained with different software for PET/CT segmentation

F. Bergesio¹, A. De Maggi¹, L. Guerra², S. Chauvie¹; ¹S. Croce e Carle Hospital, Medical Physics Unit, Cuneo, ITALY, ²S. Gerardo Hospital, Nuclear Medicine Department, Monza, ITALY.

Purpose/introduction: The aim of this work was to compare the variability in measuring the Metabolic Tumour Volume (MTV) of known lesions obtained with 4 different software (SW) for PET segmentation. **Subjects & Methods:** MTV of 24 known lesions were analysed by the same imaging expert with 4 SW: ROVER (ABX GmbH), LifeX (Universite Paris-Saclay), Fiji (petctviewer.org) and MIM (MIM software Inc.) For each lesion three different segmentation algorithm were used: 41% of SUVmax (PER), 2.5 SUV (FIX) and the proprietary segmentation algorithm (PSA). Each MTV was normalised to the average of the four SW and is reported as mean±standard deviation and range. **Results:** MTV for PER were: ROVER (0.99±0.04, range: 0.90-1.05); LifeX (0.99±0.03, range: 0.93-1.06); Fiji (1.02±0.04, range: 0.93-1.14); MIM (1.00±0.03, range: 0.92-1.06). MTV for FIX were: ROVER (1.15±0.38, range: 0.66-2.30); LifeX (0.92±0.21, range: 0.35-1.40); Fiji (0.93±0.27, range: 0.26-1.40); MIM (1.00±0.33, range: 0.22-2.23). MTV for PSA were: ROVER (Adaptive Threshold) (0.74±0.14, range: 0.30-0.98); LifeX (NESTLE Algorithm) (0.93±0.21, range: 0.34-1.30); MIM (Gradient Threshold): (1.33±0.31, range: 0.90-2.23). The mean, median, standard deviation e range of all MTV, expressed in cc, were (61.67±82.64, median: 20.26 range: 4.76-291.61), (145.97±174.26, median: 72.12 range: 6.24-719.10) and (73.10±91.59, median: 28.57 range: 5.21-325.18) for PER, FIX and PSA respectively. **Discussion/Conclusion:** PER is a robust and reproducible procedure to evaluate the MTV of PET-CT lesion even if using different software with variability below 10%. The FIX showed a high variability related to the positioning and shape of the initial VOI used for segmentation. The PSA showed a great variability related to the different segmentation algorithm emphasising the fact that different PSA are not inter-changeable. MTV measured with PER are systematically lower than with FIX.

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A new denoised deconvolution analysis in ^{99m}Tc Mag3 renography

M. Destine^{1,2}, A. Seret¹; ¹ULiège, GIGA-CRC In vivo Imaging, Liège, BELGIUM, ²CHU UCL Namur Ste Elisabeth, Namur, BELGIUM.

Aim: To obtain the relative kidney uptake and renal transit times thanks to a new deconvolution process of noisy renal time activity curves. **Material and Methods:** The method relies on a