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Generating a simulated PSMA PET map with deep learning based on anatomical MRI alone

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Aim/Introduction: PSMA PET/MRI has shown the potential to improve accuracy for lesion detection over multiparametric MRI for the detection of prostate cancer. However, the method is costly, not widely available, and not approved for prostate cancer detection, yet. Recent observations have shown that high PSMA expression might also be correlated with structural characteristics such as growth patterns. Deep learning has the potential to detect and learn such patterns, not recognized by the human eye. Therefore, this study to train a neural network based on PSMA PET/MRI scans to predict increased prostatic PSMA uptake based on the axial T2 weighted sequence alone. *Materials and Methods:* All patients undergoing PSMA PET/MRI for staging or biopsy guidance between 1st April 2020 and 1st December 2020 at our institution were selected if general consent for retrospective analysis was given. To increase the specificity of our model, the PSMA PET scans were segmented considering an SUV-threshold greater than 5 to generate positive and negative voxels; an SUV cut-off of 4 was used in patients without PSMA prostatic uptake greater than 5. T2 weighted axial sequences were semiautomatically segmented to select the prostate volume. A deep neural network (DNN) was trained on the T2 images to generate a predictive PSMA PET map. *Results:* A total of 188 scans were available (154 [^{68}Ga]Ga-PSMA-11 and 34[^{18}F]PSMA-1007). Significant cancer was present in 151 of them. 34 patients had no PSMA uptake > 5; therefore, they were re-segmented with an SUV > 4 and used as validation. In this way, the dice similarity coefficient was 69.47± 15.62%. *Conclusion:* Despite a relatively small cohort for the DNN training, we have shown that, based only on the T2 images, increased prostatic PSMA uptake can be estimated in staging PCa. Further investigation with larger cohorts and external validation is needed to assess whether PSMA uptake can be predicted accurately enough to help in the interpretation of mpMRI.

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AI-based detection and characterization of lung tumors in 18F-FDG-PET/CT including measurements of tumor dimension in CT

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Aim/Introduction: T staging for lung cancer is an accepted system to characterize the extent of disease. Manual measurements of tumor dimensions in three planes are part of the staging procedure. The aim of this study was to develop an artificial intelligence (AI)-based tool for detection and characterization of lung tumors in 18F-FDG-PET/CT including measurements of tumor dimension in CT. *Materials and Methods:* 73 patients (42 women), (mean age 63 years, range: 44 - 87) underwent 18F-FDG-PET/CT for suspected lung cancer and were included retrospectively. Manual measurements were obtained in FDG-avid lung tumors in CT axial, coronal, and sagittal views.The automatic segmentation of the lung tumor was done in two steps. A convolutional neural network (CNN) was used to detect and segment lung tumors. This CNN takes the CT, PET image and an organ mask created by a separate method as input. A second CNN was applied to the area around the main lung tumor (highest total lesion glycolysis if more than one). This CNN segments the tumor based on the tissue in the CT image, which generally doesn't correspond exactly with the high uptake region in the PET images partly due to breathing artefacts. In addition to the CT and PET images, this CNN also takes the output from the first CNN as input. Once the main tumor has been segmented in the CT image, the largest diameter in axial, coronal and sagittal planes are automatically calculated. *Results:* FDG-avid lung tumors were found in 53 of 73 patients. The AI-tool detected 47/53 tumors (sensitivity 90%) and correctly identified 16/20 without tumors (specificity of 80%). The average metabolic tumor volume was 45 cm3 and the total lesion glycolysis was 300. The median differences and interquartile ranges between AI-based and manual tumor dimensions on CT were axial -0.9mm (-2.7 to 2.2mm); coronal 0.1mm (-3.0 to 4.5mm); sagittal -0.1 mm (-3.6 to 2.9mm); maximum dimension 1.2mm (-2.6 to 4.2mm). The average tumor dimensions were 49, 50, and 49 mm in the axial, coronal, and sagittal views. *Conclusion:* This first version of an CNN developed for correct FDG-avid tumor identification in the CT of PET/CT studies showed high sensitivity and specificity. Furthermore, the automatic measurements obtained to aid T staging were quite similar in most of the correctly identified tumors. The AI method is available for research purposes on request at www.recomia.org.

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Can deep learning predict the receptors' status of breast cancer's metastases on 18F-FDG PET/CT images ?

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Aim/Introduction: Breast cancer is the most common among women, and approximately 34% of these women develop metastases. To choose the best treatment, assessing receptors' status from tumor biopsy for subtype classification is essential. However, tumor biopsies are invasive and cannot be done for all metastases from a patient and therefore cannot detect histopathologic

heterogeneity between lesions which can affect treatment efficacy. This study aims to evaluate the potential of deep learning to predict receptors' status of metastases using PET/CT images. **Materials and Methods:** Seventy-two metastatic lesions from 66 patients included in the prospective EPICUREseinmeta metastatic breast cancer study (NCT03958136) were manually delineated by two nuclear physicians from the ICO cancer center on PET/CT images. These lesions were biopsied and their receptor status (estrogen (ER), progesterone (PR), and HER2) are known. We used the experts' manual segmentations to extract 3D bounding boxes centered on the lesions in the PET and CT images. Twelve deep learning methods were compared to predict the receptors' status (ER, PR, and HER2): three for ER status, three for PR status, three for HER2 status, and three for multi-task prediction of the three receptors' status. For each group of tasks, we tested different combinations of input channels: i) only PET images of metastases, ii) PET, and CT images of metastases, and finally iii) PET, CT images, and automatic segmentation performed by a previously trained network. We used the DenseNet architecture from the Monai framework (https://github.com/project-monai/monai) for all experiments and trained all networks for 500 epochs following a 3-fold cross-validation scheme. **Results:** To compare networks and given class unbalances for ER and HER2 status, we used the weighted accuracy, which is computed by taking the average, overall the classes, of the fraction of correct predictions in this class. Best performances were obtained by single class prediction networks with three input channels for PET, CT images, and automatic segmentations. Best weighted accuracies for these networks were 0.65, 0.61, and 0.61 for ER, PR, and HER2 status respectively. Networks using only PET images as input channel had worst performances. **Conclusion:** Deep learning methods seem to be able to predict receptors' status of breast cancer metastases on PET/CT images, as we obtained weighted accuracies superior to 0.60. New experiments should be conducted using more data, with different and more complex architectures to improve predictions. Explanation methods should also be used to identify regions important for receptors' status prediction.

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Image Augmentation for Image-to-image Translation in ^{18}F-FDG PET imaging: Does it make a difference?

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Aim/Introduction: Lowering radiotracer dosage in Positron Emission Tomography (PET) imaging reduces the radiation risk at the expense of increasing noise levels in the images. With the rise of deep learning applications in medical imaging, this problem of PET imaging is addressed with image-to-image translation techniques to replicate the image quality of higher radiotracer dosage scans. With the increase of training data, the performance of the deep learning model tends to improve, but that is not always possible for most research cases. A method used for increasing training image datasets is image augmentation. We aim to study whether image augmentation techniques are worth the effort in the case of short-to-standard scan duration image translation of PET images. **Materials and Methods:** Whole-body 18F-FDG PET image data of 10 patients scanned with the standard scan duration (StdSD) were post-reconstructed to 1/32nd of StdSD to provide short scan duration (ShrSD) counterparts. A two-dimensional multi-slice input cycle-

consistent generative adversarial network (Cycle-GAN) was used to predict the StdSD images using the ShrSD inputs. Random up and down, right to left, and 45-degree rotation of ShrSD-StdSD training pairs were implemented as a simple augmentation approach after each training epoch. The model's performance trained with either of the approaches (with and without augmentation (WA and WOA)) was tested on the image data of two patients using parameters including the peak signal-to-noise ratio (PSNR), structural similarity index (SSIM), Normalized root mean squared error (NRMSE) metrics were compared to the reference ShrSD images. Paired-sample t-test will measure the statistical significance (p-value = 0.05) of the differences between the two approaches. **Results:** The model trained using both approaches (with and without augmentation) was capable of improving the PSNR (ShrSD=27.88, WA=31.12, and WOA=30.82), SSIM (ShrSD=0.9291, WA=0.9446, and WOA=0.943), and NRMSE (ShrSD=0.049, WA=0.0316, and WOA=0.0321) metrics of the ShrSD inputs with p-values lower than 0.05 indicating the statistical significance of the results. **Conclusion:** Image Augmentation using the simple approaches did improve the performance of the model. While the difference between the two approaches was statistically significant, it was not substantial. More advanced augmentation techniques that change the input pixel values can be implemented, but whether they adversely affect the resultant images needs to be further explored. However, the model trained with both approaches was capable of improving the image quality of the short-scan duration images.

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Using Visual Recognition Based Machine Learning For The Prediction Of Survival In Patients With Colorectal Cancer With Liver Metastasis

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Aim/Introduction: Colorectal carcinoma (CRC) is one of the leading causes of malignancy-related deaths worldwide. Metastatic tumor burden in the liver is one factor that determines survival in CRC. Our study aimed to reveal the relationship between image classification and survival prediction using visual recognition data obtained from FDG PET data of CRC patients. **Materials and Methods:** Fifty-five PET images of 38 patients who underwent FDG PET/CT or PET/MR for colorectal carcinoma between January 2017 and May 2019 were included in the study. Whole-body PET MIP images of the patients were processed with semi-automatic segmentation, and liver MIP images were obtained. A total of 55 images were divided into two main groups: training(20 images) and analysis(35 images). The custom mode of the IBM Watson Studio was used for machine learning and analysis of the data. Two subgroups (<6 months and >6 months) were defined for image classification in custom mode **Results:** According to the machine classification analysis, 30 out of 35 images were evaluated correctly (85.7%). Five images were considered false (14.3%). While 14 (93.3%) of 15 images of patients who lived for less than 6 months after PET was evaluated correctly. One patient was considered false because the classification confidence score was below the threshold value. Otherwise, 16 (80%) of 20 images from patients who lived longer than 6 months after PET were classified correctly. However, the remaining 4 images were misclassified. **Conclusion:** Visual recognition-based machine