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optimized for a smaller amount of coincidence data. The TA is a necessary scanner procedure, designed for an arbitrary object. The proposed TA based TOF resolution assessment method, mostly performed in projection space, can be a suitable replacement of the current NEMA method, mostly performed in image space and designed for line sources only. **References:** None

EPS-139

Development of an automatic calculation method for the specific binding ratio in [¹²³I]ioflupne SPECT

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Aim/Introduction: A fully-automatic method for specific binding ratio (SBR) calculation in [¹²³I]ioflupane (FP-CIT) SPECT studies was proposed by creating volumes of interest of the striatum (VOI_{st}) and reference region (VOI_{ref}) without manual-handling steps to avoid operator-induced variability with rapid quantitative calculation. **Materials and Methods:** The present study involved 105 patients (72±10 years) suspected of parkinsonian syndrome (PS) who underwent FP-CIT SPECT. All patients were classified into PS and non-PS groups according to the results of clinical follow-up and SPECT images. The data from 200 patients in our previous study were used for evaluation and validation of the new program. The SPECT images were reconstructed with two methods; CT-attenuation correction with scatter (ACSC) and without scatter correction (CTAC). Consecutive slices containing striatal intensive counts were selected and a trapezoidal volume of interest (VOI_t) was created automatically. VOI_{st} was then created using our previous method [1]. SBR values were calculated from the mean values of VOI_{st} and VOI_{ref} determined by the whole brain region outside of VOI_t. To exclude low count voxels in the VOI_{ref}, several thresholds were applied for choosing an appropriate cut-off level. The SBR values from the new method were compared with those from our previous semi-automatic method and the Tossic-Bolt (TB) method [2]. **Results:** The fully-automatic method with the VOI_{ref} threshold of 75% maximum reference count, determined from the previous data (200 patients), showed a good linear correlation between the SBRs from the semi- and fully-automatic methods in both patient data sets ($r > 0.98$). The areas under the curves (AUCs) of receiver operating characteristics (ROC) analysis showed no significant difference between the semi- and the fully-automatic methods for both our previous (AUC > 0.99) and new (AUC > 0.95) data. Diagnostic accuracy of the two methods with ACSC and CTAC reconstruction showed similar results (> 92%), and both were better than the TB method. The mean running time of the fully-automatic method was 9±1 sec for each patient. **Conclusion:** The proposed method

successfully created the automatic VOIs and calculated SBR rapidly without any manual operation, avoiding the operator-induced variability and providing objective SBR results. **References:** 1) Rahman MGM, et al. Count-based method for specific binding ratio calculation in [¹²³I]FP-CIT SPECT analysis. Ann Nucl Med. 2019; 33: 14-21. 2) Tossic-Bolt, et al. Quantification of [¹²³I]FP-CIT SPECT brain images: an accurate technique for measurement of the specific binding ratio. Eur J Nucl Med Mol Imaging. 2006; 33: 1491-9.

EPS-140

A new automated method for analysis of cerebrovascular reserve capacity deficiency by rCBF SPECT with acetazolamide test: Preliminary results

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Aim/Introduction: The rCBF SPECT with acetazolamide test is a well-known, reliable method for the evaluation of cerebrovascular reserve capacity. The investigation could predict the increased risk for stroke in patient population with significant hemodynamic ischemia. Most nuclear medicine clinicians use visual assessment for the interpretation of rCBF SPECT. Quantitative assessment of the presence and degree of cerebrovascular reserve capacity could lead to more precise, patient-based treatment strategies. The aims of this study was to develop a new, automated method for quantification the difference between rCBF SPECTs before and after acetazolamide test and to validate with visual assessment. **Materials and Methods:** The automated method consists of five main steps: 1) SPECT brain images were translated into the MNI space (to ICBM Average Brain - ICBM152) using rigid and affine image registration methods; 2) Brain images were normalized by the average voxel value of the cerebellum (cerebellum atlas [1]); 3) the difference image obtained by subtracting the two aligned normalized SPECT images; 4) abnormal regions were detected using automated IQR analysis based on cortical and subcortical regions (Harvard-Oxford atlas); 5) for each detected subregion the size, median difference and anatomical region are extracted. The validation process contained two steps. Firstly, the founded subregions were evaluated based on the visual probability of decreased vascular reserve capacity using three main groups (proved, probable or not proved). Secondly, a region based comparison was performed between the visual assessment and the automated method. 15 patients' (7 men, 8 women, mean age: 66 years) rCBF SPECT images were evaluated. **Results:** All pathological cortical and subcortical regions were recognized by the automated method. In total 129 subregions with decreased vascular reserve were identified by the method. Forty two (32,56%)

visually proved or probable subregions were confirmed. The volume determined by our automated method in proved and probable subregions differed significantly from the not proved subregions (Kruskal-Wallis, $P < 0.0001$). The proved subregions do not differed from probable subregions (Kruskal-Wallis, $P > 0.05$). **Conclusion:** A new, automated method for analysis of brain perfusion reserve was developed. Based on the evaluation the method detected all of the affected regions. Despite the detected subregions large number based on our study in the future the clinically relevant subregions can be separated from the clinically irrelevant areas. **References:** [1] Diedrichsen, J. et al., A probabilistic MR atlas of the human cerebellum, *Neuroimage*, 2009 May 15;46(1):39–46

EPS-141

Quantification of 18F-Florbetapir amyloid brain PET scans using commercial software: a comparison with an experienced and independently reviewed clinical report

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Aim/Introduction: BRASS software can be used to quantify 18F-Florbetapir amyloid PET/CT scans performed for suspected Alzheimer's disease. BRASSv4.0 applies an automated PET-only registration method utilising an adaptive template based on principal component analysis. Work by our group has shown accurate registration of amyloid PET images to a template is possible without need of an MR(T1) driven template registration ($R^2=0.996$). Previous versions of BRASS used a standard rather than adaptive PET template. The aim of this work was to assess the potential of the BRASSv4.0 software to aid interpretation of 18F-Florbetapir scans. **Materials and Methods:** The clinical report for 226 18F-Florbetapir scans was agreed by two experienced readers following independent review. The scans were classified as type A (typical features) or non-type A (atypical features including image noise and atrophy) for both positive and negative scans. Quantitative analysis was performed using BRASSv4.0 and the regional values were normalised using the Pons region to give regional amyloid uptake ratios (SUV_R). The mean SUV_R across the regions was recorded (mean SUV_R) together with a coefficient identified in the linear model that correlated with amyloid load ($A\beta$ -index). The quantitative values were compared with the clinical report. ROC curves were used to evaluate regions and threshold values which minimised disagreement to

the clinical report (false positive and false negative scans). These results were compared to those obtained using the software with standard template. **Results:** 183(81%) scans were classified as type A (87 positive, 96 negative). 43(19%) scans were classified as non-type-A (23 positive, 20 negative). In BRASSv4.0 the optimum threshold for $A\beta$ -index and mean SUV_R was found to be -0.05 (AUC 0.96) and 0.74 (AUC 0.96, 94% sensitivity and 93% specificity) respectively. The left and right (i)lateral temporal cortex ($SUV_R=0.75$, AUC=0.97; $SUV_R=0.76$, AUC=0.96), (ii)Precuneus ($SUV_R=0.73$, AUC=0.95; $SUV_R=0.76$, AUC=0.95) and (iii) frontal cortex ($SUV_R=0.75$, AUC 0.95; $SUV_R=0.77$, AUC=0.95) brain regions showed best separation between positive and negative cohorts. For atypical studies an increase in specificity (79% versus 37%) with preserved sensitivity (79%) was found when comparing results from BRASSv4.0 with the previous version. A small improvement in agreement with the report was seen for typical scans (97% compared to 89% agreement previously, 99% sensitivity, 91% specificity). **Conclusion:** The updated BRASSv4.0 software utilising an adaptive template registration shows improved agreement with clinical report for 18F-Florbetapir PET/CT scans compared to a standard template registration. This study has shown very good agreement of atypical scans which are often difficult to interpret and require high degree of experience. **References:** None

EPS-142

Evaluation of myocardial perfusion images in patients with left ventricular dilatation using software program provided Artificial Neural Network (ANN)

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Aim/Introduction: Left ventricular (LV) dilatation has several causes such as ischemic heart disease (IHD) or cardiomyopathy. Patients with LV dilatation and severely impaired LV function will be under heart failure condition. Heart failure is expected poor prognosis and is the leading cause of hospital admission in over 65s. Myocardial perfusion images (MPI) analyzed by ANN provides various indices. To investigate these indices, it will be possible to define the characteristic of myocardium and to approach proper treatment. We compared these indices of patients with LV dilatation caused by IHD and non-IHD. **Materials and Methods:** Thirty patients with LV dilatation were enrolled in this study. They were divided into two groups, IHD group (group A) and non-IHD group (group B). All of them underwent MPI. In visual assessment, two expert physicians in nuclear medicine detected myocardial abnormality. Indices from MPI analyzed by ANN were compared. **Results:** The age of