DatScan SPECT Image Processing Methods for Calculation of Striatal Binding Ratio (SBR)

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Summary

DatScan SPECT imaging was acquired at PPMI imaging centers per the PPMI imaging protocol and sent to IND for processing and calculation of SBRs. All baseline SPECT scans have been analyzed utilizing the processes in the method section.

Method

SPECT raw projection data was imported to a HERMES (Hermes Medical Solutions, Skeppsbron 44, 111 30 Stockholm, Sweden) system for iterative (HOSEM) reconstruction. This was done for all imaging centers to ensure consistency of the reconstructions. Iterative reconstruction was done without any filtering applied. The HOSEM reconstructed files were then transferred to the PMOD (PMOD Technologies, Zurich, Switzerland) for subsequent processing. Attenuation correction ellipses where drawn on the images and a Chang 0 attenuation correction was applied images utilizing a site specific mu that was empirically derived from phantom data acquired during site initiation for the trial.

Once attenuation correction was completed a standard Gaussian 3D 6.0 mm filter was applied. These files were then normalized to standard Montreal Neurologic Institute (MNI)space so that all scans were in the same anatomical alignment. Next the transaxial slice with the highest striatal uptake was identified and the 8 hottest striatal slices around it were averaged in to generate a single slice image. Regions of interest (ROI) were then place on the of left and right caudate, the left and right putamen, and the occipital cortex (reference tissue). Count densities for each region were extracted and used to calculate striatal binding ratios (SBRs) for each of the 4 striatal regions. SBR is calculated as (target region/reference region)-1.

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