

Play a Part in Parkinson's Research

AV-133 PET Image Processing Methods for Calculation of Striatal Binding Ratio (SBR)

Gary Wisniewski, John Seibyl, Ken Marek, Institute for Neurodegenerative Disorders (IND)

Summary

18F-AV-133 PET images are acquired as part of an imaging substudy at several PPMI imaging centers per a specified PPMI imaging protocol. Reconstructed, attenuation, scatter and random corrected image volumes were sent to IND for processing and calculation of striatal binding ratios (SBRs). All AV-133 PET scans are analyzed according to the procedures described below.

Method

PET dynamic data are imported to a PMOD system (PMOD Technologies Ltd., Sumatrastrasse 25 CH - 8006 Zürich, Switzerland) for processing and analysis following technical and scientific QC performed at the IND core imaging lab.

Dynamic PET frames are assessed for motion and where necessary motion correction is performed. These files are then averaged (time weighted mean) to create a single PET volume. The PET volume is coregistered to the subject's MRI. The MRI is normalized to standard Montreal Neurologic Institute (MNI) space and the transformations from that normalization are applied to the coregistered PET volume so that all scans are in the same anatomical alignment. A standardized striatal template created at IND is then placed on the normalized MRI volume. VOI placement may be adjusted, especially on scans where there is atrophy or the VOI template does not exactly align. The VOI placement is saved for each subject specifically. The subject specific VOI template is then transferred to the normalized PET volume.

Quantitative measurements (count densities or average SUV per voxel) are extracted from the regions and used to calculate SBRs for all of the striatal areas (left and right caudate, ant putamen, and post putamen).

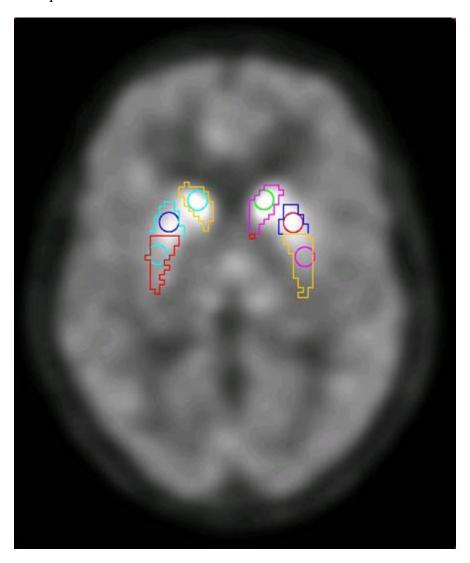
SBR is calculated as (target region/reference region)-1. The reference region is the occipital lobe..

Follow up scans are preprocessed in the same manner with motion correction and averaging. They are then coregistered to the baseline PET volume and the transformations from the baseline normalizations are applied. The VOI template is then applied but not typically adjusted on the follow up scans as the VOIs are subject specific and already properly fit on the baseline data. Quantitative measurements are extracted in the same manner as for the baseline scan.



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Example of VOI on PET scan



About the Authors

This document was prepared by Gary Wisniewski, Director of Imaging Science and John Seibyl, Executive Director and Senior Scientist, Institute for Neurodegenerative Disorders, New Haven, CT. For more information please contact Gary Wisniewski at (203) 401-4300 or by email at gwisniewski@indd.org

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