Purpose: To apply factor analysis technique to a sequence of 11C-DTBZ dynamic PET images to healthy and diseased subjects in order to extract factor curves (or time activity curves) and associated factor images and develop a metric to detect extent of Parkinson's disease.

Methods: Philips Gemini (C) PET/CT scanner (with 4mm isotropic voxels) is used to collect a dynamic dataset consisting of a time sequence of 16 frames (with unequal temporal spacing) of the brain from healthy and diseased subjects. Several image preprocessing techniques (e.g. noise reduction using singular value decomposition, voxel-averaging) are used on these dynamic datasets prior to implementing factor analysis using projected gradient method in the framework of non-negative matrix factorization to extract physiologically meaningful structures. A priori information (region-of-interest based time activity curves) is used to warm start the optimization process in order to reduce the number of possible solutions.

Results: The factor analysis technique separates each dynamic dataset into two time-dynamic factors – one factor represents the striatum (directly related to the disease) while the other factor represents the non-striatum tissues. The factor curves and images related to the former show clear difference in the tracer uptake among the healthy and diseased subjects. Our metric, which relies on such difference, indicates that the tracer uptake in striatum tissue for the healthy subject is roughly four times higher than that of the diseased subject.

Conclusions: This study suggests that the technique can decompose large dynamic datasets into parts-based images (or volumes) that represent the underlying physiological structures, and has the potential to significantly aid in the review process for evaluating dynamic datasets by clinicians. The technique is not limited to dynamic PET images and can be applied to any sequence of dynamic images.