Introduction

It has been shown that Logan analysis is more appropriate than the Gjedde-Patlak analysis for the assessment of [F-18]FDOPA PET dynamic data (Sossi et al., Kawatsu et al.). The aim of this study was to investigate the feasibility of simplified reference tissue model, solved by basis function approach (BF-SRTM), in computation of parametric maps of dopamine turnover as its inverse, effective dopamine distribution volume (EDVR).

The potential of this approach in discriminating Parkinson’s disease patients and age-matched healthy subjects is compared to the traditional analysis method, Gjedde-Patlak.

Results and discussion

BF-SRTM fits time-activity curves (TACs) reasonably well, demonstrated by the model fits to regional average TACs (fig 2).

Parametric EDVR maps computed using BF-SRTM have a visibly good quality, especially in cortical regions (fig 3).

Mean values of $K_i$ and EDVR inside caudatus, putamen, occipital cortex and frontal cortex were calculated from the parametric maps produced using the two methods, Gjedde-Patlak analysis and BF-SRTM. Both methods separate the two study populations well in striatal areas, and neither of them gives any difference in cortical areas (Table 1).

Although Gjedde-Patlak and BF-SRTM are based on opposite assumptions (irreversible uptake vs. reversible uptake) and the outcomes theoretically represent different physiological phenomena (net uptake rate vs. distribution volume), in practice the results $K_i$ and EDVR show good correlation (fig 4). Gjedde-Patlak analysis does not account for the loss of [F-18]FDOPA metabolites from the brain, and therefore the outcome $K_i$ is strongly biased. $K_i$ does not reflect “net uptake”, but instead correlates to the more relevant measure, EDVR, which can be calculated using more appropriate methods, Logan analysis or BF-SRTM.

Conclusions

BF-SRTM is useful method for producing EDVR maps from [F-18]FDOPA PET studies.

BF-SRTM separates advanced PD patients from controls at least as accurately as Gjedde-Patlak analysis.

Apparently, the $K_i$ from Gjedde-Patlak analysis with reference tissue input does not reflect net uptake rate but is correlated to EDVR.